Forensic DNA Evidence: Science and the Law § 1:1

Forensic DNA Evidence: Science and the Law | June 2024 Update
Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 1. Introduction

§ 1:1. Overview of forensic DNA

With the advent of the Human Genome Project in 1990, the rate of genetic information available for use worldwide was set to increase exponentially. A short 12 years later, scientists determined the order of the three billion chemical base pairs that make up the building blocks of human DNA (deoxyribonucleic acid).[1] Since then, our understanding of the human genome, scientific advancements in CRISPR Cas-9 genome editing, FDA approved treatments for sickle cell anemia, HIV-1, and other human maladies that affect global populations has added to our knowledge and well-being at a blazing pace. Application of this information has been creative and crosses many fields, including medicine, biotechnology, neurology, anthropology, animal husbandry, agriculture, and, of course, law.

It has been said that the 21st century will be the century of biology.[2] But the opening of this new age arguably occurred during the 20th century, in 1953, when James Watson and Francis Crick, using information Rosalind Franklin developed, first elucidated the DNA molecule's structure.[3] It took another 13 years to determine how the DNA molecule actually codes information.[4] Laboratory techniques soon followed, allowing scientists to isolate DNA from cells and to manipulate DNA fragments.[5] In 2020, two scientists, Emmanuelle Charpentier and Jennifer Doudna, received the Nobel Prize in Chemistry for their work in developing the CRISPR-Cas9 gene editing tools.[6]

In humans, about one-tenth of one percent of DNA (about three million bases) differs from person to person. In other words, the order of the bases in humans varies *on average* by one base in 1,000. As researchers began to recognize these sites of variation, others imagined using them as a type of individual identification system. In the mid-1980s, Dr. Alec Jeffreys, an English geneticist, found that certain regions of DNA contained DNA sequences that repeated over and over again next to each other. He also discovered that the number of repeated sections in a sample could differ from one person to another. He developed a method for examining variations in the lengths of these DNA repeat sequences, thus creating the ability to perform human identity tests.

Since then, forensic use of DNA as a tool of human identification has become widespread. Although initial data were somewhat crude by today's standards, DNA evidence offered courts an independent, science-based and reliable identification method. Subsequent improvements in technology have dramatically increased both the sensitivity and specificity of DNA forensics data.

Forensic use of DNA typically begins with a sample of biological material, which often is collected from a crime victim or a crime scene. Scientists identify a limited number of genetic markers in the sample by deploying small pieces of manufactured chemical sequences (primers) that seek out and bind to complementary DNA sequences of interest in the sample. A series of primers bound to a DNA sample permits amplification of the original sample to the point that the analyst can determine a DNA “profile” for the known or unidentified individual who deposited the sample.

With a DNA sample from an unknown source, the next step in the forensic identification process is comparing the sample to the known forensic DNA profile of a suspect or to the millions of DNA profiles now stored in computer databases throughout

the country. Any known profile that does not match eliminates that person as the source of DNA collected from the victim or at the crime scene.

If a match is found, however, scientists must determine its significance. Even unrelated people share, on average, two or three genetic markers, so a match is of little significance absent information about the probability that it occurred solely by chance. The smaller the probability of a random match, the greater the chance that the source of the comparison sample was also the source of the DNA found at the crime scene. To reduce the chance of a random match, 13 or more DNA regions, or loci, that vary from person to person are generally used to create the DNA profile. Given the frequency with which DNA characteristics of interest appear in populations, any given "target" forensic DNA profile is going to be exceptionally rare. To quantify this chance, forensic scientists use a statistical method called the "product rule," which involves estimating the frequency with which each genetic marker appears in the populations and multiplying the frequencies together to produce the complete profile's frequency. This result is often also expressed as the probability that the DNA of a single person selected at random from the relevant population will match the evidentiary sample.

The use of DNA identification technology has transformed the work of those in the criminal justice system. Police, prosecutors, and defense counsel rely heavily on DNA evidence to do their jobs. Throughout the country, huge DNA databases are being compiled with DNA-based identification information of convicted offenders, arrestees, suspects, victims and their family members, and even witnesses, which can later be tested against samples from crime scenes. Using these databases, law enforcement authorities have been able to make arrests in crimes that have gone unsolved for decades. "The National DNA Index (NDIS) contains over 16,532,335 offender profiles, 5,190,279 arrestee profiles and 1,282,418 forensic profiles as of August 2023. Ultimately, the success of the [Combined DNA Index System, or CODIS] program will be measured by the crimes it helps to solve. CODIS's primary metric, the 'Investigation Aided,' tracks the number of criminal investigations where CODIS has added value to the investigative process. As of August 2023, CODIS has produced over 674,405 hits assisting in more than 656,893 investigations."[7]

Of course, DNA identity evidence can aid the accused and the already-convicted as well as the accuser. As of November, 2022, there had been over 375 postconviction DNA exonerations in the U.S., including 21 people who served time on death row and 44 who pleaded guilty to crimes they did not commit.[8] The statistics show an incredible 69% of the DNA exonerations involved eyewitness misidentifications—including 34% from in-person lineups and 52% from photo arrays.[9] In 2023, the Innocence Project documented an additional nine new exonerations "from Hilo, Hawaii to Syracuse, New York. Together, the nine clients exonerated [last] year persevered through a combined time of 212 years in prison."[10]

But the impact of DNA evidence in criminal trials is not confined simply to matters of identity. As information about variation within genes has given us a clearer understanding of the genetic component of behavior, disease, and other traits,[11] criminal defendants have increasingly sought to use their own DNA to deny responsibility for and to mitigate their unlawful conduct. They hope to prove they have a genetic predisposition for violent, impulsive, or other antisocial behavior, and therefore are not culpable for their offenses.

More broadly, the impact of forensic DNA extends well beyond criminal law. For example, in personal injury cases, plaintiffs and defendants may offer genetic evidence on issues of causation and damages. In family law cases, judges may turn to genetic evidence to settle questions of paternity and to decide questions about parental rights.

In the future, advances in genetic science will inevitably raise new legal questions. As DNA testing offers us more effective disease prevention and treatment, medical professionals will have to consider new liability issues in choosing which of the hundreds of available genetic tests to give to a patient. Other legal and ethical issues are arising with breakthrough medical advances like gene therapy, gene editing, stem cell research, and reproductive technologies. Competition among labs has become fierce and is subject to ongoing patent litigation.[12] Advancements in genetics also create risks of privacy invasion, discrimination

in employment, and denial of health or life insurance. And the use of genetically modified organisms in agriculture and environmental science remains highly controversial.

Beyond genetic science, researchers are developing and refining sophisticated brain testing techniques that can shed light on both the truth of our statements and the motivations behind our actions. Researchers have already used brain imaging technology to identify simple abstract thoughts with 70% accuracy.[13] Scans have likewise already "been used to identify brain signatures of disgust, drug cravings, unconscious racism, suppressed sexual arousal, and a possible propensity in some individuals to engage in socially deviant behavior.[14,15]

As technology evolves and advances, science and law will become more deeply entwined. Technological strides have forced people to change and expand their ways of thinking about concepts such as privacy, discrimination, the food they consume, and life itself. To accommodate these changes, our legal system must be prepared.

Footnotes

1 A press conference marking completion of the Human Genome Project was held April 14, 2003, with former President William J. Clinton presiding. The sequence was published the same day. International Consortium Completes Human Genome Project, available online at www.genome.gov/11006929 (Mar. 2, 2024).

The entire issue of NATURE dated February 15, 2001, is dedicated to the publication of the sequence of the human genome and related commentary. It is available online at www.nature.com/nature/journal/v409/n6822/index.html (as of Mar. 2, 2024).

2 John Carey, We Are Now Starting the Century of Biology, BusinessWeek.com, Aug. 30, 1998, www.bloomberg.com/news/articles/1998-08-30/we-are-now-starting-the-century-of-biology (as of Mar. 2, 2024).

3 The first description of DNA's structure appeared in a paper titled "Molecular Structure of Nucleic Acids," published in NATURE, Vol. 171, p. 737, 1953. For their efforts, the paper's authors, James Watson and Francis Crick, received the Nobel Prize for Physiology or Medicine.

4 The genetic code, the mechanism by which DNA codes for proteins, was published by Holley, Khorana, and Nirenberg. For their work, they were jointly awarded the 1968 Nobel Prize in Medicine.

5 A timeline chronicling major events in this process is available online at www.dna-worldwide.com/resource/160/history-dna-timeline (as of Mar. 2, 2024).

6 Heidi Ledford & Ewen Callaway, Pioneers of revolutionary CRISPR gene editing win chemistry Nobel, Oct. 7, 2020, www.nature.com/articles/d41586-020-02765-9 (as of Mar. 2, 2024).

7 Federal Bureau of Investigation, CODIS-NDIS Statistics, https://le.fbi.gov/science-and-lab/biometrics-and-fingerprints/codis/codis-ndis-statistics (internal footnote omitted) (as of Feb. 23, 2024).

8 Innocence Project, DNA Exonerations Nationwide, www.innocenceproject.org/dna-exonerations-in-the-united-states/ (as of Feb. 23, 2024).

9 Ibid.

10 Innocence Project: *Innocence Projects' Uplifting Moments from 2023* (12/04/23) https://innocenceproject.org/innocence-projects-uplifting-moments-from-2023/ (as of Feb. 23, 2024).

11 See generally, Broeckel and Schork, Identifying genes and genetic variation underlying human diseases and complex phenotypes via recombination mapping, 554 (Pt. 1) J. Physiol. 40 (Jan. 1, 2004).

12 Jon Cohen, Science Insider, *CRISPR's Nobel Prize winners defeated in key patent claim for genome editor*) March 1, 2022, https://www.science.org/content/article/latest-round-crispr-patent-battle-has-apparent-victor-fight-continues (as of Mar. 2, 2024).

13 John Dylan-Haynes, et. al., Reading Hidden Intentions in the Human Brain (Feb. 20, 2007) 17 Current Biology 4, pages 323-328 in ScienceDirect, available online at www.sciencedirect.com/science/article/pii/S0960982206026583 (as of Mar. 2, 2024).

14 William Saletan, Full-Mental Nudity, Slate, Mar. 17, 2007, https://slate.com/technology/2007/03/the-arrival-of-mind-reading-machines.html (as of Mar. 2, 2024).

15 Jiang W, Zhang H, Zeng L, Shen H, Qin J, Thung K, Yap P, Liu H, Hu D, Wang W, Shen D. Human Brain Mapping. 2020 Oct 16; 42(2): 329-344, www.ncbi.nlm.nih.gov/pmc/articles/PMC7776000. (as of Mar. 2, 2024).

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Chapter 1. Introduction

§ 1:2. Matters covered

Chapter Two provides an overview of the DNA profile and explains how DNA testing technology identifies the individual. It begins with a history of forensic DNA testing. It summarizes DNA biology and the PCR-STR (polymerase chain reaction and short tandem repeat) testing process.

The portions of the DNA molecule used for forensic identification purposes, when considered collectively in the form of a profile, are particularly useful as an identifier because of the high degree of variability among individuals. This chapter explains how DNA's structure, its cellular organization, and its function (replication and cell division, transcription, and translation) serve the process of DNA testing for forensic DNA identification. This chapter likewise explains the analysis of short tandem repeats as the most widely used form of forensic DNA testing and details the advantages of this form of testing.

Chapter Three addresses the tasks and procedures involved in developing a DNA profile from crime scene to laboratory. It begins by discussing evidence collection. Any time evidence from a crime scene or physical examination is collected for DNA testing, it is intended to represent the biological material present at the time of a crime or assault. However, it ultimately is a representation of the biological material present at the time of collection. For this reason, careful sample collection, handling, packaging, and record keeping are essential to any crime scene investigation or examination.

The chapter explains the importance of reference samples. Reference samples are known samples taken from an individual to be used for comparison with profiles from evidence items. Reference samples may be saliva, blood, hair, or other bodily fluids or tissue. When evidence of a crime includes a perpetrator's DNA profile, a primary objective of investigators is to obtain a reference sample or samples from the suspect or other known persons for comparison purposes. DNA database programs represent automated means of accomplishing this, but more traditional methods can also be employed, such as: applying for a search warrant, collecting an “abandoned” DNA sample, obtaining valid consent from the person of interest, or using trickery and ruse (so long as the tactics comply with constitutional protections for individual rights).

Sampling crime scene evidence is the first step in the process of developing a DNA profile that takes place in the laboratory. The chapter traces when evidence is received, and what investigators do with it. Evidence can come into a laboratory in many forms, ranging from swabs in a sexual assault kit to an entire automobile. Several tests exist to test for blood, semen, saliva, and fecal matter, and to determine whether certain biological fluids are of human origin. The chapter examines presumptive tests, sampling techniques, and evidence handling.

Before a DNA profile can be developed, DNA must be extracted from the nucleus of the cell and separated from all other cellular material the sample contains. To do this, the membranes of DNA-containing cells must be disrupted, and the DNA must be separated from the cellular components. Several methods exist, and the chapter discusses them in turn: organic extraction, differential extraction, resin and magnetic bead extraction, and purification of DNA extract.

After DNA is extracted from a sample, it is usually preferable to determine how much DNA is present. Currently, the most widely used method for DNA quantitation is quantitative real-time polymerase chain reaction (qPCR). Polymerase chain reaction

(PCR) is the process of amplifying specific regions of the DNA molecule. qPCR takes advantage of this process by targeting human-specific regions of the DNA molecule. The chapter discusses this process in depth. It also discusses two methods of electrophoresis, including gel and capillary. Electrophoresis is done at the end of the PCR amplification process. After a genetic analyzer run is complete, the next step in the process is to size each peak detected and assign allele designations. This can be done manually by an analyst but is almost exclusively accomplished by software programs. The chapter surveys such data analysis and interpretation processes.

During the evidence evaluation and sampling process, every effort is made to conserve an adequate amount of sample for subsequent testing. The chapter briefly discusses consuming a sample in the event this does not occur.

Chapter Four addresses quality assurance standards, mechanisms, and procedures that govern forensic DNA laboratories. The chapter charts forensic DNA technology's rapid emergence and growth without uniform testing techniques, quality control measures, or requirements of professional education and experience for the scientists performing the DNA analyses. It traces how the forensic science community developed quality assurance standards, monitoring bodies, conformance procedures, and certification of personnel to address judicial concerns with the validity of the results presented.

The chapter begins by defining quality assurance and the standards first developed by the DNA Advisory Board (DAB), appointed by the Director of the Federal Bureau of Investigation (FBI). It highlights current standards for forensic DNA testing laboratories and DNA databasing laboratories ("Quality Assurance Standards for DNA Testing Laboratories" and "Quality Assurance Standards for Databasing Laboratories," respectively). It discusses national accreditation for both testing and databasing labs (American Society of Crime Laboratory Directors/Laboratory Accreditation Board—ASCLD/LAB), in addition to international standards and accreditation (International Organization for Standardization—ISO standards and International Laboratory Accreditation Cooperation/InterAmerican Accreditation Cooperation—ILAC/IAAC accreditation), and the cooperation between the bodies that address conformity assessment infrastructure in the Americas (ASCLD/LAB-International).

The chapter focuses on the accreditation process and procedures. Upon accreditation, the laboratory must conform with reporting and monitoring requirements. These requirements include self-reporting, surveillance visits, and external testing. If the accredited laboratories and their employees fail to conform to ASCLD/LAB standards, a review procedure commences, which may result in sanctions.

In addition to ASCLD/LAB accreditation in the United States, the Forensic Quality Service (FQS) accredits forensic science laboratories. FQS is a full signatory member of the ILAC/IAAC bodies and conforms with their accreditation standards and procedures. FQS is recognized by the FBI to perform Quality Assurance Standards DNA assessments and the National Institute of Justice as a provider of accreditation to forensic science laboratories.

The chapter describes how forensic DNA examiners, analysts, and criminalists complete training and certification. It notes the DNA Identification Act (42 U.S.C.A. § 14132(b)), which specifies the requirements for participating in the National DNA Index System or NDIS. A complement to federal law, California Penal Code § 295 (the DNA Forensic Identification Database and Data Bank Act of 1998), also spells out the state Department of Justice DNA Laboratory's accreditation reporting requirements.

The chapter concludes with a discussion of state and federal efforts to review and improve forensic science in the United States. It details the work and recommendations of the National Academy of Sciences, which was commissioned to study forensic science in the United States by a U.S. Congress that was concerned about highly publicized crime laboratory errors. It also discusses the work and recommendations of the California Crime Laboratory Review Task Force, which was established to study the issue by a California Legislature that was likewise concerned about forensic science in the United States.

Chapter Five covers statistical considerations associated with forensic DNA evidence. Statistics give meaning to a DNA match by providing information about the likelihood the match occurred solely by chance. The chapter begins by explaining the random

match probability statistic, which expresses the probability that a person randomly selected from a population of unrelated people will have a DNA profile that matches the DNA profile of a sample collected at the scene of a crime or from a crime victim. This statistic is calculated using the product rule, which involves estimating the frequency with which each genetic marker (allele) appears in the relevant population and multiplying the frequencies together to produce the complete profile's frequency in the population.

A premise of the product rule is that the alleles at any one locus are inherited independently of the alleles at any other given locus. The chapter discusses other statistical considerations, including: (1) Hardy-Weinberg Equilibrium, which is a measure of the independent inheritance of alleles within a single locus; (2) population substructuring, which factors into statistical calculations the circumstance that humans do not mate randomly; and (3) kinship considerations, which estimate the probability that one or more of a defendant's siblings shares the defendant's DNA profile.

The chapter then discusses the prosecution and the defense “fallacies,” which are ways in which the parties to a criminal case may incorrectly describe to the fact finder the significance of a random match probability statistic. It then discusses the process of determining allele frequencies for forensic testing loci. The chapter ends by discussing statistical measures that may be used in database search cases as alternatives to the product rule, including: (1) the database probability statistic, which estimates the chance of a random match in “cold hit” cases, where investigators compare the DNA profile of a sample found at a crime scene with DNA profiles in a database; (2) the National Research Council's suggested approach, which involves using one set of loci to establish a match and then calculating a frequency estimate for separate set of loci; and (3) the likelihood ratio, which compares the probability of a match occurring from the database search if the suspect is the source of the sample to the probability of a match occurring from a database search if the suspect is not the source of the sample.

Chapter Six covers DNA mixtures, i.e., when biological evidence samples contain DNA from more than one source. The chapter discusses how to identify and evaluate such mixtures using single source short tandem repeat (STR) profile characteristics. Depending on the quality of the mixture data, it may be possible to determine to a high degree of certainty the absolute number of contributors to a mixture.

After a mixture is identified and the number of potential contributors determined, the next step is evaluating the sample for possible genotypes. This process is referred to as deconvolution, or mixture interpretation. The process of deconvolution takes into consideration the properties of a single-source profile and applies them as a logical tool to determine mathematically genotypes for possible contributors. To determine the possible genotypes for a locus, an analyst first considers how many alleles are present (four-, three-, two-, or one-allele loci), and then how many contributors are assumed to be in the mixture.

After all possible genotypes have been determined, the list of genotypes may be narrowed further by considering pairings with respect to peak height ratios (PHR). The PHR for any two alleles is the ratio of the smaller allele to the taller allele, expressed as a percentage. The chapter provides examples of this concept.

In addition to peak height ratios, the amount of DNA each contributor donates to a mixture relative to the other contributors can be determined and used to assist in deconvolution. A donor ratio is calculated by dividing the sum (Sigma) of the peak heights from one contributor (C1) by the sum of the peak heights from a second contributor (C2). A mixture proportion is calculated by dividing the sum of either the peak height or peak area of the minor (smaller) alleles by the sum of all alleles in the locus.

When performing mixture interpretation calculations, an analyst must be conscious of peaks in stutter positions. Stutter peaks are DNA peaks that occur four bases in size away from an allelic peak. Stutter is a result of dynamic effects of the polymerase chain reaction and is a well-documented phenomenon. A more detailed discussion on stutter can be found in § 6:2.

The chapter also considers assumed donors—where forensic DNA samples are analyzed under the assumption that a particular donor is present. An assumed donor's profile can be an extremely useful tool for mixture deconvolution. With the ability to attribute a genotype to one contributor, the amount of possible foreign contributor genotypes may be greatly decreased.

Just as with single-source DNA profiles, mixtures are susceptible to effects from environmental factors. However, these effects can be either amplified or masked in mixture samples. Patterns specific to inhibition (interference with amplification) and degradation (deterioration of DNA in a sample) seen in single-source samples can act as a guide to recognizing and interpreting these effects in mixtures. The effects should be treated with even more caution in mixed samples. If a mixture has been evaluated as suitable for comparison, and once all possible genotypes have been determined, it is appropriate to compare reference samples for inclusion or exclusion as possible contributors to the mixture.

The chapter next discusses mixture statistics. Any inclusion of a reference profile as a potential contributor to a mixture must be qualified by a statement of the significance of the inclusion. If a single-source profile is determined from a mixture, the random match probability (RMP) can be applied just as with nonmixed samples. When a mixture interpretation includes more than a single profile as a potential contributor, a different calculation is appropriate. This may be a modified version of the RMP, the likelihood ratio (LR), or the combined probability of exclusion/inclusion (CPE/CPI). The appropriate calculation can be selected based on the stated assumptions used for interpretation.

The chapter closes with a discussion of software tools that are available to perform the calculations necessary for mixture deconvolution. These programs are structured to use analyst and laboratory established parameters and assumptions to evaluate, interpret, and determine possible contributor profiles from DNA mixture data.

Chapter Seven covers DNA testing methods that are alternatives to PCR-STR testing. It begins with Y chromosome STR testing (Y-STR testing), which involves sequencing of the Y chromosome. The Y chromosome is one of the sex chromosomes and, barring anomalies, is passed only from father to son. Because each male has only one Y chromosome, a Y-STR profile will have only one allele present at each locus and is referred to as a haplotype. For this reason, Y-STR testing can, at best, match a questioned haplotype to that of a male lineage, rather than to a particular individual. In other words, a Y-STR match means that neither the suspect who supplied the tested sample nor any of his paternally related male relatives may be excluded as the potential source of the male DNA collected from the victim or at the crime scene. Y-STR testing may be useful in cases where collected DNA evidence consists of a large quantity of female DNA mixed with a low quantity of male DNA. By amplifying only Y-STRs, the female DNA in the sample is undetected, thereby allowing analysis of the sample's male DNA. Efforts are underway to create a large, centralized Y-STR database, with the ability to calculate frequencies for haplotypes at 49 loci and within specific racial groups.

The chapter next discusses testing of mitochondrial DNA (mtDNA), which is found outside of the cell's nucleus. Because a sperm cell's mtDNA is inactivated when the sperm enters an egg, only females transmit their mtDNA to the next generation. Thus, all maternally related relatives in a lineage will share mtDNA. Like Y-STR testing, mtDNA statistics are based on haplotypes, rather than allele frequencies. mtDNA testing is routinely used in missing persons DNA programs. It is especially useful when dealing with severely compromised samples, where nuclear DNA testing has failed.

The chapter next discusses single nucleotide polymorphisms, which involve differences of one base pair at a particular location between two DNA sequences, and low copy number analysis, which involves STR testing of samples that contain low amounts of DNA.

The chapter concludes by discussing “low copy number” testing (LCN testing), which involves adding a low amount of DNA to a polymerase chain reaction. The STR data that result from such testing may exhibit characteristics not commonly seen in amplified samples with higher template input amounts.

Chapter Eight begins by describing features of DNA database programs in general, but specifically addresses California's program, as well as corresponding law and practices that have developed.

The chapter introduces the input process of DNA evidence from a crime scene into respective DNA database programs. This section begins by explaining how local public laboratories (Local DNA Index Systems or LDIS) develop DNA profiles from crime scene evidence and upload them into a state DNA database. The state-level DNA databases that receive the crime scene profiles of unknown origin from LDIS labs are known as SDIS (State DNA Index System) programs. All 50 states have an SDIS governed by each state's individual laws. SDIS programs upload the majority of their content into the NDIS (National DNA Index System), which the FBI administers. Professionals in the field refer to the acronym CODIS (Combined DNA Index System) as an umbrella label for DNA database programs in general, but the acronym specifically refers to the DNA database software developed by the FBI and licensed to state (SDIS) and local (LDIS) laboratories, thus forming a national network.

The CODIS national network forms a three-tiered network of information sharing; the NDIS constitutes the highest level in the CODIS hierarchy, but all participating laboratories at the local and state level have access to the NDIS database. All DNA profiles in the CODIS system get collected at the local level (LDIS) before flowing to operative state databases (SDIS). SDIS allows labs within states to exchange DNA profiles. California state law does not prohibit county and municipal law enforcement agencies from developing and maintaining DNA databases unaffiliated with CODIS. To maintain such independence, however, a local laboratory may not receive biological samples from the State DNA Database Program, or the direct transfer of any NDIS records.

The chapter discusses the history, purpose, funding, and management of California's program. It addresses such issues as retroactivity, suspect samples, plea bargain samples, forcible collection, and crimes related to DNA sample collection. It also covers expungement and retention of offender DNA profiles.

Municipal, county, and state law enforcement crime laboratories in California that meet accreditation requirements under Penal Code Section 297 may upload DNA profiles into the state's DNA Database. The chapter focuses on the collection and processing of crime scene samples, as well as use restrictions on data bank samples and profiles (including disclosure restrictions and penalties for violating such restrictions).

The chapter surveys case law concerning the constitutionality under the Fourth Amendment of DNA database collections and searches. This survey includes a discussion of sample collection from offenders and arrestees, as well as pending state and federal litigation on the issue. Other constitutional concerns addressed include: equal protection, due process, ex post facto considerations, the Fifth Amendment right against self-incrimination, and the free exercise of religion.

Briefly, the chapter surveys the California Department of Justice's adopted protocol for conducting “familial searching” using its DNA database, as well as the operation of the missing persons DNA database program in California.

Chapter Nine explains the operation of statutes of limitation and how DNA evidence may toll a felony offense statute. It discusses felony sex offenses in California where DNA evidence of the perpetrator's identity has been developed, or where there is no evidence available. It surveys federal law governing how DNA affects applicable statute of limitations periods. In circumstances where extended statutes of limitations are not available, but where DNA evidence exists, issuance of a “Doe” complaint, based on the perpetrator's DNA profile, may operate to commence the prosecution.

Specifically on issuance of “Doe” warrants, this chapter gives an overview of California and other states' case law on DNA-based Doe warrants and provides the elements of such warrants. It discusses the governing California case on preaccusation delay, People v. Nelson, 43 Cal. 4th 1242, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008), which held that prejudice to a defendant will never be presumed, at least in a murder case, regardless of how much time has elapsed between the crime and the arrest/filing of charges. Federal constitutional due process violations based on preaccusation delay require a finding of deliberate delay by the government in order to gain a tactical advantage over the defendant.

Chapter Ten provides a summary of California's criminal discovery law and describes items commonly provided by the prosecution related to DNA testing. It also discusses more unusual discovery-related circumstances that may arise. Of course,

the scope of appropriate discovery in any case hinges on the facts of that particular case. Thus, the chapter's discussion is a comprehensive but not all-encompassing survey of DNA discovery issues. A defendant's own retained or appointed expert, for example, may identify additional items of interest to seek as discovery from the prosecution.

In addition, the chapter addresses how the prospects of consuming a crime scene DNA sample through testing and retesting raises legal issues regarding disclosure of results.

The chapter begins by discussing discovery in California criminal cases, where both state statutory authority and federal constitutional mandates govern pretrial exchange of information between parties. California's discovery statutes provide the exclusive source of procedural and substantive authority for the reciprocal exchange of pretrial information, as informed by overlapping constitutional mandates. The chapter explains the role and function of informal discovery, motions to compel, subpoena duces tecum, as well as routing disclosures, including: laboratory reports, chain of custody information, documentation of the technical and administrative review processes, "bench notes," and electropherograms for all samples and controls.

In addition to the standard discovery materials relating to DNA casework, defense counsel may request additional information from prosecution testing laboratories if relevant to case facts and strategies. The following materials, which the chapter discusses in depth, are often among the additional items requested: electronic STR typing data, laboratory technical procedures, operations and/or policy manuals, allele frequency data tables, unintended transfer/contamination records, corrective action records, internal validation studies for particular techniques and instruments, proficiency test results, and evidence of the laboratory's accreditation status.

Requests for defense DNA testing or retesting of crime scene evidence may or may not be granted by the trial court, depending on the amount of evidence available. The chapter discusses several cases that illustrate the range of possible outcomes.

The chapter discusses discovery issues around the DNA Data Bank Program. Given the high volume of "cold hits" reported by the Department of Justice's DNA Data Bank Program, the chapter describes additional documentation generated by that program that may be available as discovery in resulting criminal prosecutions. These include: the hit notification letter, the specimen match detail report, a photocopy of the offender's sample submission card, chain of custody information including the chronology of the testing process, electropherograms for both the original analysis and the confirmation analysis, procedural check sheets, and documentation of the technical and administrative review process.

Other than the information described above pertaining to a criminal defendant's own DNA profile and related information, California law limits disclosure of other forensic identification information and other DNA profiles maintained by the DNA Data Bank Program. Specifically, no DNA profile, and no data bank or database information, is available to a criminal defendant by way of subpoena or other discovery mechanism. The chapter discusses this disclosure limitation in depth. Because California uploads the contents of its offender DNA database into the National DNA Index System (NDIS), the state is subject to federal disclosure restrictions as well.

Although a comprehensive collection of all laboratory operational and background materials would be outside the scope of practical or permissible discovery in any given case, case facts may dictate that particular attention be focused on certain aspects of those operations. Accordingly, the chapter examines several potential sources of additional discovery, including: quality control data, instrument repair and calibration records, and validation studies.

The chapter provides an in-depth discussion of the landmark United States Supreme Court case Brady v. Maryland, 373 U.S. 83, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963), including the "*Brady* obligation," case law examples involving forensic science, and examples of potential *Brady* evidence. The chapter also briefly addresses what occurs when the defense in a criminal case seeks access to the government crime laboratory so its DNA expert can observe the prosecution's DNA testing.

The chapter concludes with a discussion about the preservation of biological evidence. It reviews major state and federal case law on the issue within the context of the due process clause of the Fourteenth Amendment. The chapter also outlines the state statutory mandate to preserve biological evidence in felony cases for incarcerated offenders.

Chapter Eleven surveys California case law that has developed around application of the *Kelly* test (People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976)), as well as other key considerations and legal authorities bearing on the admissibility of scientific evidence including the California Supreme Court's decision in Sargon Enterprises, Inc. v. University of Southern Cal., 55 Cal. 4th 747, 149 Cal. Rptr. 3d 614, 288 P.3d 1237, 286 Ed. Law Rep. 1191 (2012). The chapter likewise addresses Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469, 27 U.S.P.Q.2d 1200, Prod. Liab. Rep. (CCH) P 13494, 37 Fed. R. Evid. Serv. 1, 23 Envtl. L. Rep. 20979 (1993) (*Daubert*), and its progeny, the application of these admissibility principles to DNA evidence in California courts, and the still-evolving case law concerning a defendant's Sixth Amendment Confrontation Clause right to challenge forensic scientific evidence.

The chapter initially articulates *Kelly*'s three-prong test and summarizes the principles related to the admissibility of scientific evidence as well as expert witness testimony as clarified in *Sargon Enterprises*. It then discusses how trial courts apply *Kelly*, both procedurally and as a matter of law. Finally, it covers appellate review of a trial court's *Kelly* ruling.

The chapter advises that trial courts must assess whether a disputed technique or method is actually scientific in nature, thus bringing it under the auspices of a *Kelly* evaluation. Once a court finds current DNA testing to be generally accepted, new or varied applications of that fundamentally unchanged technology do not raise a *Kelly* issue.

The chapter then proceeds to address different kinds of DNA typing technology. It notes that appellate decisions in California, as well as state and federal courts nationwide, have recognized the fundamental validity of PCR and STR analysis applications. A number of courts have deemed STR analysis of mixed DNA samples to be generally accepted in the field of forensic analysis. The same is true of capillary electrophoresis instrumentation in conjunction with PCR/STR testing.

Calculating the statistical significance of a DNA profile match has been the subject of *Kelly* scrutiny in California courts for more than 20 years. The chapter summarizes the law in this area. It moves on to address the admissibility of "source attribution" statements or DNA test results in the absence of statistics.

The courts' acceptance of DNA typing technology also includes Y-STR analysis. Y-STR analysis ordinarily occurs when there are insufficient volume or quality samples using standard 13- or 15-loci STR testing kits. The Y-STR DNA testing kit thus processes identification markers located on the Y-chromosomes. Because Y-STR analysis generally employs the same testing methods and analytical processes applicable to PCR/STR typing kits, courts considering the validity of Y-STR testing kits have generally favored admissibility. Courts have also permitted admission of mitochondrial DNA testing.

The chapter next discusses chain of custody and Confrontation Clause issues. Chain of custody considerations apply to biological evidence. The chapter highlights the unresolved question of whether a defendant has a Sixth Amendment Confrontation Clause right to cross-examine the DNA laboratory testing analyst in his or her case, and if so, under what circumstances. Cases currently pending in the California and United States Supreme Court present this question. The chapter provides a helpful tracing of United States Supreme Court case law on the issue from Crawford v. Washington, 541 U.S. 36, 124 S. Ct. 1354, 158 L. Ed. 2d 177, 63 Fed. R. Evid. Serv. 1077 (2004), to Melendez-Diaz v. Massachusetts, 557 U.S. 305, 129 S. Ct. 2527, 174 L. Ed. 2d 314 (2009), Bullcoming v. New Mexico, 564 U.S. 647, 131 S. Ct. 2705, 180 L. Ed. 2d 610 (2011), and Williams v. Illinois, 567 U.S.50, 132 S. Ct. 2221, 183 L. Ed. 2d 89 (2012).

The chapter highlights the California Supreme Court's holding in People v. Geier, 41 Cal. 4th 555, 61 Cal. Rptr. 3d 580, 161 P.3d 104 (2007), that a DNA analysis report generated in response to law enforcement requests and for possible use at criminal trial is distinguishable from testimonial witness statements that recount past events related to criminal activity. Thus, the witness in *Geier* was providing evidence of the DNA test results as an independent expert, and not as a mere conduit for another person's

scientific conclusions. It also discusses a number of other California appellate decisions that consider Confrontation Clause protections as they relate to forensic science test results and observations.

The chapter concludes with a discussion of forensic science expert witness testimony in light of the California Supreme Court's 2016 decision in People v. Sanchez, 63 Cal. 4th 665, 679, 204 Cal. Rptr. 3d 102, 374 P.3d 320 (2016), which clarified (1) the degree to which the rule of Crawford v. Washington, 541 U.S. 36, 124 S. Ct. 1354, 158 L. Ed. 2d 177, 63 Fed. R. Evid. Serv. 1077 (2004) limits expert witnesses from relating case-specific hearsay in explaining the basis for their opinions, and (2) the application of Evidence Code sections 801 and 802, relating to the scope of expert testimony.

Chapter Twelve discusses California's postconviction DNA testing law, Penal Code Section 1405. The section, enacted in 2001, allows only defendants convicted of a felony offense and currently serving a term of imprisonment to bring a motion. The section provides for appointment of counsel to assist indigent inmates before filing the actual testing motion. The motion must be filed in the trial court that entered judgment in the case, and notice must be served on the prosecuting district attorney, the Attorney General, and the court, crime laboratory, or police agency in possession of the biological evidence. The section does not specify or address potential remedies for the convicted person should test results provide exculpatory evidence.

The chapter lists the eight factually based criteria required under section 1405. After the parties stipulate to postconviction DNA testing under section 1405, or after the court grants the testing motion over opposition, the court will issue an order setting forth the parameters of the testing to be performed. The chapter describes what an appropriate court order should include and includes an in-depth discussion about section 1405's applicability to prior convictions. An order granting or denying a postconviction DNA testing request is not appealable.

The chapter reviews case law involving postconviction DNA testing starting with the seminal California case Richardson v. Superior Court, 43 Cal. 4th 1040, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008). The chapter then discusses Jointer v. Superior Court, 217 Cal. App. 4th 759, 158 Cal. Rptr. 3d 778 (4th Dist. 2013) and shifts to cases in other states in which courts have considered requests for postconviction DNA testing.

The chapter considers the constitutional implications of postconviction DNA testing. It undertakes more in-depth analysis of the United States Supreme Court decisions in District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 174 L. Ed. 2d 38 (2009), and Skinner v. Switzer, 562 U.S. 521, 131 S. Ct. 1289, 179 L. Ed. 2d 233 (2011).

The chapter next discusses California statutes that address the retention and preservation of biological evidence, including Penal Code Section 1417.9, which mandates retention of "all biological material" in felony cases, as long as the convicted person remains incarcerated in connection with the case, in order to preserve the possibility of a motion for DNA testing under § 1405. Biological evidence may be disposed of when all defendants incarcerated in connection with the case are released from incarceration. The investigating agency, crime laboratory, or other governmental entity that possesses biological evidence may destroy the evidence before that time, however, under conditions mentioned in the chapter. Other statutes include Penal Code section 680, which is the Sexual Assault Victims' DNA Bill of Rights, and Penal Code section 680.3, which creates the "SAFE-T" database and requires its updating by investigating agencies and laboratories to reflect the collection and analysis status of rape kit evidence.

The chapter next discusses a 2015 California law (Penal Code section 1405.1) that permits the court that heard a postconviction testing motion to decide, after a hearing, whether to order a resulting DNA profile uploaded into state and national DNA databases. The court "may" order uploading only if the requesting party shows that the profile is "attributable to the putative perpetrator of the crime" and meets all federal and state technical uploading requirements.

The chapter concludes with a discussion of postconviction challenges to scientific evidence received at trial. This subject has been addressed by both the California Legislature—through amendments to Penal Code section 1473 relating to postconviction

changes to expert opinion—and the California Supreme Court (In re Richards, 63 Cal. 4th 291, 202 Cal. Rptr. 3d 678, 371 P.3d 195 (2016); In re Richards, 55 Cal. 4th 948, 150 Cal. Rptr. 3d 84, 289 P.3d 860 (2012).)

Chapter Thirteen covers current issues that have arisen at the intersection of law and science, including forensic DNA evidence and genetic editing technology. The chapter explores issues that may arise in the future as technology evolves and advances. It begins by discussing the ways DNA evidence has been used as evidence of identity in courtrooms, the legal issues associated with this forensic use of DNA, and emerging techniques and issues associated with using DNA as evidence of identity. It briefly discusses People v. Turner, 5 Cal.5th 786, 272 Cal.Rptr.3d 50, 476 P.3d 676 (2020), the most recent case from the California Supreme Court on the product rule's use in a cold hit case. It then discusses ways in which DNA evidence may be used to explain, excuse, possibly predict a person's behavior, or as evidence in civil cases.

The chapter continues with a discussion of brain evidence in court. It describes techniques for measuring brain function and discusses potential use of brain testing to determine whether someone is lying, or has stored memories of certain events, or is experiencing pain. It also considers legal issues associated with forensic use of brain evidence, including questions of admissibility and potential constitutional limitations on use of this technology.

The chapter next explains advancements in the use of CRISPR Cas9 and its newly engineered variants labeled SpG and SpRY that are capable of higher genome editing efficiency for potential mutation. The legal and ethical implications of using the technology is a prominent concern. The chapter includes a discussion of genetic privacy and issues that arose from the Covid-19 pandemic, including whether requiring employees to be vaccinated before returning to work implicated California's privacy protections under the Genetic Information Nondiscrimination Act of 2008 (GINA).

The chapter also discusses the legal issues associated with advancements in DNA technology, including genetic privacy and patent issues that arose from the development of CRISPR Cas9, the revolutionary genome editing technology that has enabled scientists to modify our DNA. It notes the recent FDA approvals of gene therapies to treat such devastating illness as sickle cell anemia and HIV-1, as well as many emerging treatments for numerous genetically based issues. The chapter concludes by examining the global impact of genetic science, genome editing, and biopharma interventions on agriculture and the environment while exploring the complex international issues associated with these scientific developments.

Forensic DNA Evidence: Science and the Law Ch. 2 Introduction

Forensic DNA Evidence: Science and the Law | June 2024 Update
Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 2. What is a DNA Profile?

Introduction

"DNA testing has an unparalleled ability both to exonerate the wrongly convicted and to identify the guilty." (District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 174 L. Ed. 2d 38 (2009).)

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§ 2:1. History of forensic DNA testing

DNA testing technology has undergone rapid evolution since the mid-1980s. The first use of nuclear DNA evidence (i.e., analysis of DNA patterns in the nuclei of cells) for forensic identification purposes took place in a 1988 Florida case. (Andrews v. State, 533 So. 2d 841 (Fla. Dist. Ct. App. 5th Dist. 1988).) At the time, DNA sequencing and comparison had been in development and use for about ten years, but its application had been largely limited to the "diagnosis, treatment and study of genetically inherited diseases." (*Andrews v. State*, 533 So. 2d at 848.) The first California appellate opinion on the admissibility of forensic DNA evidence was issued in 1991. (People v. Axell, 235 Cal. App. 3d 836, 1 Cal. Rptr. 2d 411 (2d Dist. 1991) [DNA testing technology is fundamentally valid and admissible].) Early cases involved a DNA typing process known as RFLP, or Restriction Fragment-Length Polymorphism. (*People v. Axell,* 235 Cal. App. 3d at 846–848.) While highly discriminating as an identifier, RFLP testing required a sample size much larger than what is now suitable for STR (Short Tandem Repeat) test results, and was fairly time-consuming.

STR testing is the current standard in the field. (See, e.g., District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 2315, 174 L. Ed. 2d 38 (2009); People v. Johnson, 139 Cal. App. 4th 1135, 1149, 43 Cal. Rptr. 3d 587 (5th Dist. 2006).) Accurate STR test results can be achieved with less than 500 picograms of sample (or half a nanogram, with a nanogram being one billionth of a gram), representing fewer than one hundred cells. By contrast, RFLP testing required a minimum of around 50 to 100 nanograms of cellular material for analysis. Moreover, unlike RFLP analysis, STR testing methods utilize a process known as PCR (Polymerase Chain Reaction) to amplify genetic regions of interest to determine identification characteristics. (*Ibid*.)

Discussion of the following information about DNA biology and testing technology can be found in many published cases, including People v. Jackson, 163 Cal. App. 4th 313, 321–323, 77 Cal. Rptr. 3d 474 (3d Dist. 2008), as modified, (June 5, 2008); People v. Smith, 107 Cal. App. 4th 646, 654-657, 132 Cal. Rptr. 2d 230 (2d Dist. 2003); U.S. v. Trala, 162 F. Supp. 2d 336, 341–343, 57 Fed. R. Evid. Serv. 1266 (D. Del. 2001); and U.S. v. Shea, 957 F. Supp. 331, 333–336, 46 Fed. R. Evid. Serv. 1375 (D.N.H. 1997), aff'd, 159 F.3d 37, 50 Fed. R. Evid. Serv. 516 (1st Cir. 1998), as well as on-line through, for example, the United States DNA Initiative: http://www.dna.gov/.

What follows is a summary of DNA biology and the PCR-STR testing process.

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Chapter 2. What is a DNA Profile?

§ 2:2. DNA biology

Deoxyribonucleic acid (DNA) is a large molecule coiled up tightly inside the nucleus of most cells in the human body. Some cells, such as red blood cells, lack a nucleus and, consequently, nuclear DNA. The nuclear DNA molecule contains all of the information necessary for the development and growth of an individual. The portions of the DNA molecule used for forensic identification purposes, when considered collectively in the form of a profile, are particularly useful as an identifier because of the high degree of variability between individuals.

1) DNA Structure

The molecular structure of DNA is that of a twisted ladder called a double helix. The sides of the ladder are comprised of alternating sugar and phosphate molecules. Pairs of molecules called bases make up the rungs of the ladder. A nucleotide is formed by the combination of 1) a phosphate group, 2) the sugar molecule deoxyribose, and 3) a base. This is the basic building block of the DNA molecule. Nucleotides join together by linking their phosphate group to the sugar molecule of another nucleotide. This creates a single strand of DNA with a sugar phosphate backbone on one side and a sequence of exposed bases on the other. The ladder is completed by the bonding of another single strand of DNA to the exposed bases of the first strand. The completed molecule then twists to form a spiral. (See, e.g., People v. Smith, 107 Cal. App. 4th 646, 653–654, 132 Cal. Rptr. 2d 230 (2d Dist. 2003); U.S. v. Davis, 602 F. Supp. 2d 658, 663–664 (D. Md. 2009).)

All information within a DNA molecule is contained in the sequence of its approximately three billion base pairs. The DNA base alphabet is made up of only four characters. They are adenine (A), cytosine (C), guanine (G), and thymine (T). These bases are divided into two types; the purines, adenine and guanine, and the pyrimidines, cytosine and thymine. Each base has only one other with which it will pair; A pairs with T and C pairs with G.

2) Cellular Organization

Inside a cell, DNA is housed in a central core called the nucleus. The nucleus of a cell is analogous to the yolk of an egg. In order for the large DNA molecule to fit inside the nucleus of the cell, it is packaged into tightly coiled bundles called chromosomes. Humans have 23 pairs of chromosomes. Twenty-two of these, called autosomes, are pairs of different versions of the same chromosome, one inherited from each parent. The twenty-third pair is the sex chromosomes, X and Y. If a person has two X chromosomes, she is a female. An X and Y chromosome pairing results in a male individual. In the human body, each cell that contains DNA, with the exception of sex cells, has two copies of each autosome and two sex chromosomes. These cells are diploid cells, each containing 46 chromosomes. Sex cells (eggs and sperm) are haploid, containing 23 chromosomes. They contain only one copy of each autosome and one of the sex chromosomes. (See, e.g., People v. Wesley, 83 N.Y.2d 417, 611 N.Y.S.2d 97, 633 N.E.2d 451, 459 (1994).)

Each human chromosome contains coding and non-coding regions. This means that some areas of the chromosome contain DNA that, when translated, provides instructions for the synthesis of specific proteins that contribute to the biological appearance and function of the person. These coding regions are called genes. (See, e.g., People v. Soto, 21 Cal. 4th 512, 520, 88 Cal. Rptr.

2d 34, 981 P.2d 958 (1999).) Genes are the functional units of the DNA molecule. They are the method of transmitting genetic information from one generation to the next. In diploid cells, one copy of each chromosome has been inherited from a person's mother, and the other from his or her father. The way that each pair of genes interacts and is expressed determines the specific traits of an individual. Each sex cell contains only one copy of each chromosome. The 23 chromosomes contained in each sex cell can be a combination of chromosomes from the mother and the father. This is one method for ensuring continued genetic variation through successive generations of a species.

Non-coding regions of DNA, on the other hand, are sequences of bases that do not translate into information for protein synthesis. A number of these non-coding regions are of specific interest in forensic DNA typing, and have been chosen as the standardized markers used for identification purposes. (See, e.g., In re Jessica M., 399 Ill. App. 3d 730, 340 Ill. Dec. 512, 928 N.E.2d 511, 524 (1st Dist. 2010) [the standard set of DNA markers used for forensic purposes "'are in the non-coding regions of the DNA and are not known to have any association with a genetic disease or any other genetic predisposition.' J. Butler, *Forensic DNA Typing: Biology & Technology Behind STR Markers*, 241–45 (2001)"].) These non-coding regions (or "loci") are represented in all human DNA molecules, but there is a high degree of variability in type between unrelated individuals.

A specific pattern of base pairs at a given location on a given chromosome is called an allele. Because a person has two copies of the DNA molecule—one from each parent—two analogous sequences of base pairs (alleles) exist at any given location on any given complementary set of chromosomes. A specific allele may be the same or may differ slightly from the allele at the analogous location on the partner chromosome inherited from the other parent.

While a portion of the human genome is common to all people, some variation does exist—among those who are not identical twins—that can be used for identification purposes. Between individuals and in human populations, different alleles can exist at given locations (loci) on the DNA molecule. These differences are called polymorphisms, and are the reason forensic DNA identification is possible. The most common forensic DNA test in use today targets a core set of 13 loci that are highly variable between individuals, i.e., highly polymorphic. Testing 15 loci is becoming increasingly standard, and additional standardized loci continue to be considered for more discriminating comparisons.

3) DNA Function

The sequence of bases along the DNA molecule reads as a blueprint for the synthesis of proteins responsible for the development and maintenance of an individual. During its lifespan, a cell translates the DNA code into separate instructions for building individual proteins. At the end of its lifespan, the cell replicates and divides into two identical daughter cells, thus contributing to the growth of an individual.

4) Replication and Cell Division

In order for a cell to divide, it must first make a complete copy of all genetic information contained within its nucleus. For non-sex, or somatic, cells, this process is called mitosis. During mitosis, the DNA helix "unzips" and an enzyme called DNA polymerase travels along each single strand reading the sequence of bases. As each base is read, a new nucleotide with its complimentary base (A with T, and C with G) is attached, creating a second strand and completing the double helix once again. This happens on both of the original DNA strands at the same time. Thus, the end result is two new, complete, and identical DNA replicates. As the cell moves on to divide, the replicated DNA organizes into chromosome pairs lined up in the center of the cell. The chromosome replicates are then pulled apart, the cells divides in half, and one full genome will end up in each of the new diploid daughter cells.

Cellular division that results in sex cells (eggs and sperm) is called meiosis. Sex cells do not replicate, but are generated from diploid starter cells. The process of meiosis starts, much like mitosis, with the replication of the entire genome. The DNA, organized into chromosomes, then lines up in the center of the cell. However, instead of each replicated chromosome lining

up individually, each lines up with its homologous chromosome. For example, the replicated chromosome 12 passed from an individual's mother lines up with the replicated chromosome 12 from the father.

During this pairing, a process of genetic swapping, known as “crossing over,” occurs. As chromosome pairs sit adjacent along the midline of the cell, they will trade a portion of their DNA strands. This involves the same portion of each chromosome breaking off and attaching to the other chromosome of the pair. This process is one of the reasons that offspring do not have the exact gene compliment of either parent. A chromosome inherited from an individual's mother can be passed on to a sperm or egg cell with a portion from the father spliced in. Crossing over events help to promote genetic diversity throughout successive generations. It has significant implications for the use of DNA as an identification tool.

After crossing over occurs, the homologous chromosome pairs are then separated into two daughter cells. These daughter cells are not identical, and contain a random compliment of maternal and paternal chromosomes. A second cell division then takes place that creates haploid cells. Each replicated chromosome again lines up at the midline of each cell. The replicates of each chromosome are then pulled apart as each cell divides. The result is four non-identical haploid daughter cells.

5) Transcription

The DNA molecule can be thought of as an organism's assembly manual. In order for the information stored within the genes of the DNA molecule to be available, copies of specific sections are made and distributed for use outside the cell nucleus. This first step in the process of protein synthesis is called transcription. As a gene is transcribed, a messenger ribonucleic acid (mRNA) molecule is produced. RNA is a single-stranded molecule that is structurally similar to DNA. Instead of the sugar deoxyribose, the backbone of an RNA molecule contains the sugar ribose. Ribose contains an oxygen molecule that deoxyribose lacks. RNA also uses the base uracil (U) in place of thymine.

To begin the transcription process, a portion of the DNA helix untwists, the bonds between base pairs are broken, and the two strands separate from each other. This is similar to a zipper being pulled apart from its center out toward its ends. An enzyme called RNA polymerase then attaches to the exposed strand of DNA and begins to read the sequence of bases. As each base is recognized, its complimentary RNA base is added to the growing RNA molecule. For example, if RNA polymerase is reading a C on the DNA molecule, a G is added to the RNA strand. If an A is read on the DNA strand, a U is added to the RNA. As RNA polymerase reaches the end of the gene sequence, the enzyme detaches from the DNA strand, the mRNA molecule is released, and the DNA molecule regains its double stranded form. This new mRNA molecule is then used for the next step in the protein synthesis process.

6) Translation

Once the information from a gene is transcribed into mRNA, that information must be translated into the language of amino acids. Amino acids are the building blocks of proteins, which in turn facilitate the biological function of a given cell, as “instructed” by its DNA. Amino acids are composed of a central core, common to all amino acids, and a unique side chain. This side chain acts as a nametag for each individual amino acid. There are 20 standard amino acids the human body uses for protein synthesis. Some of these can be produced inside the body; others must be taken into the body.

The translation process starts when an mRNA molecule is joined with a ribosome at a specific base sequence. Ribosomes are cellular structures found outside the nucleus, in the cytoplasm of a cell. A single cell may contain thousands of ribosomes. The ribosome complex travels along the mRNA molecule reading the base sequence three bases at a time. These three base sections are called codons, and each one represents one amino acid. When a ribosome reads a specific codon, it allows a piece of RNA called transfer RNA (tRNA) to enter its complex. The tRNA is composed of a strand of RNA, an amino acid, and a three base sequence called an anticodon. The anticodon on the tRNA molecule is the compliment to the codon being read from the mRNA and is the code for the amino acid at the other end of the tRNA molecule. The tRNA binds its anticodon to the codon on the mRNA. This then signals the amino acid to be released from the tRNA and added to the growing protein strand. For example, if

a ribosome reads the sequence G-U-C from an mRNA, it allows the binding of a tRNA with the sequence C-A-G and the amino acid valine. The ribosome then shifts its position to the next codon and the valine molecule is added to the protein strand. The next shift releases the empty tRNA molecule back into the cell. This process continues along the mRNA strand until a complete protein sequence has been synthesized and is ready for use by the organism.

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§ 2:3. Short tandem repeats

Only approximately two percent of the entire human genome contains protein-coding genes. The other 98 percent does not code for proteins, but serves various regulatory functions within the cell. These non-coding regions are of particular use for DNA testing. Some areas of the genome, called satellite regions, contain large amounts of repetitive base sequences. Some of these repeated units, called variable number tandem repeats (VNTRs), are composed of sequences typically less than 100 bases in length, repeated several times in succession. Analysis of short tandem repeats (STRs), VNTRs of two to six bases, is currently the most widely used form of forensic DNA testing. The variability of STR patterns between people is due to the fact that while every person has short repeating sequences of base pairs at the loci used for forensic identification (e.g., A-G-G-T, A-G-G-T, A-G-G-T), the number of repeats differs. For example, at a particular locus, a person may have inherited 12 repeats from her mother and 14 repeats from her father. STRs are "short" because they are only two to six chemical letters long, "tandem" because they are on adjacent chromosomes, and "repeat" because the pattern repeats. One would say that this person's alleles at that locus are "12,14."

A person may receive the same allele from both mother and father at a locus, resulting in a "homozygous" allele pairing of, for example, "16,16." A locus where the two alleles differ is called "heterozygous," for example, "12,14." In forensic DNA laboratory reports, a homozygous locus is often indicated with a single number, e.g., "16." When two DNA profiles are compared side-by-side, a match means that the DNA could have come from the same source, a determination that is informed, as discussed below, by the statistical rarity of the DNA profile at issue.

1) STR Naming

Thousands of STRs have been characterized and can be found on every chromosome in the human genome. Each STR region or locus is named for its position in the genome. They can be found in non-coding regions between genes, or in non-coding regions within a gene called introns. An STR found between genes is identified by its molecular composition, its chromosome, at how many locations it appears in the genome, and the order in which it was characterized. For example, STR location (i.e., "locus") D8S1179 signifies that this location is DNA (D), found on chromosome eight (8), occurs at only one location in the genome (S), and is the 1179th locus described on chromosome eight (1179). An STR located within an intron is named for the gene in which it is found. For example, locus TH01 is located in an intron region of the gene that codes for the enzyme tyrosine hydroxylase. (See People v. Axell, 235 Cal. App. 3d 836, 845, 1 Cal. Rptr. 2d 411 (2d Dist. 1991) ["Every locus that is known has an official name and symbol assigned by the international Human Gene Mapping Workshop"].)

2) STR Structure

STRs most commonly used in forensic testing are four or five base pairs (bp) in length. These are tetra- and pentanucleotide repeats, respectively. An STR is composed of a specific sequence of bases that is repeated several times in succession. For example, the sequence G-A-T-A is the repeat sequence for the locus D7S820. This base sequence at this location is most commonly repeated between six and fifteen times. The number of times the sequence repeats is a person's "type" for that locus. For example, an individual with the sequence **G-A-T-A-**G-A-T-A-**G-A-T-A-**G-A-T-A-**G-A-T-A-**G-A-T-A would have a

D7S820 type of 6. Because humans inherit a set of chromosomes from each parent, each diploid cell has two versions, or alleles, for every STR locus. (See People v. Nelson, 43 Cal. 4th 1242, 1258, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008).) These alleles, which together are a person's genotype, may be the same or different. Individuals with two of the same alleles are considered homozygous at a particular locus. For example, a 10 allele from both one's mother and father would result in a genotype of 10,10. Individuals with two different alleles at a locus (e.g. 10,12) are considered heterozygous. (See U.S. v. Morrow, 374 F. Supp. 2d 51, 57 (D.D.C. 2005).)

In general, STR fragments are comprised of a set of complete repeat units arranged in tandem. In other words, for a tetranucleotide STR, the number of bases in the repeat motif most often is divisible by four. However, it is quite common for an STR sequence to contain a partial repeat unit due to either the insertion or deletion of one, two, or three base pairs somewhere in the repeat region. When these variations occur, they are named for the number of complete repeat units followed by a decimal and the number of "extra" bases in the repeating region. For example, one of the most common of these microvariants is the 9.3 allele in locus TH01. For this allele, one base is missing from the 10 allele. This leaves the STR fragment with nine complete repeats and one incomplete unit of three base pairs.

While the number of repeating units of an STR determine its allele designation, the sequences on either side of the repeated region are equally important. These flanking regions contain sequences that act as locators for each locus. These sequences, called primer binding sites, allow primers (engineered, complimentary DNA strands) to attach, or hybridize, to the DNA molecule on either side of the STR region of interest. The primers act as the starting point for the amplification of each STR fragment. Specific targeting of STR fragments makes it possible to analyze multiple loci in one reaction. This process is called multiplexing, and has greatly improved the efficiency of DNA testing. (See U.S. v. Morrow, 374 F. Supp. 2d 51, 58 (D.D.C. 2005) ["To minimize the chance of human error and contamination, the laboratory may use a process known as 'multiplexing.' Multiplexing allows the lab to type the DNA sample at multiple sites by adding additional primers which will bind simultaneously to their respective target sites."].)

Commercially available DNA test kits in use presently target sets of standardized, "core" loci characterized by a high degree of variability among individuals; i.e., highly polymorphic. Following the widespread use of 13-locus testing kits, technology has advanced to make 15-locus kits (such as IdentiFiler™) and 24-locus kits (such as GlobalFiler™) common in laboratories offering forensic DNA services. Each locus in a kit is tagged with a fluorescent dye of a particular color. The colors can be read separately by a genetic analyzer, thus allowing analysis of different fragments of similar size at the same time. (See People v. Smith, 107 Cal. App. 4th 646, 654–657, 132 Cal. Rptr. 2d 230 (2d Dist. 2003) [describing SRT testing process]; People v. Henderson, 107 Cal. App. 4th 769, 778–779, 132 Cal. Rptr. 2d 255 (4th Dist. 2003) [same].) Each color has a set of loci that range in fragment size from 100 to 400 base pairs. Using primers and spacing sequences of different sizes, the loci can be sufficiently spread out to avoid overlap. For more detail on the mechanics of STR testing, see §§ 3:1 et seq.

3) Advantages of STR Testing

STR analysis has many advantages over other methods of DNA testing. Until the advent of STR typing and its adoption by crime laboratories in the late 1990's, the most common method of DNA analysis was restriction fragment length polymorphism (RFLP) analysis. (See People v. Venegas, 18 Cal. 4th 47, 60-62, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998) [detailing RFLP methodology]; People v. Barney, 8 Cal. App. 4th 798, 806-809, 10 Cal. Rptr. 2d 731 (1st Dist. 1992) (same).) This method involves using chemicals called restriction enzymes to cut the DNA molecule at specific targeted locations, thereby sectioning the genome into pieces of varying length. The fragments are then separated by agarose gel electrophoresis. This process uses an electric current to move the DNA fragments through a gel matrix. Smaller fragments will navigate through the agarose faster than the larger fragments. (An apt analogy is that of snakes winding through rock-strewn terrain; the smaller snakes will encounter fewer obstacles and can move more swiftly than the larger snakes.) The result is separation of the fragments by size. The DNA is then transferred to a membrane that locks the DNA in place. Then a specific location on the DNA molecule is targeted and tagged. Once the DNA at the locus of interest is tagged, it can be visualized and the fragments that contain the locus can be sized. Patterns from different samples can be compared for matches or exclusions.

RFLP analysis offers a high power of discrimination due to the great range of DNA sequence variability between individuals. This can be achieved with analysis of fewer loci than STRs. However, STRs offer several distinct advantages over RFLP methods. Processing time for RFLP is a matter of weeks, where STR analysis can be accomplished in 1–2 days. For RFLP, analysis requires the targeting of each locus separately over a period of days. STR analysis can be multiplexed, as well as automated.

The amount and quality of DNA required for STR analysis gives it a distinct advantage over RFLP. RFLP requires a very high amount of high quality, double-stranded DNA. To produce an RFLP profile, a minimum of 50 nanograms (one nanogram is one billionth of a gram) of DNA is needed. A complete STR profile can be reliably obtained with much less than one ng of single- or double-stranded DNA. The same is true of degraded DNA. Enzymes called endonucleases are constantly at work to dismantle, or degrade, the DNA molecule. RFLP fragments are much larger than STR fragments, which make them much more susceptible to degradation. Smaller fragment size means that STRs have a better chance of escaping endonuclease activity. Because homologous STR alleles are within a very narrow size range, there is less chance of losing one allele in a heterozygous pair. Heterozygous RFLP allele pairs may be on two fragments that very greatly in size. One may be degraded and drop out entirely.

The sizing of STR alleles is also less variable than RFLP alleles. STR analysis produces discreet alleles of specific sizes that do not vary between individuals. A 10-allele at one locus from one-person will be the same size as a 10-allele at the same locus from another individual. Because of sequence variations between individuals, specific RFLP alleles tend to show a wide range of sizes. This makes comparisons dependent on a closest fit method of comparison, called binning. With this method of sizing and comparison, alleles within a similar size range are grouped together for comparison. (See People v. Nelson, 43 Cal. 4th 1242, 1258, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008) [“RFLP testing is now obsolete …. PCR-STR testing has many advantages over RFLP testing. It can test a far smaller sample than RFLP testing requires. It is less susceptible to sample degradation. It is simpler and less time consuming”].)

Forensic DNA Evidence: Science and the Law § 2:4

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Chapter 2. What is a DNA Profile?

§ 2:4. Attributes and Advantages of Loci Chosen for Forensic Use

The ability to analyze multiple STR locations at one time is a great advantage for speeding the analysis process. This does, however, present a challenge when looking at forensic DNA analysis from a national and international perspective. In order for an STR profile to have value as an identifier, there must be another STR profile composed of the same markers with which to compare it. Because there are thousands of STR loci to choose from, without standardization of core loci for forensic testing, two profiles without common loci to compare hold no evidentiary value. This is why in 1997, 13 core STR loci were established for the Combined DNA Index System (CODIS). (See U.S. v. Davis, 602 F. Supp. 2d 658, 666 (D. Md. 2009) ["All of the samples in the CODIS data bank are typed at the same thirteen STR loci, thus enabling law enforcement to compare unknown samples with samples in the data bank. CODIS was developed by a consortium of twenty-one laboratories to test various STR markers to determine which would be the best to use in the CODIS data bank. The thirteen used in this case were selected for CODIS and are, therefore, known as the CODIS core loci"].) In order for a forensic laboratory to participate in and use CODIS, they must test their samples at the following loci: D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, CSF1O, FGA, TH01, TPOX, and VWA. These loci, all of which are tetra-nucleotide repeats, were selected for specific characteristics which include:

1) High power of discrimination;

2) Presence on separate chromosomes to avoid linked loci;

3) Performance in a multiplex system;

4) Low occurrence of stutter;

5) Low mutation rate;

6) A size range of 90-500 base pairs.

These characteristics help to ensure that each locus produces reproducible results in a variety of conditions, and functions independently of other loci targeted by a multiplex testing kit.

Moreover, courts considering the constitutionality, under the Fourth Amendment, of the suspicionless seizure of DNA samples from convicted offenders for use in criminal identification DNA databases often cite the non-coding nature of the loci analyzed as a reason why any invasion of privacy is minimal. For example, the First Circuit Court of Appeals offered the following discussion:

> Each of the targeted loci are found on "so-called 'junk DNA'—DNA that differs from one individual to the next and thus can be used for purposes of identification but which was 'purposely selected because [it is] not associated with any known physical or medical characteristics' and 'do[es] not control or influence the expression of any trait.'" [Citation.] Thus, the resulting DNA profile "'provide[s] a kind of genetic fingerprint, which

> uniquely identifies an individual, but does not provide a basis for determining or inferring anything else about the person.'" [Citation.]

(Boroian v. Mueller, 616 F.3d 60, 66 (1st Cir. 2010); see also U.S. v. Kincade, 379 F.3d 813, 818 (9th Cir. 2004) ["the Bureau analyzes the presence of various alleles 5 located at 13 markers (or loci) on DNA present in the specimen. These STR loci are each found on so-called 'junk DNA'—that is, non-genic stretches of DNA not presently recognized as being responsible for trait coding—and 'were purposely selected because they are not associated with any known physical or medical characteristics'"]; U.S. v. Amerson, 483 F.3d 73, 85 (2d Cir. 2007) ["We are mindful of the vast amount of sensitive information that can be mined from a person's DNA and the very strong privacy interests that all individuals have in this information …. Nevertheless, we are persuaded … that the federal statute provides adequate safeguards to insure that the privacy invasion occasioned by the maintenance of the DNA profiles is minimized. The so-called 'junk-DNA' sequences stored in CODIS are not currently associated with any known physical or medical characteristics"].) There is some recent research, however, that has "begun to question the notion that junk DNA does not contain useful genetic programming material." (*United States v. Kincade*, 379 F.3d at 818.)

Further, forensic testing loci potentially can remain stable in crime scene evidence despite the passage of time. Properly preserved crime scene DNA has been processed successfully more than 30 years after the crime: (See, e.g., People v. Matthews (2019) 32 Cal.App.5th 792, 795 [successful DNA testing performed on sperm swabbed from victim's body "[m]ore than 30 years later"].) DNA certainly can degrade or become contaminated, however, when subjected to unfavorable environmental conditions such as heat or humidity. (People v. Marlow, 41 Cal. Rptr. 2d 5 (App. 6th Dist. 1995), as modified on denial of reh'g, (May 24, 1995) and review granted and opinion superseded, 43 Cal. Rptr. 2d 679, 899 P.2d 65 (Cal. 1995) and review dismissed, cause remanded, 90 Cal. Rptr. 2d 225, 987 P.2d 695 (Cal. 1999).)

Forensic DNA Evidence: Science and the Law § 3:1

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Chapter 3. Developing a DNA Profile: From Crime Scene to Laboratory

§ 3:1. Sample collection

Developing a DNA profile begins with sample collection. Biological samples containing DNA may be collected from a wide range of places and sources. For example, evidence swabs of potential blood may be collected from a crime scene, a clinical examination of a victim or suspect at a medical facility may yield a sexual assault evidence kit, or a reference buccal swab for inclusion in an offender database may be collected from a known arrestee or convicted offender at a law enforcement or correctional facility. Each of these scenarios presents its own set of considerations for handling and preservation.

1) Evidence Samples

Any time evidence is collected from a crime scene or physical examination for DNA testing, it is intended to represent the biological material present at the time of a crime or assault. However, it ultimately is a representation of the biological material present at the time of collection. For this reason, careful sample collection, handling, packaging, and record keeping are essential to any crime scene investigation or examination.

Evidence collection should be conducted by personnel trained in crime scene investigation, forensic assault examination, and/or handling biological samples. This may include crime scene technicians, criminalists, or sexual assault nurse examiners. Sample collection should be done wearing gloves and other personal protective equipment, such as masks or coveralls, which may prevent the transfer of DNA from the collector to the evidence item. When using an implement to collect potential biological material from a surface or body cavity, the implement and the intended container should be new and sterile. For example, a sterile swab may be used to collect a vaginal swab from a victim during a sexual assault exam. After the swab is collected it is essential that it be allowed to dry completely before packaging. Moisture in a biological evidence sample promotes microbial growth, which can have a detrimental effect on downstream DNA processing.

After the swab has dried completely, it should be placed in a container that will allow air to circulate around the sample. Placing an evidence item in an airtight container, especially plastic, can promote microbial growth. Cardboard boxes, paper envelopes, wax paper bindles, and paper bags are all good choices for storage and transportation of evidence. Any solvent used to ease sample collection, such as water on a swab, should be de-ionized and sterile. A sample of the solvent on a sterile swab should also be provided as a testing control.

Evidence stored at a testing facility should be maintained in an environmentally controlled area with minimal fluctuation in temperature and humidity. Storage conditions may include room temperature or refrigerated or freezer environments, dependant on the type of evidence. After the completion of testing evidence is customarily returned to the submitting law enforcement agency, where similar storage conditions are recommended. DNA extracted during testing is typically stored at the testing laboratory.

Properly packaged evidence should be enclosed in appropriate evidence packaging, sealed with a proper seal, and labeled with, at a minimum, the item number, description, date, and initials of the collector. Each evidence item should be accompanied by a complete and accurate chain of custody. See § 11:9, for a discussion of chain of custody legal considerations.

2) Substrate Considerations

The substrate, or surface, on which a biological sample is deposited, can affect sample collection and/or the quality of DNA typing results. For example, certain substrates, such as soil and denim, commonly contain substances that inhibit DNA testing procedures.

DNA testing can provide an answer to the probable identity of the DNA contributor, but cannot ultimately provide an answer as to how and when the DNA present was deposited. When a potential biological sample is taken from a substrate, such as blood from a countertop, the DNA from the blood is collected along with any DNA that was on the counter before the blood was deposited. Current typing methods do not provide any information about which DNA in mixed samples came from which type of biological fluid. To help provide an insight into what DNA may have been on a surface, or item of evidence (e.g., a t-shirt) prior to the deposit of the stain of interest, a substrate sample (substrate control) may be sampled as a typing control. A visually unstained area near the stain of interest is sampled. During the DNA typing process, this sample is treated in the same manner as the stain. The idea is to produce a representation of what level of background DNA, if any, was present on the substrate. This information may aid in interpreting DNA mixtures.

3) Expedited DNA Evidence Submission and Processing In Sexual Assault Cases

California Penal Code section 680 is known as the Sexual Assault Victims' DNA Bill of Rights. It acknowledges the strong interest of both victims and society as a whole in promptly investigating and solving sexual assault crimes, and recognizes the power of DNA and DNA database technology to aid those objectives. Accordingly, section 680 sets forth several objectives for law enforcement and crime laboratories involved regarding sexual assault case investigations.

Effective January 1, 2015, section 680 was amended to address so-called “rapid turnaround” DNA processing programs in sexual assault cases. These programs are cooperative efforts between government DNA laboratories and hospitals that perform sexual assault examinations. Nurses receive specialized training in the collection and preservation of evidence samples collected in sexual assault response team (SART) examinations, and forward the most probative sample(s) to the partner laboratory in a hospital's jurisdiction for prioritized processing for the presence of any DNA that could be attributable to the perpetrator. A resulting DNA profile, if eligible, is uploaded into state and national DNA databases for searching and, ideally, prompt identification of the perpetrator.

The law defines a “rapid turnaround DNA program” programs as

> a program for the training of sexual assault team personnel in the selection of representative samples of forensic evidence from the victim to be the best evidence, based on the medical evaluation and patient history, the collection and preservation of that evidence, and the transfer of the evidence directly from the medical facility to the crime lab, which is adopted pursuant to a written agreement between the law enforcement agency, the crime lab, and the medical facility where the sexual assault team is based.

(Pen. Code, § 680, subd. (c)(5).)

In order to take advantage of statutes of limitations applicable to serious sex crimes, the Legislature has mandated that sexual assault evidence be submitted to laboratories, and subjected to DNA testing, in an expedited manner pursuant to a prescribed chronology. Accordingly, law enforcement agencies investigating specified sex crimes (violations of Penal Code sections 261,

261.5, 262, 286, 287, 289, or former section 288a), where "any sexual assault forensic evidence" was received by the agency on or after January 1, 2016, "shall"

- "Submit sexual assault forensic evidence to the crime lab within 20 days after it is booked into evidence[; and]

- "Ensure that a rapid turnaround DNA program is in place to submit forensic evidence collected from the victim of a sexual assault directly from the medical facility where the victim is examined to the crime lab within five days after the evidence is obtained from the victim."

(Cal. Pen. Code, § 680, subd. (c)(1)(A) & (B).) Note that the evidence submission deadlines are mandatory ("shall"), as added by 2019 legislation effective January 1, 2020, to replace formerly permissive ("should") language.

The amendments to section 680 impose corresponding obligations upon the crime laboratories that receive the sexual assault evidence. The laboratory "shall do one of the following for any sexual assault forensic evidence received by the crime lab on or after January 1, 2016[:]"

- "Process sexual assault forensic evidence, create DNA profiles when able, and upload qualifying DNA profiles into CODIS as soon as practically possible, but no later than 120 days after initially receiving the evidence[; and]

- "Transmit the sexual assault forensic evidence to another crime lab as soon as practically possible, but no later than 30 days after initially receiving the evidence, for processing of the evidence for the presence of DNA. If a DNA profile is created, the transmitting crime lab shall upload the profile into CODIS as soon as practically possible, but no longer than 30 days after being notified about the presence of DNA."

(Pen. Code, § 680, subd. (c)(2)(A) & (B).) The policy objective, again, is to rapidly type and upload into databases DNA profiles probative of the perpetrator's identity.

Notably, section 680 expressly "does not require a lab to test all items of forensic evidence obtained in a sexual assault forensic evidence examination," but rather, only "representative samples of the evidence …." (§ 680, subd. (b)(7)(C).) Nor does the law "require a DNA profile to be uploaded into CODIS if the DNA profile does not meet federal guidelines regarding the uploading of DNA profiles into CODIS." (§ 680(c)(3).)

Forensic DNA Evidence: Science and the Law § 3:2

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Chapter 3. Developing a DNA Profile: From Crime Scene to Laboratory

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§ 3:2. Reference samples

Reference samples are known samples taken from an individual to be used for comparison with profiles from evidence items. References may be collected from victims and suspects during criminal investigations, convicted offenders or arrestees for inclusion in a DNA database, or other individuals who may offer elimination samples for an investigation (e.g., consensual sexual partner of a sexual assault victim).

References may be saliva, blood, hair, or other bodily fluids or tissue. Victim samples are often blood that has been collected during a physical exam by a nurse or phlebotomist. Blood is collected for medical and toxicological screening so an extra blood vial is not overly invasive. Reference samples taken in a non-clinical setting are commonly saliva or buccal samples. These samples are non-invasive and can be collected by medical or law enforcement personnel without the need for specialized training. Buccal samples are also less of a biohazard than blood. Offender and arrestee database reference samples are obtained by scraping a piece of paper on a specialized collector across the cheek several times.

When evidence of a crime includes a perpetrator's DNA profile, it becomes a primary objective of investigators to obtain a reference sample or samples from the suspect or other known persons for comparison purposes. DNA database programs represent automated means of accomplishing this, but more traditional methods can also be employed. The following discussion describes several of those methods, as well as related case law that has developed concerning their use in DNA investigations.

1) Seizing and Using DNA Samples: General Principles

In cases where biological evidence has been collected from a crime scene, and a DNA profile has been developed that is attributable to the perpetrator, law enforcement efforts may focus on obtaining a DNA reference sample from a suspect for comparison purposes. Such seizures must comply with the Fourth Amendment to the United States Constitution.

Government activity constitutes a "search" for Fourth Amendment purposes only if the person claiming an illegal search exhibits an actual—i.e., subjective—expectation of privacy in the item searched, and that expectation is one which society recognizes, objectively, as reasonable. (See California v. Ciraolo, 476 U.S. 207, 211, 106 S. Ct. 1809, 90 L. Ed. 2d 210 (1986).) It is well established that the nonconsensual seizure of cellular material for DNA analysis purposes implicates a legitimate privacy interest. (See, e.g., Schmerber v. California, 384 U.S. 757, 767–771, 86 S. Ct. 1826, 16 L. Ed. 2d 908 (1966); People v. Robinson, 47 Cal. 4th 1104, 1119, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010).)

Note, however, that the strength of the privacy interest will depend upon factual context of the seizure. For example, a convicted offender who is mandated to provide a sample for DNA database identification purposes possesses a greatly reduced expectation of privacy in his personal identification by virtue of his status in the criminal justice system. (See, e.g., People v. Adams, 115 Cal. App. 4th 243, 257, 259, 9 Cal. Rptr. 3d 170 (6th Dist. 2004), as modified, (Feb. 5, 2004).) This, in part, justifies warrantless seizure of DNA database samples. (*People v. Adams,* 115 Cal. App. 4th at 257–258.)

In addition, the chemical analysis of cellular material is generally regarded as a separate search falling under the auspices of the Fourth Amendment. (See County of San Diego v. Mason (2012) 209 Cal.App.4th 376, 381 ["[I]t is well established that the analysis of a DNA sample is independent from the taking of that sample, and presents its own distinct privacy concerns"]; see Skinner v. Railway Labor Executives' Ass'n, 489 U.S. 602, 109 S. Ct. 1402, 103 L. Ed. 2d 639 (1989) [chemical analysis of employees' blood and urine for presence of drugs is a search]; Cupp v. Murphy, 412 U.S. 291, 295, 93 S. Ct. 2000, 36 L. Ed. 2d 900 (1973) [fingernail scraping is search because analysis of dried blood retrieved goes "beyond mere physical characteristics … constantly exposed to the public … [and] constitutes the type of severe, though brief, intrusion upon cherished personal security that is subject to constitutional scrutiny"]; U.S. v. Davis, 657 F. Supp. 2d 630, 644 (D. Md. 2009).)

However, once the government is in lawful possession of DNA seized by warrant, with valid consent, or abandoned, the chemical testing of that sample does not require a separate warrant. (People v. Baylor, 97 Cal. App. 4th 504, 509, 118 Cal. Rptr. 2d 518 (4th Dist. 2002), opinion modified on denial of reh'g, (May 6, 2002) [once a blood sample has been lawfully seized, it may be maintained and used by law enforcement for criminal investigations without further constitutional restriction]; State v. Glynn, 38 Kan. App. 2d 437, 166 P.3d 1075 (2007) [no constitutional violation or infringement of privacy rights when police used a DNA profile obtained in one case by search warrant to investigate and charge a different case]; People v. King, 232 A.D.2d 111, 117–118, 663 N.Y.S.2d 610 (2d Dep't 1997) ["Privacy concerns are no longer relevant once the [DNA] sample has already lawfully been removed from the body, and the scientific analysis of a sample does not involve any further search and seizure of the defendant's person"]; Williamson v. State, 413 Md. 521, 993 A.2d 626, 641–642 (2010), cert. denied, 131 S. Ct. 419, 178 L. Ed. 2d 327 (2010); Patterson v. State, 742 N.E.2d 4, 9–11 (Ind. Ct. App. 2000), on reh'g, 744 N.E.2d 945 (Ind. Ct. App. 2001); Myles v. State, 54 So. 3d 509, 512 (Fla. Dist. Ct. App. 3d Dist. 2010), review denied, 72 So. 3d 746 (Fla. 2011) [DNA sample provided with defendant's consent to eliminate him as a suspect in one investigation lawfully used by police as point of comparison in subsequent, unrelated, investigation].)

This conclusion, however, is less certain where the DNA sample is seized surreptitiously from a crime victim not under suspicion at the time of the seizure. (*United States v. Davis*, 657 F.Supp.2d at 649, 653–654.) In this situation, a warrant is at least preferable. (*Ibid*.) Finally, the First Circuit Court of Appeals has opined that "it may be time to reexamine the proposition that an individual no longer has any expectation of privacy in information seized by the government so long as the government has obtained that information lawfully." (U.S. v. Weikert, 504 F.3d 1, 16 (1st Cir. 2007).)

Similarly, the government's search of a lawfully possessed DNA profile in an identification database does not implicate the Fourth Amendment. (People v. Roberts (2021) 68 Cal.App.5th 64, 104 "[R]epeated comparison of an arrestee's validly obtained and recorded DNA profile to the profiles in CODIS is no more a search than are future uses of mugshots for photo lineups or comparisons of fingerprints to latent prints found at an unrelated crime scene"; Johnson v. Quander, 440 F.3d 489, 498 (D.C. Cir. 2006) ["accessing the records stored in the CODIS database is not a 'search' for Fourth Amendment purposes. As the Supreme Court has held, the process of matching one piece of personal information against government records does not implicate the Fourth Amendment;" citing Arizona v. Hicks, 480 U.S. 321, 107 S. Ct. 1149, 94 L. Ed. 2d 347 (1987)].) The *Johnson* court added that "the consequences of the contrary conclusion would be staggering," creating "an intolerable burden" on law enforcement "if every 'search' of an ordinary fingerprint database were subject to Fourth Amendment challenges." (*Johnson v. Quander*, 440 F.3d at 499.) And the *Roberts* court conceptualized a lawfully maintained DNA database profile as something that is "essentially in the plain view of law enforcement." (*People v. Roberts*, 68 Cal.App.5th at 104) "[T]here is no constitutional impediment to matching information against other governmental records when that information is in law enforcement's plain view as the result of a valid search," concluded the court. (*People v. Roberts*, 68 Cal.App.5th at 104)

2) Search Warrant

When a suspect is implicated by evidence sufficient to generate probable cause, the investigating agency may seek issuance of a search warrant, signed by a magistrate, authorizing the collection of a reference DNA sample for comparison purposes. The execution of a search warrant often occurs simultaneously with the arrest of the suspect.

The Fourth Amendment requires that all warrants be supported by a showing of probable cause, in addition to a sufficiently particular and specific description of the person to be searched and the evidence to be seized. (4th Amend., U.S. Const.) The United States Supreme Court described the meaning and nature of "probable cause" in the Illinois v. Gates, 462 U.S. 213, 103 S. Ct. 2317, 76 L. Ed. 2d 527 (1983):

> The task of the issuing magistrate is simply to make a practical, common-sense decision whether, given all the circumstances set forth in the affidavit before him, including the "veracity" and "basis of knowledge" of persons supplying hearsay information, there is a fair probability that contraband or evidence of a crime will be found in a particular place.

(462 U.S. at 238; see also Maryland v. Pringle, 540 U.S. 366, 370–371, 124 S. Ct. 795, 157 L. Ed. 2d 769 (2003) [explaining that the probable cause standard is a "practical, nontechnical conception that deals with the factual and practical considerations of everyday life on which reasonable and prudent men, not legal technicians, act" and one that provides a "reasonable ground for belief of guilt"].) Moreover, "probable cause is a fluid concept—turning on the assessment of probabilities in particular factual contexts—not readily, or even usefully, reduced to a neat set of legal rules." (*Illinois v. Gates*, 462 U.S. at 232.)

Even if probable cause exists to arrest a subject, a DNA reference sample for case investigation purposes—as distinguished from mandatory DNA samples for DNA database purposes—should be obtained pursuant to warrant or valid consent, as is consistent with Fourth Amendment principles. Seizing a warrantless DNA sample for investigation purposes is not properly considered a search incident to arrest. (See People v. Clark, 5 Cal. 4th 950, 993–994, 22 Cal. Rptr. 2d 689, 857 P.2d 1099 (1993) (disapproved of on other grounds by, People v. Doolin, 45 Cal. 4th 390, 87 Cal. Rptr. 3d 209, 198 P.3d 11 (2009)) [probable cause to seize blood sample after defendant's arrest would have been provided by incriminating taped statements made 30 minutes later; thus, suppression motion based on warrantless seizure of blood sample properly denied based on doctrine of inevitable discovery].)

A DNA database sample taken upon arrest or conviction, by contrast, may be used for database purposes only, pursuant to the specific collection, use, and disclosure parameters set forth in controlling statutory authority. (See Pen. Code, §§ 296, subd. (a)(2); 296.1, subd. (a)(1).) Law enforcement may not use the statutory warrantless DNA database sample as a means to avoid constitutional strictures governing seizure of physical evidence for use in a case investigation. In other words, DNA database laws are not to be viewed as convenient "shortcuts" around the Fourth Amendment's warrant requirement.

Should investigators desire a DNA sample from an arrestee for direct comparison to crime scene evidence in that case or an unrelated case, ordinary principles governing searches apply. Most often a sample will be obtained by search warrant or consent. (But see discussion below of abandoned DNA collection.) DNA sampling does not qualify as an exigent circumstance justifying a warrantless search pursuant to arrest, because a DNA profile is not evidence that will be lost or destroyed if a sample is not taken immediately. (See, *e.g.*, Friedman v. Boucher, 580 F.3d 847, 858 (9th Cir. 2009).) Of course, in some circumstances a warrantless swab of an arrestee's body (*e.g.*, a penile swab) may be justified if the facts indicate that probative evidence of the crime (*e.g.*, a rape victim's DNA) may be present that would be wiped or washed away if not collected immediately. (See Schmerber v. California, 384 U.S. 757, 770, 86 S. Ct. 1826, 16 L. Ed. 2d 908 (1966) [warrantless seizure upon arrest permissible where officer "might reasonably have believed that he was confronted with an emergency, in which the delay necessary to obtain a warrant, under the circumstances, threatened 'the destruction of evidence.' [Citation.]"].)

3) Abandoned DNA Samples

Collecting an "abandoned" DNA sample has become an increasingly common tactic for law enforcement investigators who seek a reference sample for comparison purposes but lack the requite probable cause for issuance of a search warrant. The legality of this approach is premised on the established principle that no reasonable expectation of privacy attaches to property abandoned in public and thus accessible to anyone. (California v. Greenwood, 486 U.S. 35, 39–40, 108 S. Ct. 1625, 100 L. Ed.

2d 30 (1988) [search of defendant's trash container left for curbside pickup did not infringe upon protected privacy interest]; People v. Parson, 44 Cal. 4th 332, 345, 79 Cal. Rptr. 3d 269, 187 P.3d 1 (2008).)

Two published California decisions thus far have applied the "abandoned property" principle to surreptitious DNA collection by police. In People v. Gallego, 190 Cal. App. 4th 388, 117 Cal. Rptr. 3d 907 (3d Dist. 2010), review denied, (Mar. 16, 2011), police identified Gallego as a "person of interest" in a 1991 murder involving a victim who had been stabbed more than 50 times. (*People v. Gallego,* 190 Cal. App. 4th at 390–391.) During the initial crime scene investigation, technicians had collected samples of blood attributable to the perpetrator on a bloody towel. (*People v. Gallego,* 190 Cal. App. 4th at 393.) DNA testing in 2006 revealed a usable DNA profile. (*Ibid*.) Shortly thereafter, police conducting surveillance of Gallego surreptitiously recovered a cigarette butt he had thrown down on a public sidewalk. (*Ibid*.) DNA testing of saliva on the cigarette resulted in a match to the DNA on the bloody towel from the 1991 homicide. (*Ibid*.) The court held that Gallego had abandoned the cigarette butt in a public place "'particularly suited for public inspection'" and thus retained no reasonable expectation of privacy in it or in its use for DNA testing and comparison to the unknown crime scene DNA profile. (*People v. Gallego,* 190 Cal. App. 4th at 395–396.)

The court characterized Gallego's actions as "conscious activity—indeed, an unlawful act of littering: voluntarily discarding his cigarette butt onto a public sidewalk. We do not face the situation of DNA being deposited in a truly nonvolitional way of unconsciously shedding cells." (*People v. Gallego,* 190 Cal. App. 4th at 396–397.) It did not matter that Gallego would not have anticipated the police use of his DNA. (*People v. Gallego,* 190 Cal. App. 4th at 397.) And, noted the court, the abandonment of the cigarette terminated any privacy interest both in the cigarette itself and in the chemical contents of the cells left on it—or at least the chemical contents used for forensic criminal identification purposes. (*Ibid*.) Ultimately, opined the Gallego court, there is no constitutional distinction between the police use of an abandoned cigarette for DNA testing and recovering it to lift a fingerprint. (*People v. Gallego,* 190 Cal. App. 4th at 398.)

In People v. Thomas, 200 Cal. App. 4th 338, 132 Cal. Rptr. 3d 714 (2d Dist. 2011), review filed, (Dec. 5, 2011), defendant Thomas was a suspect in a string of residential burglaries. A DNA profile attributable to the perpetrator had been developed based on biological material left at several of the crime scenes. (*Id*. at p. 340.) While conducting surveillance of Thomas, police officers stopped him for suspected driving under the influence of alcohol. He was given a preliminary alcohol screening (PAS) device breath test. Although Thomas was not arrested for DUI, officers surreptitiously retained the plastic mouthpiece from the PAS test and submitted it for laboratory analysis of the DNA left behind on it by Thomas. The testing identified Thomas as the burglary suspect based on a DNA profile match. (*Id* at p. 340.)

The court of appeal held that Thomas had voluntarily abandoned the saliva on the PAS test mouthpiece; thus its use by police for DNA testing did not constitute a search that implicated the Fourth Amendment. (*Id*. at pp. 342–343.) Specifically, noted the court,

> defendant in this case had no privacy right in the mouthpiece of the PAS device, which was provided by the police, and he abandoned any expectation of privacy in the saliva he deposited on this device when he failed to wipe it off. Whether defendant subjectively expected that the genetic material contained in his saliva would become known to the police is irrelevant since he deposited it on a police device and thus made it accessible to the police. The officer who administered the PAS test testified that used mouthpieces are normally discarded in the trash. Thus, any subjective expectation defendant may have had that his right to privacy would be preserved was unreasonable.

(*Id*. at pp. 342–343; but see U.S. v. Davis, 657 F. Supp. 2d 630, 649–650 (D. Md. 2009) [rejecting argument that DNA present on clothing seized from gunshot wound victim while in hospital emergency room has been "abandoned" for Fourth Amendment purposes]; Imwinkelried, *DNA Typing: Emerging or Neglected Issues*, (2001) 76 Wash. L. Rev. 413, 437 ["depositing DNA in the ordinary course of life when drinking, sneezing, or shedding hair, dandruff, or other cells differs from placing papers in

a container on the street to be collected as garbage. Depositing paper in the trash is generally a volitional act …. Leaving a trail of DNA, however, is not a conscious activity"]; Joh, *Reclaiming "Abandoned" DNA: The Fourth Amendment and Genetic Privacy*, (2006) 100 Nw. U. L. Rev. 857, 883–883.)

Of additional interest in People v. Thomas was the court of appeal's observation that while using a subject's saliva from the mouthpiece of an alcohol breath test to investigate an unrelated crime was constitutional, the result might have been different had police conducted DNA testing on blood or urine provided pursuant to Vehicle Code section 23612, California's "implied consent" statute for DUI investigations. (*Id*. at pp. 343–344.) That statute limits the scope of the driver's consent to chemical analysis of his or her blood by specifying that "[a] person who drives a motor vehicle is deemed to have given his or her consent to chemical testing of his or her blood or breath *for the purpose of determining the alcoholic content of his or her blood*." (Veh. Code, § 23612, subd. (a)(1)(A) & (B); see also People v. Ryan, 116 Cal. App. 3d 168, 182, 171 Cal. Rptr. 854 (1st Dist. 1981) ["the immediate purpose of … the implied consent law, is to obtain the best evidence of blood alcohol content at the time of the arrest of a person who is reasonably believed to be driving while intoxicated"].)

The Thomas court pointed out that, "[i]n cases where a driver consents to give a blood sample under a state's implied consent law and the sample is afterwards genetically tested, some courts have concluded that the scope of the driver's consent does not permit genetic testing, either because the driver expressly limited his consent or because the express statutory purpose for testing the blood sample is to ascertain the presence of alcohol or drugs in the blood." (People v. Thomas, 200 Cal. App. 4th 338, 132 Cal. Rptr. 3d 714 (2d Dist. 2011), review filed, (Dec. 5, 2011), citing State v. Binner, 131 Or. App. 677, 886 P.2d 1056, 1059 (1994) and State v. Gerace, 210 Ga. App. 874, 437 S.E.2d 862, 863 (1993).) In Thomas, by contrast, the statutory breath sample provided by the defendant was used exclusively for determining alcohol content and only the incidentally abandoned cells on the instrument mouthpiece were collected for independent investigatory purposes.

Case law from other states addressing abandoned samples is in accord. For example, in Williamson v. State, 413 Md. 521, 993 A.2d 626 (2010), cert. denied, 131 S. Ct. 419, 178 L. Ed. 2d 327 (2010), a rape suspect was arrested on unrelated charges. While awaiting booking at the jail, he was given a meal from McDonald's, which he accepted, consumed, and then discarded the cup and wrappers on the floor of the cell. (993 A.2d at 630.) Officers retrieved the cup, and submitted it for DNA testing. The results implicated Williamson in a 2002 rape. (*Ibid*.) The court held that "Williamson unequivocally abandoned the McDonald's cup after he had been offered a meal, accepted it, and then threw the debris from the meal on the floor. He certainly did not retain the cup as his own and clearly, while in the premises of the prison, could not reasonably expect that the police would not collect, and potentially investigate, the trash he discarded in his cell." (993 A.2d at 635.)

Further, the Williamson court reiterated that the privacy interests attached to the content of one's DNA are qualitatively lower when the DNA testing is performed on a limited number of markers that do not code for biological traits, and when the government's use of the information is limited to criminal identification purposes:

> In *State v. Raines* [(2004) 857 A.2d 19, 33], we already recognized that the only information collected from testing and storage of DNA profiles is the identity of the person whose DNA is being tested under the Maryland DNA Collection Act, and the purpose of uploading DNA profiles to CODIS is "akin to that of a fingerprint." Our sister courts also have recognized, as we did in Raines, that testing and storage is limited to identification purposes, such as in the present case. See *State v. Hauge* [(Haw. 2003) 79 P.3d 131] (rejecting a parade of horribles argument where DNA is being used for identification purposes only); *United States v. Davis* [(D.Md. 2009) 657 F.Supp.2d 630, 656, fn. 6] (noting that DNA profiles contained in CODIS consist of analyses of 13 "junk" loci consisting of stretches of DNA, which do not presently recognize traits and were purposely selected because they are not associated with any known physical or medical characteristics).

(*Williamson v. State*, 993 A.2d at 639.) Consequently, concluded the court, no warrant was needed to conduct testing of the biological sample lawfully in the possession of the police. (*Williamson v. State*, 993 A.2d at 641.)

In Com. v. Perkins, 450 Mass. 834, 883 N.E.2d 230 (2008), defendant Perkins was accused of raping and killing a woman in 1990. Although DNA was recovered from the victim's body, the case went unsolved for six years. (*Commonwealth v. Perkins,* 883 N.E.2d at 236.) In 1996, police investigators interviewed Perkins about the crime. "The defendant smoked two cigarettes and drank a can of soda during the interview that were made available to him." (*Commonwealth v. Perkins,* 883 N.E.2d at 237.) These items were later retrieved and subjected to DNA testing, and the results implicated Perkins. (*Ibid.*) The Massachusetts Supreme Court held that the cigarette butts and soda can had been abandoned by Perkins and, as a result, the police seizure and testing did not infringe upon a Fourth Amendment privacy interest. (*Commonwealth v. Perkins,* 883 N.E.2d at 239.) "Nothing prevented the defendant from bringing [the items] with him after the interview had ended, as he had done with the balance of the pack of cigarettes. Whatever reasonable expectation of privacy he may have had in the cigarette butts was abandoned under both the State and Federal Constitutions." (*Ibid.*) In reaching this conclusion, the court relied on the facts that Perkins had asked for the cigarettes and soda, and had not been induced through promises or other means to leave them behind when he left the room. (*Ibid.*) Further, the court was influenced by the fact that the defendant knew that he could not take the soda can with him when he left, and made no effort to sanitize or exert control over it. (*Commonwealth v. Perkins,* 883 N.E.2d at 240.)

In Piro v. State, 146 Idaho 86, 190 P.3d 905 (Ct. App. 2008), a suspect (Piro) was taken into custody for questioning regarding an attempted lewd conduct. He was placed in an interrogation room at the police station and questioned for approximately an hour. At that point the officers left the room and returned with a bottle of water, a pencil, and paper. The officers left the room again so that Piro could complete a witness statement. When the officers returned to the interrogation room, they told Piro to leave the water bottle, placed him under arrest for the attempted lewd conduct, and took him to a holding cell. The officers returned to the interrogation room and collected the bottle of water from which Piro had been drinking, and submitted it for DNA testing. A CODIS database hit linked Piro to an unrelated and unsolved rape case from the previous year. (*Piro v. State,* 190 P.3d at 906.) The reviewing court held that "Piro had no legitimate subjective expectation of privacy in the water bottle …. Although Piro was asked to leave the bottle on the table, he was not holding the bottle in his hand when this occurred. Furthermore, even someone new to the system would not reasonably believe that he could permanently retain possession of a used water bottle while incarcerated in jail." (*Piro v. State,* 190 P.3d at 910.)

Other cases have reached a similar conclusion. (Com. v. Ewing, 67 Mass. App. Ct. 531, 854 N.E.2d 993, 1001 (2006), aff'd, 449 Mass. 1035, 873 N.E.2d 1150 (2007) [offering defendant cigarettes and a straw during interrogation]; Com. v. Cabral, 69 Mass. App. Ct. 68, 866 N.E.2d 429 (2007) [defendant did not retain a reasonable expectation of privacy in spit he left on a public sidewalk, or the DNA extracted from his saliva]; People v. Sterling, 57 A.D.3d 1110, 869 N.Y.S.2d 288 (3d Dep't 2008) [no reasonable expectation of privacy in DNA from milk carton discarded by an imprisoned defendant]; Com. v. Bly, 448 Mass. 473, 862 N.E.2d 341, 356–537 (2007) [suspect linked to murder by DNA analysis of water bottle and cigarette butts abandoned following police interview].)

Case facts dictated a different outcome in State v. Reed, 182 N.C. App. 109, 641 S.E.2d 320 (2007), writ denied, review denied, appeal dismissed, 361 N.C. 701, 653 S.E.2d 155 (2007). There, investigators questioned Reed on the patio of his home after asking him to provide a DNA sample for an ongoing investigation. During the conversation, Reed smoked a cigarette and then "took apart the butt, removing the filter's wrapper and shredding the filter before placing the remains in his pocket. As he did so, [Reed] mentioned watching the popular network television police procedural, CSI: Crime Scene Investigation." (*State v. Reed,* 641 S.E.2d at 320.) He smoked another, but this time flicked the butt onto a pile of trash on the patio. A police detective kicked the cigarette butt off the patio into a grassy common area, and retrieved it later for DNA testing. The testing implicated Reed in a crime. The appellate court held that the seizure violated the Fourth Amendment because Reed had a reasonable expectation of privacy on his patio and demonstrated intent to preserve private possession of the cigarette butts. (*State v. Reed,* 641 S.E.2d at 323.) The affirmative removal of the cigarette butt from Reed's property unlawfully interfered with those privacy rights.

4) Consent

As in other search and seizure contexts, officers may lawfully obtain a DNA reference sample by obtaining valid consent to do so from the person of interest. A person's consent to a search provides an exception to the warrant requirement. (People v.

James, 19 Cal. 3d 99, 106, 137 Cal. Rptr. 447, 561 P.2d 1135 (1977).) The consent, however, must be a voluntary "product of … free will and not a mere submission to an express or implied assertion of authority." (*Ibid*.; Schneckloth v. Bustamonte, 412 U.S. 218, 219, 93 S. Ct. 2041, 36 L. Ed. 2d 854 (1973); Florida v. Jimeno, 500 U.S. 248, 250–251, 111 S. Ct. 1801, 114 L. Ed. 2d 297 (1991); People v. Smith, 190 Cal. App. 4th 572, 577, 118 Cal. Rptr. 3d 483 (2d Dist. 2010), review denied, (Mar. 2, 2011).)

Whether consent is voluntary depends upon all of the surrounding factual circumstances, including whether the consenting person was restrained or under arrest at the time, and whether officers employed deceptive or coercive tactics in eliciting the consent. (*People v. James*, 19 Cal.3d at 109–110.) "[N]o single factor is dispositive of this factually intensive inquiry." (People v. Avalos, 47 Cal. App. 4th 1569, 1578, 55 Cal. Rptr. 2d 450 (4th Dist. 1996); see also *Schneckloth v. Bustamonte*, 412 U.S. at 227 ["the question whether a consent to a search was in fact 'voluntary' or was the product of duress or coercion, express or implied, is a question of fact to be determined from the totality of all the circumstances"].)

The scope of consent may be limited or conditioned by a person agreeing to relinquish a DNA sample, and determines the subsequent use to which that sample may be put. (See Florida v. Jimeno, 500 U.S. 248, 251, 111 S. Ct. 1801, 114 L. Ed. 2d 297 (1991); People v. Crenshaw, 9 Cal. App. 4th 1403, 1408, 12 Cal. Rptr. 2d 172 (5th Dist. 1992) ["The standard for measuring the scope of a suspect's consent under the Fourth Amendment is that of 'objective' reasonableness—what would the typical reasonable person have understood by the exchange between the officer and the suspect?"].) See People v. Pickard, 15 Cal. App. 5th Supp. 12, 17, 222 Cal. Rptr. 3d 686 (Cal. App. Dep't Super. Ct. 2017) [secondary testing of blood alcohol sample for drugs fell outside the scope of consent and thus violated the Fourth Amendment]. For example, several courts have held that implied consent laws authorizing seizure of a biological sample to measure blood alcohol content preclude future DNA analysis or other use of those samples for unrelated investigations. (State v. Binner, 131 Or. App. 677, 886 P.2d 1056, 1059 (1994); State v. Gerace, 210 Ga. App. 874, 437 S.E.2d 862, 863 (1993).) Incomplete or misleading representations by police about the use to which a DNA sample will be put can also negate consent. (Beasley v. State, 204 Ga. App. 214, 419 S.E.2d 92, 94 (1992) [defendant did not consent to use of urine sample to develop evidence of drug use for trial purposes when told only that sample would be used to determine amount of bail that would be set].)

Other courts have held that a person's consensual DNA sample is not considered involuntary if police advisements and corresponding consent are sufficiently generalized and without express limitation, even though the person is not told that the sample may also be used for future law enforcement purposes unrelated to the current investigation. (Myles v. State, 54 So. 3d 509, 512 (Fla. Dist. Ct. App. 3d Dist. 2010), review denied, 72 So. 3d 746 (Fla. 2011) [DNA sample provided with defendant's consent to eliminate him as a suspect in one investigation lawfully used by police as point of comparison in subsequent, unrelated, investigation]; Holmes v. State, 284 Ga. 330, 667 S.E.2d 71, 73 (2008) [consent valid where defendant only told that sample would be used "for comparison purposes"]; Pharr v. Com., 50 Va. App. 89, 646 S.E.2d 453, 458 (2007); Com. v. Gaynor, 443 Mass. 245, 820 N.E.2d 233, 243 (2005); People v. Collins, 250 P.3d 668, 674 (Colo. App. 2010), cert. denied, 2010 WL 4400041 (Colo. 2010); see generally People v. Baylor, 97 Cal. App. 4th 504, 508, 118 Cal. Rptr. 2d 518 (4th Dist. 2002), opinion modified on denial of reh'g, (May 6, 2002) ["there is no constitutional violation or infringement of privacy when the police in one case use a DNA profile, which was lawfully obtained in connection with another case"]; cf. Colorado v. Spring, 479 U.S. 564, 577, 107 S. Ct. 851, 93 L. Ed. 2d 954 (1987) ["a suspect's awareness of all the possible subjects of questioning in advance of interrogation is not relevant to determining whether the suspect voluntarily, knowingly, and intelligently waived his Fifth Amendment privilege"].)

5) Trickery and Ruse

Applying Fourth Amendment principles, courts have approved the use of law enforcement trickery or ruses to obtain abandoned or consensual DNA, so long as the police tactics are not coercive.

The United States Supreme Court has recognized that law enforcement may use deception during the investigation of criminal offenses, so long as such tactics comply with constitutional protections for individual rights. (Lewis v. U.S., 385 U.S. 206, 208–212, 87 S. Ct. 424, 17 L. Ed. 2d 312 (1966) [undercover agent posed as narcotics buyer to gain consensual entry into home for

purpose of buying drugs]; see also People v. Lucatero, 166 Cal. App. 4th 1110, 1117, 83 Cal. Rptr. 3d 364 (5th Dist. 2008), as modified on denial of reh'g, (Oct. 8, 2008).) Police trickery as to the purpose of a search does not, therefore, necessarily render a subject's consent to search involuntary. (People v. Avalos, 47 Cal. App. 4th 1569, 1578, 55 Cal. Rptr. 2d 450 (4th Dist. 1996).) Although "police deception as to the purpose of the search is relevant in assessing a suspect's consent, it cannot be analyzed in a vacuum without reference to the surrounding circumstances." (*Ibid*.) When confronted with an unlawful search or seizure claim based on police trickery, courts will consider whether the deception materially misled the defendant into surrendering the privacy rights implicated. (*People v. Avalos,* 47 Cal. App. 4th at 1579; see also People v. Reyes, 83 Cal. App. 4th 7, 11–13, 98 Cal. Rptr. 2d 898 (4th Dist. 2000).)

In State v. Athan, 160 Wash. 2d 354, 158 P.3d 27, 34 (2007), defendant Athan was suspected by Seattle police of committing raping and murdering a young girl 20 years earlier, but investigators were unable to generate probable cause to support a search warrant for a DNA sample to compare to the perpetrator's DNA. Instead, investigators created a ruse. They sent Athan a letter that purported to be from a law firm inviting him to participate in a class action lawsuit. The letter was mailed to Athan in New Jersey and included a return envelope. Athan sent back the envelope, which was submitted for DNA testing of the saliva used to lick the seal. Athan's DNA matched the homicide evidence sample, and Athan was found guilty of murder. On appeal, the Washington Supreme Court concluded that Athan retained no reasonable expectation of privacy in his saliva. (*State v. Athan,* 158 P.3d at 33–34.) "[T]here is no subjective expectation of privacy in discarded genetic material just as there is no subjective expectation of privacy in fingerprints or footprints left in a public place," held the court. (*State v. Athan,* 158 P.3d at 37.) The court observed further that "[t]he analysis of DNA obtained without forcible compulsion and analyzed by the government for comparison to evidence found at a crime scene is not a search under the Fourth Amendment." (*Ibid*.) As for the police trickery involved, the Athan court stated that "[p]ublic policy allows for a limited amount of deceitful police conduct in order to detect and eliminate criminal activity," and reasoned that the police conduct here was not so outrageous or shocking as to offend a sense of justice and require dismissal as a remedy. (*State v. Athan,* 158 P.3d at 38–39, 44.) The court was influenced by the facts that the police did nothing to affect the voluntariness of Athan's actions, and did not trick him into committing a crime or revealing confidential information. (*Ibid*.)

A Florida appellate court reached a different result in State v. McCord, 833 So. 2d 828 (Fla. Dist. Ct. App. 4th Dist. 2002). There, defendant McCord was a suspect in a string of armed robberies that included DNA evidence, but investigators lacked probable cause for a warrant to obtain a reference DNA sample. After arresting McCord on unrelated charges a detective told him that he was a suspect in a rape case—which was untrue—and asked for a DNA sample so that they could "exclude him" as the rapist. (*State v. McCord,* 833 So.2d at 829.) McCord provided the sample, which ultimately linked him to the robberies. The court held that McCord's sample was obtained in violation of the Fourth Amendment: "McCord consented to giving a sample only because he wanted to clear his name in a non-existent case[,] … this deception, while McCord was in jail, was so manipulative that his 'consent' did not 'validate the search.'" (*State v. McCord,* 833 So.2d at 830.)

In a subsequent discussion of State v. McCord, the Florida Supreme Court observed that the stigma of a rape accusation played a role in determining the voluntariness of the alleged consent: "While we do not believe that a defendant's consent to a search should be interpreted as being conditioned on the resulting evidence being used only in investigations of crimes that the defendant knows that he or she did not commit, we recognize that a defendant's understandable desire to clear his or her name of the stigma of a rape accusation is a circumstance to consider. McCord's being told that he was a suspect in a serious sex crime for which DNA could clear him is a circumstance relevant to the analysis of whether McCord's consent was voluntary or coerced." (Wyche v. State, 987 So. 2d 23, 31 (Fla. 2008) [in-custody rape suspect told he was a suspect in fictitious burglary series and asked for DNA sample for use in that investigation; held that consent valid despite police deception].)

Finally, in People v. LaGuerre, 29 A.D.3d 820, 815 N.Y.S.2d 211 (2d Dep't 2006), the court considered a more elaborate law enforcement ruse. Detectives posing as employees of a chewing gum manufacturer asked a sex crime suspect to chew a stick of gum and deposit it in a cup as part of a contrived "Pepsi taste test challenge." (*People v LaGuerre*, 815 N.Y.S.2d at 213.) The gum was analyzed for DNA type. The court held that the suspect "freely discarded and abandoned [the gum] inside a cup that he handed to a police detective during the supposed taste test," and thus was not denied due process as a result of police deception.

(*Ibid*.) That deception was "'not coercive or so fundamentally unfair as to deny due process' [citations]." (*Ibid*.; see also Com. v. Ewing, 67 Mass. App. Ct. 531, 854 N.E.2d 993, 1001 (2006), aff'd, 449 Mass. 1035, 873 N.E.2d 1150 (2007) [ruse to induce suspect to abandon refuse that could be subjected to DNA testing does not violate Fourth Amendment if not coercive].)

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Forensic DNA Evidence: Science and the Law § 3:3

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Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 3. Developing a DNA Profile: From Crime Scene to Laboratory

§ 3:3. Sampling crime scene evidence

Sampling crime scene evidence is the first step in the process of developing a DNA profile that takes place in the laboratory. When evidence is received, it is generally accompanied by a request that offers details of the incident and which items, if any, are of particular interest to investigators. Investigators may also consult with a laboratory before or during evidence transfer to discuss details of the case and possible strategies for testing.

Evidence can come into a laboratory in many forms, ranging from swabs in a sexual assault kit to an entire automobile. The analyst will perform an inventory of items and evaluate each one for potential probative value. The object of any analysis is to analyze the items that have the best chance of answering the question presented by investigators. This may be one sample or several, depending on the facts of the individual case.

1) Presumptive Tests

Once evidence items are selected for further processing, presumptive tests may be conducted to determine if biological fluids of interest are present. Several tests exist to screen for blood, semen, saliva, and fecal matter, as well as test that determine if certain biological fluids are of human origin. Some of these tests are presumptive, meaning that a positive result reveals the presence of a substance found in the fluid of interest. For example, acid phosphatase is an enzyme found in large quantities in semen; however, it is also present in several other bodily fluids at lower concentrations. Therefore, the mere presence of acid phosphatase in a sample does not necessarily mean that a stain is semen. Rather, it simply means that semen may be present. Confirmatory tests are specific to a bodily fluid. A protein known as “p30” is specific to semen, and is present even in individuals who do not produce sperm as a result of, for example, a vasectomy. A positive p30 test can confirm the presence of semen in an evidence sample. Vaginal swabs from a sexual assault are commonly tested with these two methods, among others including microscopic observation of spermatozoa. Depending on laboratory policy, some negative presumptive tests may halt the analysis process, while other samples will continue forward regardless of the presumptive test results.

2) Sampling Techniques

Once an analyst had determined which items will be sampled, a portion of each item is sampled for processing. This may involve cutting a piece from the item, such as a portion of the cotton from a vaginal swab, or cutting a bloodstain from a piece of clothing. A stain may also be swabbed. For example, a portion of a bloodstain on a piece of leather may be easily removed with a moistened sterile swab. The swab would then be sampled and tested. Swabbing may also be used to sample trace or wearer DNA from large areas. For example, the inside of a hat band may be swabbed to test for DNA from anyone who may have worn the hat.

3) Evidence Handling

Evidence items should always be handled separately from one another to prevent possible DNA transfer. An analyst should open one item, sample it and repackage it before proceeding to another. Evidence from victims should always be examined separately from suspect evidence. It is preferable for laboratories to have separate examination areas for victim and suspect evidence. Evidence should always be handled separately from references. In some cases all evidence items may be processed completely before any references are sampled.

It is an analyst's responsibility to wear appropriate personal protective equipment while handling evidence. This includes gloves and lab coat. A face mask or shield, a cap or hairnet, disposable sleeves, and booties may also be worn depending on the case and the analysts comfort level. Personal protective equipment is intended to protect evidence form contamination from the analyst, but is also intended to protect the analyst from any potentially infectious materials that may be present.

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Forensic DNA Evidence: Science and the Law § 3:4

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Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 3. Developing a DNA Profile: From Crime Scene to Laboratory

§ 3:4. Extraction, amplification, and determination of a DNA profile

1) DNA Extraction Methods

Before a DNA profile can be developed, DNA must be extracted from the nucleus of the cell, and separated from all other cellular material contained in the sample. To do this the membranes of DNA containing cells must be disrupted, and the DNA must be separated away from the cellular components. Several methods exist.

a) Organic extraction

Organic extraction takes advantage of the different chemical properties of cellular components. DNA is hydrophilic, which means it has an affinity for water. The outer layer of the cell, known as the cellular membrane, and other cellular components composed of lipids (fats), are hydrophobic, or non-water soluble. Because the main goal of the DNA extraction process is to separate DNA from other cellular components, the difference in these elements' affinity for water can be exploited. A buffer containing sodium dodecyl sulfate (SDS) and proteinase K (prok) is added to a tube with a sampled evidence item. The tube is then heated. After DNA has been released from the cells, an organic (non-water soluble) solvent is introduced into a tube containing the DNA extraction mixture. The DNA extraction mixture is water-based, so the addition of the organic solvent causes two separate layers, or phases, to form, much like oil and vinegar salad dressing. The tube is then agitated causing the two phases to commingle. During this blending of phases, the cellular components in the tube are attracted to either the water phase or the organic phase. The tube is then centrifuged (spun at a high gravitational force). This causes the components in the tube to choose sides and separate. After spinning, the two phases are once again separated with the water (aqueous) phase on top and the organic phase on bottom. DNA and other hydrophilic components stay in the aqueous, or water, phase. The cell membrane pieces and other hydrophobic components separate into the organic phase. The DNA containing aqueous phase is then removed from the top of the organic phase and placed in a clean tube, leaving behind unwanted cellular debris.

b) Differential extraction

Sexual assault cases frequently contain samples that are a mixture of a perpetrator's semen and a victim's own cellular material (e.g., epithelial cells from the vaginal wall or the inner cheek). If an evidentiary vaginal swab from a sexual assault were to be processed with an extraction designed to maximize DNA yield from a sample into a single extract, there is a great chance that most male DNA in that sample would go undetected, possibly preventing identification of the perpetrator.

Spermatozoa contained in semen are coated with proteins that make the cells resistant to chemicals used in standard extraction methods. The conditions of a standard organic extraction can be adjusted to allow for the extraction of sperm cells; however, the resultant DNA extract would contain all DNA from the original sample in one tube. This is problematic, as it is very common for a vaginal swab to contain hundreds or thousands of times more DNA from cells of the victim's vaginal lining than from the perpetrator's sperm. Because current analysis methods rely on the amount of DNA in a sample as well as each contributor's relative contribution of DNA, it is likely that a male perpetrator's DNA could be overwhelmed by the amount of female DNA present.

The ability to separate a perpetrator's DNA away from a victim's DNA leads to a great analytic advantage. A sperm cell's resistance to standard extraction methods can be exploited to allow for the differentiation of DNA from different cell types (sperm vs. non-sperm) originating from the same evidence sample. The goal of this extraction method is to produce two separate DNA extracts: one containing sperm DNA, the other containing DNA from all other non-sperm cells.

First described in 1985, the differential extraction process begins similarly to a standard extraction. The initial step of the extraction breaks apart non-sperm cells contained in the sample. This releases DNA from non-sperm cells into solution, while leaving sperm cells intact. The solution containing non-sperm DNA (non-sperm fraction) is removed from the portion of the extraction containing intact sperm cells (sperm fraction). The sperm fraction is then washed to either rinse away, or chemically eliminate any residual non-sperm DNA remaining in the sperm fraction. After the sperm cells have been washed, the sperm fraction undergoes a second extraction step. This extraction is designed to create an environment capable of disrupting the chemical bonds of the protein coat on the sperm cells. Once the protein coat is disrupted, the sperm cells are susceptible to digestion. At the end of the differential extraction process, there exist two DNA extracts from one original sample: one with sperm DNA, and one with non-sperm DNA.

While the goal of the differential extraction is to produce two completely separated DNA fractions from the same sample, the process is not always 100% efficient. It is common to detect carryover from one fraction into the other. For example, vaginal samples that contain a large number of non-sperm cells may show carryover of non-sperm DNA in the sperm fraction. If the evidence sample has a high ratio of non-sperm to sperm cells, a small amount of residual non-sperm DNA may be easily detectable. Also, if any intact non-sperm cells were present after the initial digestion, they would then be subsequently digested with the sperm cells, causing carryover to be detected in the typing results. It is also possible to detect carryover of sperm DNA in the non-sperm fraction. One example of this occurs with sperm cells that have weakened protein coats prior to extraction. Age, storage conditions, or pre-collection environmental effects can all have an impact on the integrity of a sperm cell's protein coat. If the protein coat is weakened in some way, the sperm is subject to premature digestion during the initial non-sperm extraction step.

c) Resin and magnetic bead extraction

Another method of DNA extraction commonly employed is resin, or magnetic bead, extraction. This method of extraction introduces small particles that target either DNA molecules or organic components in the extraction mixture. The particles rely on acid/base characteristics and positive or negative charges to capture and bind to either DNA or cellular components. In the case of a DNA binding reaction, beads with a positive charge are added to an extraction mix. DNA will be captured by the beads and leave unwanted cellular debris and inhibitors free in solution. The beads are then collected through centrifugation or magnetism, and the effluent separated from the DNA bound beads. The charge of the beads is then altered to release the DNA into buffered solution, and the magnetic particles are separated away from the DNA extract.

Other methods will employ a resin added to an extraction mix to capture cellular debris. The resin is polar (hydropobic) and attracts the cellular components. The resin is then pelleted by centrifugation and the remaining extraction mix with DNA and other hydrophilic compounds is left behind. This, however, produces a DNA extract that may contain chemicals that inhibit later laboratory processing.

Resin and magnetic bead extractions are popular due to their potential for automation and efficiency. The extractions can be carried out by robots or with minimal analyst time investment and sample manipulation.

d) Purification of DNA extract

After DNA from a sample is extracted from the cell nucleus, it is generally desirable to “clean up” the extract to remove residual cellular components. The result is a solution consisting of isolated DNA in a buffered solution. Not all extraction processes

involve this step. Some rapid throughput methods of extraction proceed directly from cell lysis to quantitation or amplification. However, these methods also allow for the continued presence of potential inhibitors to downstream processing that purified extracts are able to more easily avoid. Magnetic bead extraction methods usually result in a purified DNA extract without a separate step.

Purification of DNA extracts generally employs some type of filtration device. This usually is in the form of a column of resin or a cup-type device fitted with filter paper or silica. The DNA extraction mix is introduced to the filtration device and DNA adheres to the resin or filter while the remaining cellular debris is washed away. The DNA bound to the filter is then washed and eluted from the column or filter. The elution step can either involve changing the pH of the resin or column, or rely on gravity and inversion of the filtration device. The result of this step is a DNA extract in a buffered solution that is free of cellular debris and hopefully inhibitors to downstream processing.

2) Quantitation

Once DNA is extracted from a sample, it is usually preferable to determine how much DNA is present in an extract. There are several methods that can be used to determine DNA quantity in a sample; however, for human identification there are some considerations that guide the selection of a method. First, for human identification purposes, it is best to employ a quantitation method that is human-specific. It is common for an evidence or reference sample to contain non-human DNA, so methods that detect all DNA present in an extract can result in an inaccurate estimate of DNA available for human testing. For example, a saliva sample from a human contains not only DNA from the individual donating the sample, but also DNA from the bacteria native to the individual's mouth.

Currently, the most widely used method for DNA quantitation is quantitative real-time polymerase chain reaction (qPCR). Polymerase chain reaction (PCR), which will be discussed in detail in the next section, is the process of amplifying specific regions of the DNA molecule. qPCR takes advantage of this process by targeting human specific regions of the DNA molecule.

As a DNA sample is amplified with this technique, targeted regions are copied and amplification product is produced. This product accumulates at a predictable rate. Therefore, by detecting the amount of product present at several times during the reaction, an estimate of the amount of human DNA present in an extract can be determined.

qPCR has another advantage: by targeting specific regions of DNA, a large amount of information can be learned about an extract at an early stage, which in turn can guide downstream processing of the sample. For example, by targeting a region on the Y chromosome, the amount of male DNA in a sample can be estimated. This, compared to the total amount of DNA in a sample, can offer information about the presence of a mixture, or the probative nature of a sample. It may also guide the course of further testing. In a case with suspects where an evidence sample contains a large amount of total DNA and a small quantity of male DNA, it may be preferable to continue forward with male specific STR testing for that sample instead of potentially masking any male DNA present in the sample with the overwhelming amount of female DNA present. By targeting regions of different sizes, information regarding potential inhibition and degradation (DNA quality) can be assessed and technical procedures chosen to overcome the effects in further testing.

3) Polymerase Chain Reaction

Polymerase chain reaction (PCR) is the process of targeting and amplifying specific regions of interest on a DNA molecule. (See People v. Hill, 89 Cal. App. 4th 48, 57–60, 107 Cal. Rptr. 2d 110 (2d Dist. 2001) [PCR/STR testing process generally accepted by the relevant scientific community]; People v. Wright, 62 Cal. App. 4th 31, 41, 72 Cal. Rptr. 2d 246 (1st Dist. 1998) [PCR process generally accepted by the relevant scientific community]; People v. Morganti, 43 Cal. App. 4th 643, 663–666, 50 Cal. Rptr. 2d 837 (1st Dist. 1996), as modified on denial of reh'g, (Mar. 27, 1996) [PCR process generally accepted in the scientific community].) The process takes advantage of the mechanism behind DNA replication by moving the process outside of the body and into a reaction tube. A DNA molecule from a single cell, though large for a molecule, is virtually undetectable

by genetic analysis instrumentation. Therefore, in order to develop a DNA profile, it is necessary to amplify specific regions of DNA. This is made possible through the use of PCR.

PCR in the form it is known today was developed in the 1980's by scientists at Cetus Corporation in Emeryville, CA. In 1993, the Noble Prize in Chemistry was awarded to Kary Mullis for the development of the technique. The procedure involves guiding a DNA molecule through a series of heating and cooling steps in the presence of bases and chemicals that facilitate replication of the specific regions of interest. To begin the process, a quantity of DNA extract is placed in a tube with a mix of reagents that include:

a) DNA primers: These are small sequences of DNA that are complimentary to sequences found on either end of the target region. For STR analysis, these are sequences that are present in all humans, and do not change relative to the amount of repeating chemical sequences between primer sites. There is one set of primers for each locus in a multiplex kit. Most often these primers are labeled with a fluorescent dye which aids in detection by the genetic analyzer, the instrument used to develop a DNA profile.

b) Taq polymerase: Polymerase is an enzyme that facilitates the addition of bases to a replicating strand of DNA. In essence it is the enzyme responsible for assembling the new DNA fragments. Taq polymerase is derived from the bacterial species, *Thermus aquaticus,* which lives near thermal vents and is capable of withstanding and reproducing at extreme temperatures. Taq's ability to remain intact under extreme temperature conditions helped to revolutionize the PCR process. Originally, heat-sensitive polymerases were used in the reaction. This posed a problem because the first step in the PCR is the extreme heating of the sample (e.g., 95°C) to facilitate the break-up (denaturation) of the DNA molecule. This extreme heating, however, also denatured and inactivated the polymerase. In order to overcome this limitation of the enzyme, the analyst conducting the test would be required to add fresh polymerase for each elongation cycle. The introduction of Taq, a polymerase that remains stable at high temperatures, eliminated the need for repeated addition of polymerase. In today's reaction mixes, Taq polymerase is most often held in a temperature neutral (thermostable) mode until activated by an initial high heat step in the process.

c) Deoxyribonucleotide triphosphates (dNTPs): These are the chemical “letters” (bases), used to make the amplified DNA fragments. They are an altered chemical form of the four bases found in the DNA molecule, and are named; deoxyadenosine triphosphate (dATP), deoxycytosine triphosphate (dCTP), deoxyguanine triphosphate (dGTP), deoxythymine triphosphate (dTTP).

d) Buffer solution: This solution of chemicals gives the DNA molecule a stable environment in which to exist. It closely replicates the pH (acid/base balance) and chemical conditions found in the body.

e) Potassium and magnesium ions: These charged particles are present to draw chemicals and molecules that can get in the way of the PCR away from the reaction.

Once the reaction mix is prepared and DNA is added to the reaction tube, the DNA sample, or template, is placed in an instrument called a thermalcycler. This device consists of a programmable heating and cooling block that can rapidly cycle between high and low temperatures. A full PCR run takes between two to five hours, and consists of several cycles of heating, cooling, and holding at specific temperatures that allow chemicals and enzymes in the reaction mix to amplify the template DNA. The phases of the PCR are:

a) Initialization: This phase is used for reactions that contain thermostable Taq. This phase involves high temperature for a sustained period of time (e.g., 95°C for 11 minutes). The Taq is activated and the DNA template undergoes its first denaturation step.

b) Denaturation: This phase is generally at or near the initialization temperature and lasts for approximately one minute. The high temperature denatures (splits apart) the DNA strands and makes the base sequence available to the primers.

c) Annealing: The temperature is quickly lowered from the denaturation temperature to a temperature that promotes the binding of the primers to the DNA template (e.g., 58°C) and held for approximately one minute. Primers in this phase arrange themselves on the template and remain there through the next phase. The base composition of the primers will affect their ability to anneal to the template. Accordingly, the temperature used for this phase will generally vary from kit to kit. This becomes a concern during the development of primer sequences for new kits. If primers for different loci vary by too wide a range (e.g., ±3°C), amplification may be affected for some loci and not others.

d) Extension: The temperature is now raised again to promote the action of the Taq. The temperature for this phase is hotter than the annealing phase but not so hot as to denature the primers from the template or inhibit the action of the Taq (e.g., 72°C). In this phase the Taq seeks out the primer template hybridization point and uses this as a starting point for DNA synthesis. One by one the base sequence of the template is read and complimentary dNTPs are added to the growing DNA product strand. This phase continues for one minute.

At this point in the reaction, the second through fourth steps are repeated several times. Generally, between 25 and 30 cycles are performed. Because the PCR product grows exponentially, by the end of the reaction millions of copies of each targeted region exist. The number of cycles is optimized for each kit through developmental validation. Because the template DNA is double-stranded, when denatured it produces two single strands, both with an STR region and primer binding site. Each locus, therefore, has two primers; a forward and reverse, one on each strand. As the extension phase begins, dNTPs are added beginning at the bound primer and continuing along the length of the DNA template. There is no inherent stop signal for the Taq polymerase, so the extention phase of the reaction continues along each of the template strands until the temperature ramps up for the next denaturation cycle.

In the first PCR cycle, the extension of the product will continue on past the end of the STR region in both directions. This produces two double-stranded amplification products with one complete strand from the original template molecule and one amplified product strand that is longer than the STR region, but not as long as the original template strand. The next extension phase produces four double-stranded products; two with the original template strands paired with new strands that are longer then the STR region, but shorter than the template, and two products with the product strands from the previous cycle (the new template strands) paired with new product strands that extend from the primer site to the end of the template strand. By the time the third cycle reaches its extension phase, most of product being produced is only the length of the targeted STR region. The production of PCR product then grows exponentially from the third cycle on.

e) Final extension: This final step in the PCR is a hold phase at 60°C for anywhere from 30 to 90 minutes. The time varies by kit and is determined through validation. This final extension is performed to overcome a phenomenon specific to PCR. At the end of each PCR product, one dATP is added. The final hold step is to ensure that all double stranded product receive this addition.

4) Capillary Electrophoresis

At the end of the PCR amplification process, the template DNA that was introduced at the beginning of the reaction is now a solution of millions of fluorescently labeled copies of STR fragments from different genome locations. In order to visualize and analyze the STR fragments present in the sample, they must first be separated and identified. Electrophoresis is an analysis technique that separates STR fragments based on size. To do this, DNA is applied to a gel or polymer matrix. Then an electric current is applied which causes the DNA in the sample to migrate through the matrix. Over a period of time, different sizes of DNA in a sample will become separated according to their ease of movement through the gel or polymer. The smaller a DNA fragment is, the faster it will migrate through the matrix; larger fragments will migrate at a slower rate. Once the fragments in a DNA sample are separated, they can be individually identified, sized, and characterized.

Two types of electrophoresis used for DNA analysis are gel electrophoresis and capillary electrophoresis. Gel electrophoresis involves loading a DNA sample onto a solidified molded gel. The gel is submerged or surrounded by a buffer solution that conducts an electric charge through the gel. Capillary electrophoresis uses a thin glass tube only a fraction of a millimeter

wide, filled with a viscous liquefied polymer. Capillary electrophoresis is currently the most widely used method of DNA fragment separation. (See People v. Henderson, 107 Cal. App. 4th 769, 785, 132 Cal. Rptr. 2d 255 (4th Dist. 2003) [capillary electrophoresis generally accepted in the relevant scientific community].) The software predominantly used with the capillary electrophoresis process is GeneMapper®, with GeneScan® and Genotyper® software also used by some laboratories. (See People v. Smith, 107 Cal. App. 4th 646, 656, 132 Cal. Rptr. 2d 230 (2d Dist. 2003).)

A capillary electrophoresis system is comprised of: two charged terminals (the positively charged anode and the negatively charged cathode), housed in a buffer solution, and bridged by a capillary filled with liquid phase polymer. DNA is a negatively charged molecule. When an electric current is applied to the system, single stranded DNA fragments are drawn into the polymer filled capillary at the cathode end and migrate toward the positively charged anode. In order to keep the DNA fragments single stranded, the amplified product is mixed with the chemical formamide, heated, and then cooled rapidly to prevent recoupling of the complimentary DNA strands. As the fragments travel through the polymer matrix inside the capillary, they separate according to their size. In order to record the data about the migration and size of the amplified fragments, the capillary electrophoresis system is housed inside an instrument called a genetic analyzer.

a) Genetic analyzer

Inside a genetic analyzer, the electrophoresis system is mounted with the capillary housed inside an oven. This keeps the capillary at a constant temperature and facilitates efficient and consistent migration from one sample injection to the next. The electrophoresis system includes a mechanism for filling the capillary with fresh polymer before each new sample injection. This mechanism may either be a syringe or set of syringes that are operated with an automated plunger to dispense polymer, or by a self-contained automated pump system. Buffer reservoirs surround an anode and cathode, and are coupled with the ends of the capillary. Depending on the model of genetic analyzer, an instrument may have anywhere from one to 96 capillaries in one instrument. The most common configurations used are the 4-, 8-, 16-, and 24-capillary array instruments.

The genetic analyzer's detection system consists of a laser and camera that capture light emissions from the fluorescent dyes tags attached to each amplified DNA fragment. As each fragment passes by a window at the anode end of the capillary, they are exposed to laser light. The laser's energy excites the fluorescent dye attached to the fragment and causes it to emit light at a specific wavelength. The emitted light is detected by the camera's color filters and registers as a peak in the baseline of the instrument's data display. The intensity of the fluorescence, and ultimately the height of the peak, is directly proportional to the amount of DNA amplified.

b) Spectral calibration and pull-up

As fluorescently tagged fragments are detected by the genetic analyzer's camera, each wavelength of light emitted by a fragment is recorded and sorted by the camera filter. The bulk of the fluorescence is detected by the color filter associated with the emitted light's wavelength. However, a portion of the fluorescence is also detected by the other color filters. This overlapping fluorescence, during data interpretation, translates into allelic peaks in one color channel also showing up as peaks in one or more other channels. These peaks are referred to as spectral pull-up. In order to avoid having the detection of erroneous signal in other color channels interfere with data interpretation, the amount of spectral overlap routinely observed from a genetic analyzer is measured and corrected for. This correction, referred to as a spectral calibration, is applied to each sample as data are collected from the instrument.[1]

The amount of spectral overlap varies between instruments. As the amount of spectral overlap observed in the data from an instrument will fluctuate over time, each instrument needs to have a spectral calibration performed periodically to ensure that the correction factor is accurate. The spectral calibration for an instrument is generally stable for several months, and commonly for more than a year. An increase in observed pull-up peaks in analyzed data is an indication that a new spectral calibration is necessary.

For forensic STR fragment genetic analysis, a capillary 36 centimeters long is used. Each DNA sample takes approximately half an hour to migrate through the capillary with all of its fragments passing by the detection window. As each fragment reaches the end of the capillary, it is discarded into the anode buffer chamber. When a sample run is over, the polymer in the capillary is replaced and a new sample is injected and run. Therefore, the set of data collected by the camera as each fragment passes by the detection window is the enduring record of each run. This is referred to as the raw data, and is the merged collection of images collected from the camera at rapid intervals throughout the run. The actual DNA fragments injected produce no permanent physical record. However, each amplified DNA sample contains enough product for numerous injections. Two or more injections of each sample may be performed on each run to ensure reproducible results.

5) Data Analysis and Interpretation

After a genetic analyzer run is complete, the next step in the process is to size each peak detected and assign allele designations. This can be done manually by an analyst, but is almost exclusively accomplished by software programs.

a) Data analysis software

Software programs can carry out the thousands of complex calculations involved in data analysis in a matter of minutes. The same process may take an analyst days to complete. The first step in this process is peak detection. Each laboratory, through its internal validation, must determine the criteria for identifying allelic DNA peaks. These criteria include:

1) Analytical threshold: Fluorescence detected by a genetic analyzer camera is measured in relative fluorescence units (RFUs). The more fluorescence measured by the camera, the higher the peak represented on the data display. The analytical threshold is the level at which peaks above a set height are considered possible DNA peaks and not just background fluorescence. Every amplified sample will exhibit a level of background fluorescence. A laboratory must determine an analytical threshold for each test kit and instrument platform used. Peaks that do not cross the analytical threshold are considered indistinguishable from background fluorescence and are not labeled by the software. These peaks are typically not used for data interpretation. (See State v. Bander, 150 Wash. App. 690, 208 P.3d 1242, 1247 (Div. 1 2009) ["Testing laboratories determine the threshold RFU value that must be exceeded in order to report the presence of a specific allele and to declare that two profiles have matching alleles at particular loci"].) However, the fact that different laboratories may subscribe to different RFU thresholds for interpretive purposes does not render any particular protocol unreliable in that respect as a matter of law. In People v. Stevey, 209 Cal. App. 4th 1400, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013), the court held that no admissibility hearing was required to assess whether the laboratory's RFU threshold "fell within generally accepted scientific guidelines or standards." (209 Cal. App. 4th at 1417.) It noted that appellate decisions from other parts of the country "suggest that the county crime lab's protocol of identifying only peaks above 75 RFU's as alleles appears to be within the range of protocols used throughout the country. Moreover, the fact that some laboratories interpret results more conservatively than others does not indicate the absence of general acceptance of a scientific technique." (*Id*. at 1418.)

In a litigation context, the evidentiary implications of "inconclusive" results may be a subject of *in limine* motions. For example, the prosecution may seek to permit its expert witness to testify that the below-threshold RFU results are "consistent" with the defendant being the source of the DNA sample, without actually identifying the data observed. The defense may seek to preclude this type of testimony as scientifically invalid and speculative.

2) Peak morphology: A true alleleic DNA peak is shaped like a thin steep bell curve. Assessing each peak's shape helps to determine if it is a true allelic peak or simply an artifact of amplification or electrophoresis. An allelic peak will be roughly symmetrical and exhibit a slope up from the baseline, a rounded apex that is neither too pointed or too broad, and similar slope back down to the baseline. Peaks or spikes that are thin and extremely pointed are often attributable to electrical surges during a run. Squat, broad peaks are often attributable to conglomerations of fluorescent dye present in the PCR product

(dye blobs). Genetic analysis software uses a set of algorithms to evaluate each peak detected. If a detected peak above the analytical threshold falls outside of the peak morphology parameters specified by the laboratory, those peaks may be flagged for evaluation by the analyst. The analyst then has the responsibility to determine the nature of the peak, and whether to interpret it as an artifact or an allelic peak.

b) Size standards

In order to determine the size, in base pairs (bp), of each peak detected by the genetic analyzer, a size standard is run with each sample. A size standard is a set of engineered DNA fragments of known sizes that acts as a ruler to measure the size of the DNA fragments in a sample. DNA fragments will separate at a constant rate over time relative to their size. Therefore, an unknown fragment's size may be determined by comparing its migration with that of the known DNA fragments in the size standard. The size standard may also be referred to as an internal lane standard. While DNA fragments will migrate at a constant rate within a run, subtle fluctuations in environmental conditions in the capillary or ambient run conditions (i.e., the air temperature in the room) make comparison of DNA peaks in one run to sizing peaks in a separate run inaccurate. Therefore, each amplified DNA sample is mixed with a size standard before injection on the genetic analyzer. Analysis software then identifies the sizing peaks in each run and compares and sizes peaks from the test sample to the internal standard.

c) Allelic ladder

Each genetic analyzer run will also include one to several allelic ladder samples. An allelic ladder is a DNA sample with a range of common alleles for all loci in an amplification kit as determined by the manufacturer. It generally contains the most commonly characterized alleles from each locus tested. However, allelic ladders may vary slightly between amplification kits and manufacturers. After all peaks in a sample are sized, the sized peaks are then compared against the allelic ladder(s) from the run. The unknown peak is then assigned an allele value according to the ladder allele to which it matches in size.

d) Non-allelic peaks

Not all peaks detected in a sample will match, or size, to a corresponding ladder allele. These peaks will be tagged as “off-ladder alleles.” There are two main reasons that this occurs.

1) Microvariants: One reason a peak may be tagged as an off-ladder allele is if the peak is a true allele that does not correspond directly to an allele represented in the ladder. These peaks are called microvariants and are actually quite common. In fact, several microvariants are included in allelic ladders from each manufacturer (e.g., the 9.3 allele at TH01). (Butler, *Forensic DNA Typing,* Second Edition (2005) Appendix 1.) Microvariants occur when an STR fragment includes a partial repeat motif somewhere in its repeat region. These alleles are denoted by the number of full repeats, followed by a decimal, then the number of bases in the partial repeat. For example, the 32.2 microvariant in D21S11 has 32 full repeats and two additional bases.

It is also possible for a microvariant to occur that is not included in the allelic ladder. These microvariants are tagged as off-ladder alleles. In order to assign an allele value to the peak, the analyst must calculate which microvariant it is based on where the peak falls between two sized ladder alleles. For example, if an off-ladder peak that has been evaluated as a microvariant sizes approximately one base size larger than the ladder allele directly proceeding it in size (e.g., 13 allele at D8S1179), and approximately three bases in size from the next ladder allele (e.g., the 14 allele), then the microvariant is sized manually as a 13.1 allele.

2) Artifacts: The function of the camera on a genetic analyzer is to record all fluorescence observed through the detection window of the capillary. As it does so, the camera does not discriminate between true, labeled, allelic DNA fragments and erroneous fluorescence. As the analysis software sizes and labels each peak detected, any peak above the analytical threshold that falls within the allelic range for a locus will be labeled. These may be labeled as allelic peaks or as off-ladder alleles. However, not all peaks labeled by analysis software are true allelic DNA peaks. They may be what are referred to as artifacts,

and are unintended by-products of the testing process rather than actual genetic characteristics. (See Roberts v. U.S., 916 A.2d 922, 931 (D.C. 2007).)

Artifacts can be a result of the amplification process or occur during electrophoresis. One of the most common amplification artifacts occurs when an extra nucleotide, usually an adenine (A), is added to the end of an amplified STR fragment by the polymerase. This addition results in an STR fragment that is one base pair longer than the intended target length. This phenomenon is well characterized and compensated for in the allelic ladders of commercially available amplification kits. If this process is not completed on all DNA fragments in the PCR, the resulting electrophoresis data will exhibit DNA peaks that are split with one point labeled as a full repeat (e.g., a 7 allele at locus TH01) and another point one base pair smaller (e.g., 6.3 allele, or an off-ladder allele at the 6.3 position).

To overcome this effect, at the end of the PCR a sample is held for a time at a temperature that promotes the A addition (e.g., 45 minutes at 60°C). The amount of time required to ensure compete addition varies by amplification kit and should be optimized by a laboratory during validation. Even with the final extension step of amplification, incomplete nucleotide addition (-A) may appear in analyzed data. In samples with high amounts of template DNA, and consequently copious amounts of PCR product, the optimized final extension time or adenine resources of the PCR mix may be insufficient to complete the A addition on every fragment. This may result in labeled -A peaks. In samples with extremely high concentrations of PCR product, -A peaks as high as the adenylated peak may be observed.

During electrophoresis conglomerations of fluorescent dye can be detected and labeled as a DNA peak. Electrical spikes can also occur during the run. These may be detected as a sharp spike in the baseline of a sample. Both of these phenomena are usually easily distinguishable from allelic DNA peaks and are handled by the analyst according to laboratory technical procedures.

e) Stutter

As an STR fragment is amplified, it is common for either the strand that is being copied, or the newly replicated strand of DNA, to “slip” and result in the formation of a PCR product that is one base repeat shorter than the intended fragment length. These peaks are called stutter. This particular type of stutter is sometimes referred to as N-4 stutter because the resulting peak is four base pairs shorter than the intended fragment. During analysis, this manifests as a small peak, one repeat in front of the actual allelic peak. The amount of stutter varies between loci and even between alleles within a locus. Generally, the amount of stutter observed increases with the number of repeats and the size of the locus. Laboratories may choose to apply a stutter filter during the analysis process. This filter allows the software to identify peaks approximately four base pairs away from an allelic peak that are below a certain percentage of the allelic peak height. The software then will omit the label from these peaks. The stutter percentage is calculated by dividing the peak height (RFU) of the potential stutter peak by the peak height of the allelic peak. For example, if a locus has a 10% stutter filter, a peak at the 12 allele position that is 200 RFU will be filtered as stutter for the 2500 RFU allelic peak at the 13 position.

Stutter slippage can also result in a one repeat increase, sometimes referred to as N+4 stutter. This type of stutter, though not uncommon, occurs at a much lower rate, and at a lower percentage than N-4 stutter.

Footnotes

1 For single capillary instruments (e.g., the ABI Prism 310), spectral overlap is corrected for by a matrix. A matrix applies the same spectral correction function as a spectral calibration, but is applied to data after it has been collected from the instrument.

Forensic DNA Evidence: Science and the Law § 3:5

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Chapter 3. Developing a DNA Profile: From Crime Scene to Laboratory

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§ 3:5. Consuming a sample

During the evidence evaluation and sampling process, every effort is made to conserve an adequate amount of sample for subsequent testing. In the case of a single swab, one half may be taken. In the case of a set of swabs, (e.g., four vaginal swabs from a sexual assault kit), an analyst may take one whole swab. However, oftentimes an evidence sample is not large enough to reasonably expect that reliable DNA typing results may be detected from a portion of the item (e.g., a single, very small blood stain). In this situation, where splitting an evidence item may interfere with the ability to detect any meaningful DNA typing results, the analysis will likely consume the sample. In order to do this, laboratory practice may require the analyst to first retain permission to consume the sample from an appropriate source, such as the case prosecutor (who presumably will coordinate response to the request with opposing counsel), or from the investigating or reporting law enforcement officer if the case has not yet been assigned for prosecution. For additional discussion of sample consumption and splitting, see § 10:4.

Because permission to consume a sample is obtained before sampling occurs, the success of the extraction process at that time is generally unknown. Even if an evidence item is consumed during sampling, however, the possibility for further testing may still exist. If enough DNA was extracted from an evidence item, a portion of extract may still be available for amplification.

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Forensic DNA Evidence: Science and the Law § 3:6

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§ 3:6. Observation of analysis by opposing party

If the need arises to consume a sample for testing, the opposing party may seek an opportunity to have an expert of their choosing present to observe the testing process. Observation may include only the initial examination and evidence sampling, or the entire testing process, which could span several days. For additional discussion of requests by an opposing party to observe testing, see § 10:9.

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Forensic DNA Evidence: Science and the Law § 4:1

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Chapter 4. Quality Assurance, Training, and Accreditation

§ 4:1. Quality assurance in a forensic DNA laboratory

1) Overview

In 1985 Sir Alec Jeffreys used a DNA technology technique he developed to solve the rape homicides of two teenage girls in England. In 1986, a private laboratory used a different DNA technology technique in a case in Pennsylvania and during that same time, the FBI began developing yet another DNA technique for use in their casework.[1] This rapid emergence of forensic DNA technology proceeded without uniform testing techniques, quality control measures, or requirements of professional education and experience for the scientists performing the DNA analyses. As this new technology began to demonstrate its power to associate a suspect to a crime, the forensic science community realized that quality assurance standards needed to be established to address concerns that the courts had with the validity of these new tests.

2) Quality Assurance Defined

Quality assurance is the systematic approach of monitoring and evaluating the quality of a work product. For forensic DNA technology, the quality assurance system must include elements that address the education and experience of the personnel, the specifications and calibration for equipment and critical reagents, the validation of analytic methods, the use of appropriate controls and standards, the procedures for handling samples, the interpretation of data and report writing, proficiency testing, internal and external audits, and policies that specify corrective actions to address deficiencies.[2] To implement a quality assurance system, appropriate standards for each of the above elements need to be written and adhered to.

Footnotes

1 Lawrence A. Presley, The Evolution of Quality Standards for Forensic DNA Analysis in the United States, Profiles in DNA 10, 10–11 (Sept. 1999).

2 National Research Council, DNA Technology in Forensic Science 98-103 (1992).

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Forensic DNA Evidence: Science and the Law § 4:2

Forensic DNA Evidence: Science and the Law | June 2024 Update
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Chapter 4. Quality Assurance, Training, and Accreditation

§ 4:2. Quality assurance DNA standards

In 1988, a group of scientists, organized and sponsored by the Federal Bureau of Investigation, began addressing the issue of quality assurance in a forensic DNA laboratory. This group, the Technical Working Group on DNA Analysis Methods (TWGDAM), consisted of scientists from the US and Canada. In 1989, TWGDAM issued the guidelines for quality assurance in DNA analysis. Two other revisions were released in 1991 and 1995. Although compliance with these standards was not mandatory, many laboratories attempted to follow them, and these guidelines became the basis of the DNA quality assurance standards that followed.

1) DNA Advisory Board (DAB)

In 1994, Congress passed the DNA Identification Act. It included requirements for the development of quality assurance and proficiency testing standards. Specifically, the law charged the Director of the FBI to appoint an advisory board on DNA quality assurance methods. Board members were to be selected from nominations from the head of the National Academy of Sciences and professional societies of crime laboratory officials. The board members were to include members from State, local, and private laboratories, along with molecular geneticists and population geneticists not affiliated with a forensic laboratory and a representative from the National Institute of Standards and Technology. Nobel laureate Dr. Joshua Lederberg served as the board's first chairman. The DNA Advisory Board issued the first set of quality assurance standards for DNA testing laboratories in 1998 and in 1999 issued the Quality Assurance Standards for Databasing Laboratories. The standards defined and specified the requirements for meeting the standards in the following categories: planning and organization, personnel qualifications and training, facilities, equipment calibration and maintenance, evidence handling procedures, validation, analytical procedures, proficiency testing, casework report writing and review, corrective action, audits, safety and subcontracting of analytical testing. Although the DAB was only funded for five years, the FBI sponsored Scientific Working Group on DNA Analysis Methods or SWGDAM (formally TWGDAM) took over for DAB, revising and updating the forensic DNA quality assurance standards.[1]

The DNA Identification Act of 1994 did not make compliance legally binding, but it did require all federally operated DNA laboratories, all DNA laboratories receiving federal funds (federal grants), and those laboratories receiving the Combined DNA Index System or CODIS software to comply with the DAB Quality Assurance Standards.

2) SWGDAM/FBI Standards

As stated above, the DAB issued two quality assurance documents: the Quality Assurance Standards for Forensic DNA Testing Laboratories and the Quality Assurance Standards for Databasing Laboratories. With DAB no longer in existence, the FBI called upon SWGDAM to assist in reviewing and updating the sets of standards. A version was released in 2004, followed by revisions in 2009 and 2011. And the latest, now binding version, went into effect in 2020.

The categories or breakdown of the standards specified in the 2009 documents are the same as those established by the DAB in its original set of standards. The complete listing of the standards can be found at the FBI's website, but the following provides examples of the requirements necessary to meet each categorized standard:

a. Quality Assurance Standards for Forensic DNA Testing Laboratories (July 1, 2009)

i. Quality Assurance Program

1. Documented and appropriate for testing program.

2. Have a proficiency test program, procedure for corrective action, policy regarding audits, maintain training records, continuing education program, and have policies regarding case file management and court testimony monitoring.

ii. Organization and Management

1. Have a managerial staff with the authority and resources to discharge their duties.

2. Have a technical manager or leader who is accountable for the technical operations.

3. Have a casework CODIS administrator.

iii. Personnel

1. Have a written job description for personnel that include responsibilities, duties, and skills.

2. Have a documented training program.

3. Maintain records on the relevant qualifications, training, skills, and experience of technical personnel and maintain a continuing education program.

4. Degree requirements for the technical leader is at minimum a Master's degree in Biology, Chemistry, or forensic science related area and successfully completed a minimum of 12 semester or equivalent hours of a combination of undergraduate and graduate course work covering the subject areas of biochemistry, genetics, and molecular biology (molecular genetics, recombinant DNA technology), or other subjects which provide the basic understanding of the foundation of forensic DNA analysis as well as statistics and/or population genetics as it applies to forensic DNA analysis.

5. The degree requirements for the technical leader may be waived by the American Society of Crime Laboratory Directors (ASCLD) or other organization designated by the Director of the FBI. The waiver is permanent and portable.

6. The examiner/analyst shall have a minimum of a BA/BS or its equivalent degree in biology, chemistry, or forensic science related area and must have completed college course work covering subject areas of biochemistry, genetics, and molecular biology, as well as course work and/or training in statistics and population genetics as it applies to forensic DNA analysis.

7. Examiners must complete a qualifying test before beginning independent casework responsibilities.

8. The casework CODIS administrator shall participate in the FBI sponsored training in CODIS software within six months of assuming the duties of the casework CODIS administrator. The casework CODIS administrator shall complete the FBI sponsored auditor training within one year of assuming their CODIS administrator duties.

iv. Facilities

1. Access to the laboratory shall be controlled and limited.

2. Prior to PCR amplification, evidence examinations, DNA extractions, and PCR setup are conducted at separate times or in separate spaces.

3. Amplified DNA product is generated, processed and maintained in a room separate from the evidence examination, DNA extractions and PCR set-ups area.

v. Evidence Control

1. Evidence is marked with a unique identifier.
2. Chain of custody for all evidence is maintained.
3. Where possible, the laboratory shall retain or return a portion of the evidence sample or extract.
4. The laboratory shall have and follow a documented policy for the disposition of evidence that includes a policy on sample consumption.

vi. Validation

1. Developmental validation shall precede the use of a novel methodology for forensic DNA analysis.
2. Peer-reviewed publication of the underlying scientific principle(s) of a technology shall be required.
3. Internal validation of all manual or robotic methods shall be conducted by each laboratory and reviewed and approved by the laboratory's technical leader prior to using a procedure for forensic applications.

vii. Analytical Procedures

1. The laboratory shall have and follow written analytical procedures approved by the technical leader.
2. The laboratory shall use reagents that are suitable for the methods employed.
3. The laboratory shall identify critical reagents and evaluate them prior to use in casework.
4. The laboratory shall monitor the analytical procedures using the following controls and analytical standards.

   a) Quantitation standards when quantitation procedures are used.

   b) Positive and negative amplification controls associated with the samples being typed shall be amplified concurrently with the samples at all loci and with the same primers.

5. The laboratory shall have and follow written guidelines for the interpretation of data.
6. The laboratory shall have and follow a documented policy for the detection and control of contamination.

viii. Equipment Calibration and Maintenance

1. The laboratory shall use equipment suitable for the methods employed.
2. The laboratory shall have a documented program for conducting performance checks and calibration of instruments and equipment.

ix. Reports

1. The laboratory shall have written procedures for taking and maintaining casework notes to support the conclusions drawn in laboratory reports.

x. Review

1. The laboratory shall conduct administrative review and technical reviews of all case files and reports to ensure conclusions and supporting data are reasonable and within the constraints of scientific knowledge.

2. The laboratory shall have a procedure to address unresolved discrepant conclusions between analysts and reviewer(s).

xi. Proficiency Testing

1. Analysts, technical reviewers, technicians, and other personnel designated by the technical leader, shall undergo semi-annual external proficiency testing in each technology performed in which they participate in casework.

2. The laboratory shall use an external proficiency test provider that is in compliance with the current proficiency testing manufacturing guidelines established by the American Society of Crime Laboratory Directors/ Laboratory Accreditation Board or be in compliance with the current International Organization for Standardization.

xii. Corrective Action

1. The laboratory shall establish a corrective action plan to address when discrepancies are detected in proficiency tests and casework analysis.

xiii. Audits

1. The laboratory shall be audited annually in accordance with these standards.

2. At least every two years, an external audit shall be conducted.

xiv. Safety

1. The laboratory shall have and follow a documented environmental health and safety program.

xv. Outsourcing

1. A vendor laboratory performing forensic DNA analysis shall comply with these standards and the accreditation requirements.[2]

b. Quality Assurance Standards for Forensic DNA Testing Laboratories (Revisions effective September 1, 2011)

Minor revisions were implemented in September, 2011. These revisions to the quality assurance standards provided states with additional flexibility in data processing, analysis, and technical review. The revisions can be found on the FBI's website. Some of the notable changes include:

i. Personnel

1. A contract employee who may be also employed by other NDIS[3] participating laboratories may be hired if it is found that no conflict of interests exist.

2. Contract employees working as an analyst must meet the same education and experience requirements as regular employees of the laboratory.

3. The laboratory's technical leader may be a contract employee.

ii. Outsourcing

1. Prior to the upload or search of DNA data from a vendor laboratory in SDIS, qualified personnel employed by a NDIS participating laboratory must review the DNA data to verify specimen eligibility and the correct specimen category for entry into CODIS.

2. If a NDIS participating laboratory outsources technical review to a vendor, an on-site visit is not required.

3. A technical leader of a NDIS participating laboratory may accept an on-site visit of a vendor laboratory that is conducted by a designated FBI employee.

c. Quality Assurance Standards for DNA Databasing Laboratories

The official Quality Assurance Standards for DNA Databasing Laboratories can also be found at the FBI's website. The categories of standards are the same as those for the Quality Assurance Standards for Forensic DNA Testing Laboratories and most of the specific requirements for each standard are the same. The main differences between the two standards are:

i. Sample Control (The Quality Assurance Standards for Forensic DNA Testing Laboratories specifies the requirements for evidence as opposed to samples)

1. The laboratory shall have a documented sample inventory control system to ensure the integrity of database and known samples.

2. Where possible, the laboratory shall retain the database sample for retesting for quality assurance and sample confirmation purposes.

ii. Analytical Procedures

1. The laboratory shall have a documented procedure for the resolution, verification and reporting of database matches.

iii. Review

1. The laboratory shall have written procedures for reviewing DNA records and DNA database information, including the verification and resolution of database matches.

2. The laboratory shall perform a technical review of all DNA records prior to uploading or searching in the state's DNA index system (CODIS).

3. The release of personally identifiable information associated with a database hit shall require an administrative review of the official correspondence.

iv. Proficiency Testing

1. Laboratories that use a team approach to database analysis may do so, on external proficiency tests.

v. Outsourcing

1. A contract or vendor laboratory performing DNA databasing analysis shall comply with these Standards and the accreditation requirements of federal law.[4]

d. Addendum to the Quality Assurance Standards for DNA Databasing Laboratories (December, 2014)

With the advent of Rapid DNA testing technology and the acceptance of this technology by the FBI, quality assurance standards were developed and specified in an addendum to the existing databasing standards. These standards can be found at the FBI's website. Some of the important additions to the Quality Assurance Standards for DNA Databasing Laboratories include:

i. Analytical Procedures

1. Rapid DNA analysis is a fully automated process of developing a CODIS CORE STR profile. The process consists of an automated extraction, amplification, separation, detection and allele calling without human intervention. The analytical process incorporates a preassembled set of reagents contained in a Rapid DNA cartridge. For each new rapid DNA cartridge, the laboratory must evaluate at least one cartridge from the cartridge lot number. A positive sample control and a negative sample control must be processed for each new rapid DNA cartridge lot number.

2. The laboratory must check its Rapid DNA Analysis procedure annually against an appropriate and available NIST or standard reference material traceable to a NIST standard.

3. The laboratory must include an allelic ladder with each Rapid DNA instrument run.

4. The laboratory must include an Internal Lane Standard with each sample.

5. The laboratory is not required to analyze quantitation standards, reagent blanks controls, positive amplification controls, and negative amplification controls on a Rapid DNA Instrument.

ii. Equipment Calibration and Maintenance

1. Laboratories must complete performance checks their Rapid DNA Instruments on a quarterly basis. The minimum requirement for a performance check is to run a positive sample control in each lane prior to analysis of reference samples.

iii. Proficiency Testing

1. Individuals performing Rapid DNA analysis using a Rapid DNA instrument with an NDIS approved STR typing kit and an internally validated expert system are not required to be proficiency tested on Rapid DNA Testing Analysis.

2. Analysts and technical reviewers who only complete the interpretation or technical reviews for Rapid DNA Analysis and do not participate in other scheduled DNA proficiency tests must be externally proficiency tested twice per year.

e. Quality Assurance Standards for Forensic DNA Testing and Databasing Laboratories (Revisions effective July 1, 2020)

Significant revisions to the quality assurance standards were released in July 2020. The most notable of the changes was the consolidation of the discussion sections, previously included at the end of each standard, into a separate guidance document. The Guidance Document for the FBI Quality Assurance Standards for Forensic DNA Testing and DNA Databasing Laboratories applies to both the forensic and databasing QAS audit documents, and provides additional guidance to assist in determining compliance. Some of the notable changes include:

i. Scope

1. The standards are applicable to laboratories using Rapid DNA instruments on casework reference samples.

ii. Quality Assurance Program

1. The laboratory shall conduct an independent, annual review of case files deemed by the technical leader to be representative of cases worked. This review is independent of the external audit.

iii. Organization and Management

1. The laboratory shall have a contingency plan for a vacated technical leader position, or if the laboratory has less than two full-time qualified analysts.

2. The laboratory shall define the date of hire or the date of qualification as the criteria by which it will determine the applicable version of the Quality Assurance Standards used for education, experience, and training requirements.

iv. Personnel

1. The technical leader shall be qualified or have received training in each technology used in the laboratory within one year of appointment.

v. Facilities and Sample Control (DNA Databasing document only)

1. The laboratory shall have a policy for securing samples and work product in progress.

vi. Validation

1. All validation data must be retained and available for review.

vii. Analytical Procedures (Casework document only)

1. The laboratory shall have a procedure addressing the reinterpretation of legacy data.

viii. Equipment Calibration and Maintenance

1. The laboratory must document all performance checks.

ix. Corrective Action

1. The laboratory must have and follow a procedure for addressing non-conforming work.

x. Professional Development

1. The laboratory shall have a documented program to ensure technical personnel maintain qualifications through continuing education, literature review, and testimony review.

xi. Outsourcing Ownership

1. The laboratory shall have a procedure to verify the integrity of DNA data for purposes of ownership.

Revisions to The Guidance Document for the FBI Quality Assurance Standards for Forensic DNA Testing and DNA Databasing Laboratories went into effect January, 1, 2023. The revisions include updated guidance relating to:

i. Personnel

1. Coursework requirements used to assess the qualifications of a Technical Leader.

2. Defining the duties and authority of a Technical Leader.

3. Coursework requirements used to assess the qualifications of an analyst.

ii. Validation

1. Internal validation compliance requirements for software used as “a component of instrumentation, for the analysis and/or interpretation of DNA data, or for statistical calculations.”

2. Requirements for the use of certified reference material prior to the implementation of an NDIS approved Rapid DNA system or for a Rapid DNA instrument used for modified Rapid DNA analysis.

3. The use of modified procedure evaluations to fulfill critical equipment performance check requirements.

4. Validation requirements for modified procedures.

5. Validation and performance testing requirement for software products.

iii. Analytical Procedures

1. Criteria for the evaluation of analytical standards and controls and the use of sample data processed with failed controls.

2. Appropriate controls for quantification methods.

iv. Equipment

1. Validation and performance check requirements based on the nature of new and/or modified methods.

v. Reports

1. Identification of evidence examined and samples collected from and evidence item in the report.

vi. Review

1. The assessment of all work by two individuals.

2. Training requirements for technical reviewers.

vii. Proficiency Testing

1. The interval between proficiency tests for an analyst.

2. Testing interval requirements for analysts authorized to perform more than one testing methodology.

viii. Audits

1. The qualifications for individuals on an audit team.

2. Timing requirements for internal and external QAS audits.

3. Evaluation of and approval of validations during audits.

4. Submission requirements for external audit documentation.

ix. Outsourcing Ownership

1. Compliance requirements for laboratories transferring ownership of DNA extracts for testing and analysis.

Footnotes

1 Ragsdale & Butler, Introduction to the DNA Advisory Board Standards, President's DNA Initiative Workshop at NFSTC (Aug. 24, 2005).

2 FBI-Quality Assurance Standards for Forensic DNA Testing Laboratories www.fbi.gov/about-us/lab/codis/qas_testlabs.

3 National DNA Index System.

4 FBI Quality Assurance Standards for DNA Databasing Laboratories www.fbi.gov/about-us/lab/codis/qas_databaselabs.

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Forensic DNA Evidence: Science and the Law § 4:3

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Chapter 4. Quality Assurance, Training, and Accreditation

§ 4:3. Accreditation

Accreditation is a process in which a professional association or organization grants recognition to a laboratory for demonstrated ability to meet predetermined criteria for established standards. For forensic laboratories, accreditation means that the laboratory has set up a quality management system that adheres to established standards. To qualify for grants from the National Institute of Justice and to participate in the Combined DNA Index System (CODIS), individual laboratories are required to be accredited.[1]

1) The American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB)

In 1973, forty-seven crime laboratory directors from around the United States met with the Director of the FBI with the intention of opening channels of communication. At a follow-up meeting in 1974, the American Society of Crime Laboratory Directors (ASCLD) was officially formed. One of the early committees formed was the Laboratory Evaluation and Standards Committee and this committee soon began focusing on accreditation and reorganized to become the American Society of Crime Laboratory Directors Committee.[2]

In 1981, the American Society of Crime Laboratory Directors Committee on Laboratory Accreditation separated from ASCLD with its own board of directors and became known as the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB). The first version of the standards were released in August of that same year. In 1984, the first forensic laboratory was accredited by what is now referred to as ASCLD/LAB Legacy Accreditation Program.[3]

ASCLD/LAB continued with the legacy accreditation program until 2009, at which time the ASCLD/LAB International Accreditation program was fully adopted. Because a laboratory's accreditation under the legacy program lasted five years, by 2014, every laboratory was required to be accredited by the ASCLD/LAB International Accreditation program that began in 2004. This became the only accreditation program offered.

In April of 2016, the ANSI National Accreditation Board (ANAB) announced the merger of ASCLD/LAB into ANAB. (See § 4:3 subsection 10).)

2) ASCLD/LAB Legacy Accreditation Program

The objectives of the legacy accreditation program were:

> "To improve the quality of laboratory services provided to the criminal justice system."

> "To develop and maintain criteria which may be used by a laboratory to assess its level of performance and to strengthen its operation."

> "To provide an independent, impartial, and objective system by which laboratories can benefit from a total operational review."

- "To offer to the general public and to users of laboratory services a means of identifying those laboratories which have demonstrated that they meet established standards."[4]

The program's three major divisions: Laboratory Management and Operations, Personal Qualifications, and Physical Plant, included approximately 140 standards, some of which were applicable to specific disciplines. Laboratories conducting DNA analysis applied for accreditation in the sub discipline of Biology. This sub discipline included evidence screening and stain identification. Laboratories that applied for accreditation in the Biology sub discipline of DNA were also inspected under the applicable standards of the ASCLD/LAB Accreditation Program and the applicable standards of the FBI's Quality Assurance Standards for Forensic DNA Testing Laboratories and Offender DNA Databasing Laboratories.[5]

To be accredited, a laboratory underwent an inspection, carried out by ASCLD/LAB trained assessors, to determine if the lab was compliant with the standards. ASCLD/LAB designated each standard as "essential," "important," or "desirable." These terms are defined as follows:

> "Essential—Standards which directly affect and have fundamental impact on the work product of the laboratory or the integrity of the evidence."

> "Important—Standards which are considered to be key indicators of the overall quality of the laboratory but may not directly affect the work product nor the integrity of the evidence."

- "Desirable-Standards which have the least effect on the work product or the integrity of the evidence but which nevertheless enhance the professionalism of the laboratory."[6]

Examples of the standards considered essential included:

- Having Technical Procedure Manuals

- Having a Quality Manual

- Having a Documented training program

- Proper identification and storage of evidence

- Secure facility

- Laboratory examination documentation

- Protection of evidence from loss, cross transfer, contamination and/or deleterious change

- External proficiency testing

- Technical review of the work product

- Monitoring of court testimony

In order to pass an accreditation inspection, a laboratory must achieve 100% of the essential standards, 75% of the important, and 50% of the desirable.[7]

If ASCLD/LAB was made aware that an accredited laboratory had become non-compliant with some of the accreditation standards and the laboratory failed to take the required corrective actions in a timely manner, the following sanctions may result:[8]

> "Probation for a specified time during which the laboratory must comply with specified requirements or conditions."

- Suspension for a specified time during which the laboratory has demonstrated that the problem has been remediated."

- Revocation for a specified time after which the laboratory may submit a new application for accreditation."

3) International Standards

The International Organization for Standardization (ISO) is the world's largest developer and publisher of international standards. ISO is a network of the national standard institutes of 162 countries, with a Central Secretariat in Geneva, Switzerland, that coordinates the system. In a joint effort with the International Electrotechnical Commission (IEC), which is also a leading organization in preparing and publishing standards, ISO has combined the relevant knowledge of experts working in related areas and produced the ISO/IEC 17025 International Standards or the "General requirements for the competence of testing and calibration laboratories."[9]

ISO established standards to "ensure desirable characteristics of products and services as quality, environmental friendliness, safety, reliability, efficiency and interchangeability and safeguard consumers, and users in general, of products and services."[10]

ISO identifies three phases in the development of standards:

- The first phase involves the definition of the technical scope of the standard and is carried out in working groups which are comprised of experts from countries interested in the subject matter.

- The second phase involves the different countries negotiate the detailed specifications within the standards and is considered the consensus-building phase.

- The last phase is the formal approval of the International Standard which requires approval of two-thirds of the ISO members that have participated actively in the standards development process, and approval by 75% of all the members that vote.

The first edition of the ISO/IEC17025 standards were approved in 1999. The technically revised edition replaced the first, and became available in 2005.[11]

4) ISO 17025:2005 General Requirements for the Competence of Testing Laboratories and Calibration Laboratories[12]

The International Standard specifies the requirements for the competence of laboratories conducting testing and/or calibration. The Standard is organized into five chapters with the first three (Scope, Normative References, and Terms and Definitions) providing descriptions and information. Chapter Four, Management Requirements, and Chapter Five, Technical Requirements, contain the requirements that laboratories must meet to be accredited. The chapters are broken down as follows:[13]

Chapter 4 Management Requirements

1. Organization

2. Management system

3. Document control

4. Review of requests, tenders and contracts

5. Subcontracting of tests and calibrations

6. Purchasing services and supplies

7. Service to the customer

8. Complaints

9. Control of nonconforming testing and/or calibration work

10. Improvement

11. Corrective Action

12. Preventive Action

13. Control of records

14. Internal Audits

15. Management reviews

Chapter 5 Technical Requirements

1. General

2. Personnel

3. Accommodation and environmental conditions

4. Test and calibration methods and method validation

5. Equipment

6. Measurement traceability

7. Sampling

8. Handling of test and calibration items

9. Assuring the quality of test and calibration results

10. Reporting the results

5) ISO 17025:2017 General Requirements for the Competence of Testing Laboratories and Calibration Laboratories

The 2017 revision of ISO/IEC 17025, brought a reorganization and expansion of the previous standard. The chapters are broken down as follows:[14]

Chapter 1 Scope

Chapter 2 Normative References

Chapter 3 Terms and Definitions

Chapter 4 General Requirements

1. Impartiality
2. Confidentiality

Chapter 5 Structural Requirements

Chapter 6 Resource Requirements

1. General
2. Personnel
3. Facilities and environmental conditions
4. Equipment
5. Metrological traceability
6. Externally provided products and services

Chapter 7 Process Requirements

1. Review of requests, tenders and contracts
2. Selection, verification and validation of methods
3. Sampling
4. Handling of test or calibration items
5. Technical records
6. Evaluation of measurement uncertainty
7. Ensuring the validity of results
8. Reporting of results
9. Complaints
10. Nonconforming work

11. Control of data and information management

Chapter 8 Management System Requirements

1. Options
2. Management system documentation
3. Control of management system documents
4. Control of records
5. Actions to address risks and opportunities
6. Improvement
7. Corrective actions
8. Internal audits
9. Management reviews

6) Supplemental Requirements

The International Standards Organization recognizes that the requirements of ISO/IEC 17025 Standard are general and applicable to all test and calibration laboratories. However, ISO recognizes that additional explanations may be needed. ISO refers to these explanations as applications and recognizes that it may be necessary for there to be a separate document of applications that supplement the ISO Standard for specific types or group of tests or calibrations, products, materials, or technical fields of tests or calibrations. Accreditation bodies that develop these supplemental applications, also referred to as supplemental requirements, must maintain the ISO Standard as the governing document.[15]

In 2010, pursuant to the adoption of ISO Standard 17025 as the assessment document for the International Accreditation program, ASCLD/LAB published, "Supplemental Requirements for the Accreditation of Forensic Science Testing Laboratories." These supplemental requirements, approximately 140 in number, are those requirements carried over from the legacy standards. (See § 4:10, infra.) Unlike the legacy program, laboratories must demonstrate compliance with all of the requirements of the ISO standard and ASCLD/LAB- International supplemental requirements. Laboratories conducting forensic DNA analysis must also follow the FBI's Quality Assurance Standards for DNA Testing Laboratories and/or the Quality Assurance Standards for Forensic DNA Databasing Laboratories.[16]

7) International Accreditation Cooperation

At least two international accreditation cooperation organizations exist that link the calibration and testing laboratory accrediting bodies together. They are the International Laboratory Accreditation Cooperation (ILAC) and the InterAmerican Accreditation Cooperation (IAAC).

ILAC was formed in 1996 with the aim of developing international cooperation for facilitating trade by promotion of the acceptance of accreditation and calibration test results. ILAC develops a global network of accredited testing and calibration laboratories that are assessed and recognized as being competent ILAC signatory accreditation bodies. The signatories have been evaluated by their peers and shown to meet ILAC's criteria for competence.[17]

The IAAC is an association of accreditation bodies and other organizations interested in conformity assessment solely in the Americas. Created in 1996, IAAC's main objective is to promote regional and international acceptance of accreditations granted by its members and play a key role in the accreditation and conformity assessment infrastructure of the Americas by, evaluating the competence of accreditation bodies in the Americas, which in turn, evaluate and recognize the competence of certification, registration ad inspection bodies, and of testing and calibration laboratories that operate in the continent.[18]

The two forensic science accrediting bodies in the US, the American Society of Crime Laboratory Directors/Laboratory Accreditation Board and Forensic Quality Services, Inc., are both signatories for ILAC and IAAC.

8) The American Society of Crime Laboratory Directors/Laboratory Accreditation Board-International Accreditation Program (ASCLD/LAB—International)

In 2004, ASCLD/LAB initiated its forensic science laboratory international accreditation program based on the ISO/IEC 17025 Standard and the supplemental requirements taken from ASCLD/LAB's Legacy Accreditation Program. As of 2009, ASCLD/LAB discontinued offering accreditation under the Legacy Accreditation Program, but because accreditation was in effect for five years, many laboratories were accredited under that program through 2014.[19]

Until 2016, ASCLD/LAB operated the international accreditation program and through a Delegate Assembly, a Board of Directors, and an Executive Director. The Delegate Assembly was comprised of the directors of all laboratories and laboratory systems accredited by ASCLD/LAB. The Board of Directors were elected by the Delegate Assembly. The Executive Director managed all daily business affairs, maintained records, coordinated inspections and assessments, and maintained financial and budgetary records.[20]

9) Forensic Quality Services—International (FQS-I)

Forensic Quality Services was another organization in the USA that offered accreditation of forensic science laboratories. FQS accredited the first forensic testing agency in 1999 and the first US forensic crime laboratory to the ISO/IEC 17025 Standard in 2001. FQS is a full member of the Inter American Accreditation Cooperation (IAAC) and the International Laboratory Accreditation Cooperation (ILAC). FQS is also recognized by the FBI to perform Quality Assurance Standards DNA assessments and by the National Institute of Justice as a provider of accreditation to forensic science laboratories.[21]

Accreditation by FQS was offered in cycles covering two to five years. As with ASCLD/LAB and subsequent international standards for accrediting bodies (ISO/IEC 17011:2004), once a laboratory applied for accreditation and the application and submission of all required documents were reviewed and approved, an assessment visit was conducted.

The on-site assessment was conducted to establish if the laboratory was meeting the requirements of the ISO/IEC 17025 Standard. Unlike ASCLD/LAB, FQS did not incorporate a lengthy list of supplemental requirements into the accreditation process. FQS requirements were derived from the ILAC Guide 19, Guidelines for Forensic Laboratories.[22] The main difference between ILAC's guidelines and FQS's, is that FQS changed the requirements from, “should” to “shall.” The ILAC guideline and the FQS document also, when compared to the ISO/IEC 17025 Standard, had additional explanations of some of the ISO requirements.[23] The FQS documents “General Requirements for accreditation (GRA) and Forensic Requirements for Accreditation (FRA-I) defined the FQS-I program.”[24] FQS-I's accreditation program was similar to ASCLD/LAB, as they also followed ISO procedures were approved by ILAC and IAAC.[25]

In 2011, FQS-I was acquired by ANSI National Accreditation Board or ANAB. FQS-I became the forensic science accreditation vehicle for ANAB. The name change did not become complete until 2015 when the ANAB Accreditation Certificates were issued to laboratories that had been accredited by FQS-I.

10) ANSI National Accreditation Board (ANAB)

ANSI National Accreditation Board or ANAB is a non-governmental organization that provides accreditation services to public and private sector laboratories. Is a wholly owned subsidiary of the American National Standards Institute (ANSI), a non-profit organization.[26] In April 2016, ANAB announced the merger of ASCLD/LAB into ANAB.

ANAB accredits management certification bodies, police crime units, reference material producers, proficiency test providers and calibration and testing laboratories. ANAB also accredits forensic testing laboratories.

ANAB accredits Forensic Science Testing Laboratories to the ISO/IEC 17025 requirements. Similar to ASCLD/LAB's accreditation approach, additional forensic science requirements were added to the ISO/IEC 17025 requirements. To assist laboratories transitioning from ASCLD/LAB accreditation to ANAB accreditation, ANAB produced a correlation document called "crosswalk." This document, presented in table form, listed the ASCLD/LAB requirement by clause number to the related clause number in the ANAB Forensic Science Testing Laboratories Accreditation Requirement.

The National DNA Index System (NDIS) Procedure Board recognizes ANAB as meeting the requirements to accredit laboratories participating in NDIS.

ANAB required that all forensic science providers previously accredited by ASCLD/LAB be in conformance with the 2017 ANAB Accreditation Requirements by December 31, 2018.

11) ANAB Supplemental Requirements

With the acquisition of ASCLD/LAB, ANAB published a new set of supplemental requirements, specific to forensic testing laboratories, to accompany the 2005 version of ISO 17025. Document AR 3028, "ISO/IEC 17025:2005—Forensic Testing Laboratories Accreditation Requirements" was released on June 1, 2017, and remained in effect until the release of the release of ISO 17025:2017, in December of that year.[27] A subsequent document, AR 3125, "Accreditation Requirements for Forensic Testing and Calibration," was released in 2018, to supplement ISO 17025:2017. An updated version of AR 3125 was released on February 1, 2023.[28]

12) Achieving Accreditation

To become accredited by ANAB, a forensic laboratory must demonstrate conformance with all requirement of the ISO/IEC 17025 Standard, the supplemental requirements in AR 3125, and the requirements of their own management system. Laboratories, or laboratory systems, must apply for accreditation for each of the disciplines in which they perform testing activities. The list of testing disciplines is the laboratory's scope of accreditation.[29] A laboratory's scope of accreditation may change over time with the discontinuation or adoption of testing methods. Forensic Laboratories conducting DNA analysis will also be assessed in accordance with the Quality Assurance Standards for DNA Testing Laboratories and the Quality Assurance Standards for Databasing Laboratories.

a) Preparing for the Assessment

In preparation for an accreditation assessment, a laboratory must provide to ANAB, documentation that the laboratory meets all of the requirements for accreditation. ANAB will determine the laboratory's readiness for accreditation based on the completion of the following:

- Possession of the most current versions of all Standards and assessment documents needed to assess conformance.

- Performance of an internal audit detailing the laboratory's conformance with all Standards and requirements and details of all non-conformances and their resolution.

- A management review.

- Personnel participation in a proficiency testing program.

Once it has been determined that the laboratory is prepared for an accreditation assessment, a formal application is submitted to ANAB.

b) The Assessment Process

Depending on the size of the laboratory and the scope of accreditation, an assessment team, comprised of technical subject matter experts is assembled and overseen by a team leader. The team's objective is to "fairly and objectively evaluate the [laboratory's] competence and conformance to effectively operate within the scope of accreditation."[30] The laboratory is provided the list of assessors in advance to identify any potential conflicts of interest.

Forty-five days in advance of the beginning of the assessment activity, the Laboratory submits a completed conformance checklist to the Team Leader for review. The Team Leader reviews the checklist to identify any potential gaps in the laboratory's management system that may indicate areas of nonconformity. If excessive gaps are identified, the Team Leader may suspend the continuation of assessment activities until the issues are addressed.[31]

When the team arrives on-site, prior to any assessment activity, an opening meeting is held with key laboratory personnel to confirm the scope of accreditation, the purpose of the assessment, and any administrative or facilities related information needed for the team's operation.

After the opening meeting, the team will begin the assessment activity. Evaluation of conformance to each standard is done using a variety of techniques, including:

- "Witnessing: A sample of personnel performing authorized tasks will be observed by assessors during the assessment process.

- Interviews: A sample of personnel covered under the [laboratory's] management system will be interviewed.

- Document and record review: A sample of documents and records will be reviewed by the assessment team."[32]

Based on objective evidence gathered by the assessment team, the Team Leader will determine for each of the requirements, if the laboratory is conforming, nonconforming, or if the requirement is not applicable to the laboratory's activities. If a potential nonconformity is identified, the Team Leader may accept a correction to bring the laboratory into compliance. Any nonconformities that cannot be resolved through a simple correction, are reported as official findings.[33]

Results of the assessment activity are formally reported to the laboratory at a closing meeting with the assessment team, the laboratory's assessment point of contact, and any other personnel the laboratory wished to include. The Team Leader will present the team's assessment of compliance and competence and a list of any nonconformities. The Team Leader may also choose to include statements about opportunities for improvement. These are conforming laboratory policies or practices that may lead to noncompliance in the future.[34]

After the closing meeting, the laboratory has thirty days to provide ANAB with an update on the resolution of each nonconformity identified from the assessment. The laboratory must report:

- An evaluation of the nonconformance, including the prevalence and cause.

- A plan to resolve the nonconformance.

- A timeline for resolution.
The Team leader will make a determination as to whether the proposal is sufficient to correct the nonconformance. If the proposal is deemed insufficient, the Team Leader may request that the laboratory perform additional evaluation or action.

Within 60 days from the closing meeting, the laboratory must provide objective evidence that the proposed resolution plan has been implemented and that any corrective actions have eliminated the negative impact on the quality of the work product.

If a resolution is not completed within sixty days, or if the Team Leader determines the nonconformity was not fully resolved, the laboratory may be subject to a suspension of the accreditation process or sanctions against their existing accreditation.[35]

c) Accreditation

When all nonconformities have been resolved and results of the assessment have been reviewed by an Accreditation Manager, the Vice President of ANAB makes the decision to grant accreditation. The laboratory will be provided a Certificate of Accreditation and a Scope of Accreditation, which are specific to each laboratory location. The accreditation certificate has a unique number and an expiration date. The scope document details each of the disciplines and types of testing for which accreditation has been granted at each laboratory site.

Laboratories that have been accredited by ANAB, are granted permission to use the ANAB accreditation symbol and use the International Laboratory Accreditation Cooperation (ILAC) mark.[36]

d) Conformance Monitoring

ANAB accreditation of a forensic testing laboratory lasts for four years from the date on the Certificate of Accreditation.[37] To retain accreditation through a full, four-year accreditation cycle, a laboratory must retain conformity with all of the requirements met to attain accreditation. In order to ensure continued conformity of an accredited laboratory, ANAB conducts surveillance activities. These interim assessments are performed at the two-year interval between accreditation assessments. Surveillance activities typically focus on a subset of requirements and my include in-person or remote activities.[38] If a laboratory has failed to maintain compliance with any accreditation requirements, ANAB may perform a more extensive interim assessment.[39]

e) Nonconformity Challenge, Appeal or Complaint

A laboratory has the right to challenge a nonconformity, appeal an accreditation decision, or file a complaint against ANAB.[40]

f) Confidentiality and Conflict of Interest

All ANAB employees, designees, and volunteers involved in assessment activities and/or accreditation decisions are required to sign and abide by a confidentiality and conflict of interest agreement.[41]

13) A2LA

A2LA was established in 1978 as a non-profit public service membership society that provides formal recognition of competence testing and calibration laboratories, inspection bodies, proficiency test providers, and reference material producers. To support the recognition of competence of laboratories, it offers accreditation, training, and membership in A2LA.

A2LA's Forensic Examination Accreditation Program requires forensic testing laboratories to comply with ISO/IEC 17025 General Requirements for the Accreditation of Testing and Calibration Laboratories and additional criteria adopted from national and international sources.

In January 2014, the National DNA Index (NDIS) Procedures Board approved A2LA as an accrediting body for laboratories conducting DNA analysis on samples with the purpose of entering results into CODIS.

14) Quality Assurance Standards Compliance and Accreditation Required

The DNA Identification Act (42 U.S.C. SS14132(b)) specifies the requirements for participation in the National DNA Index System or NDIS. They include:

a) The participating laboratories must comply with the Quality Assurance Standards for Forensic DNA Testing Laboratories and/or the Quality Assurance Standards for Databasing Laboratories.

b) Laboratories submitting DNA records to NDIS must be accredited by a nonprofit professional association that is recognized by the forensic science community.[42]

c) Laboratories undergo an external audit every two years to demonstrate compliance with the Quality Assurance Standards issued by the Director of the FBI.

As follow-up to the federal law, California Penal Code Section 295 (the DNA and Forensic Identification Database and Data Bank Act of 1998) specifies that the California Department of Justice DNA Laboratory shall submit a quarterly report, confirming the laboratory's accreditation status.

The National Institute of Justice (NIJ) is the agency that awards grants to DNA testing laboratories in the US. NIJ requires laboratories receiving grants to be accredited.[43]

Footnotes

1 See infra subsection J.

2 ASCLD/LAB www.ascld-lab.org.

3 History of the ASCLD/LAB Legacy Program, ASCLD/LAB Newsletter, Mar. 26, 2009, at 1–2.

4 Id. at p. 2.

5 ASCLD/LAB, Legacy Program Review, www.ascld-lab.org/document/legacy_overview.pdf at 8.

6 Id.

7 ASCLD/LAB, www.ascld-lab.org.

8 Id.

9 Id.

10 International Organization for Standardization, Discover ISO, available at www.iso.org/about.htm.

11 Id.

12 While the original DAB standards and the current FBI Quality Assurance Standards refer to each requirement as a standard, ISO/IEC 17025:2005 is referred as a Standard and consists of requirements to meet the Standard.

13 ISO/IEC 17025:2005 General Requirements for the Competence of Testing and Calibration Laboratories 1-23.

14 https://anab.ansi.org.

15 Id. at 26.

16 ASCLD-International, Supplemental Requirements for the Accreditation of Forensic Science Testing Laboratories 2011 Edition at 4.

17 ILAC, www.ilac.org/aboutilac.html.

18 IAAC, www.iaac.org.mx/English/Intro.php.

19 ASCLD/LAB www.ascld-lab.org.

20 Program Overview 2010 Edition: An ISO/IEC 17025 Program of Accreditation at 3.

21 Forensic Quality Services www.forquality.org.

22 ILAC-G19: 2002 ILAC Guidelines for Forensic Science Laboratories at 3–15.

23 These explanations are analogous to ISO supplemental requirements.

24 Forensic Quality Services International, Forensic Requirements for Accreditation (FRA-1) at 1–12.

25 FQS did not have an extensive list of supplemental requirements to IS0/IEC 17025:2005 and overall, the accreditation program was less complex.

26 https://anab.ansi.org.

27 Id.

28 Id.

29 Id.

30 MA 3033, Accreditation Manual for Forensic Laboratories, Forensic Inspection Bodies, and Property and Evidence Control Units, Sec. 3.3, p. 8.

31 Id., p. 9.

32 Id., p. 10.

33 Id., p. 11.

34 Id.

35 Id.

36 Id., p. 12.

37 Id., p. 15.

38 Id., p. 16.

39 Id., p. 20.

40 Id.

41 Id.

42 ASCLD/LAB and FQS have been approved by the FBI.

43 DNA Initiative, Advancing Criminal Justice Through DNA Technology, available at www.dna.gov/lab_services/audits.

End of Document

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§ 4:4. Training of forensic DNA examiners/analysts

Although the education and experience requirements for DNA examiners/analysts are specified in the FBI's Quality Assurance Standards for Forensic DNA Testing Laboratories and the Quality Assurance Standards for Forensic DNA Databasing Laboratories, specific training curricula is not. However, one of the accreditation requirements is for the laboratory to have a written training program for the disciplines in which that laboratory seeks accreditation. Forensic DNA laboratories generally use the SWGDAM Training Guidelines and/or the DNA Analyst Training Manual that was developed as part of the President's DNA initiative to train their DNA examiners/analysts thereby meeting both the requirements of the FBI's Quality Assurance Standards and the requirements of accreditation.

The SWGDAM Training Guidelines were developed with the primary emphasis on providing a model program of standardized training for laboratory personnel throughout the forensic DNA community. The guidelines can be used by laboratory directors to assist them in developing a training program applicable to the analytical methods used by their laboratories. The training program guidelines employ a module system with the expectation that a new employee would complete them all and an examiner/analyst with prior training in DNA might only be required to take some of the modules. Specific content of each module should be customized by the laboratory to include all aspects of the procedures and policies of the laboratory. The modules in the SWGDAM guidelines are as follows:

1. An introduction (topics to be covered include quality assurance and quality control).

2. Evidence handling (topics to be covered include sample collection, packaging and storage, contamination of evidence, chain of custody, and consumption of evidence).

3. Foundational Scientific Knowledge (DNA examiners/analysts must have documentation of college-level course work covering genetics, biochemistry, and molecular biology as applied to forensic DNA analysis).

4. Applied Scientific Knowledge (in-depth theoretical knowledge to be provided on the various forensic DNA techniques and typing systems used in the laboratory).

5. Laboratory Analysis (practical instruction provided on the analytical procedures used in the laboratory and each examiner/analyst must keep a training notebook documenting experiences in the laboratory with at least 50 samples for nuclear DNA analysis and if applicable, 50 successful mitochondria DNA amplifications.

6. Report Writing (instruction given on the interpretation guidelines used by the laboratory, statistical calculations, and writing the report. Included in the assessment of the examiner/analyst in training with this module, the examiner/analyst in training must review 20 sets of data representative of casework and provide a written interpretation according to laboratory policy.).

7. Legal Issues (instruction given in the presentation of DNA evidence in court, court testimony practice, etc.).

8. Final Evaluation.

The training guidelines specify that modules one through seven are organized to include a goal for the module, specific tasks, reading assignments, and an assessment. In addition to the reading assignments associated with each module, the SWGDAM Training Guidelines state that the technical leader and the examiner/analyst receive and complete the reading of a list of references specific to issue in forensic DNA. The list must include primary source material from scientific journals. The laboratory should retain all training records and formal recognition documentation that the examiner/analyst in training successfully completed the training program. The training will take a minimum of six months.[1]

The DNA Analyst Training/Laboratory Training Manual User Guide was developed with funds from the President's DNA Initiative. Incorporating the SWGDAM DNA Training Guidelines, this manual provides an electronic format for adding a laboratory's specific policies, procedures, protocols and exercises. Additionally, it includes trainer and trainee responsibilities.[2]

Prior to a DNA examiner/analyst commencing forensic DNA analysis, they must pass a competency test. The FBI Quality Assurance Standards define a competency test as "a written, oral and/or practical test or series of tests designed to establish that an individual has demonstrated achievement of technical skills and met minimum standards of knowledge necessary to perform forensic DNA analysis."[3] Competency testing is different than proficiency testing which is defined as "a quality assurance measure used to monitor performance and identify areas in which improvement may be needed."[4]

Footnotes

1 Scientific Working Group on DNA Analysis Methods, Training Guidelines, January 23, 2001, Forensic Communications, Oct. 2001, available at, http://www.fbi.gov/about-us/lab/forensic-science-communications/fsc/oct2001/kzinski.htm.

2 DNA Analyst Training/Laboratory Training Manual/User Guide, www.static.dna.gov/lab-manual/pdi_labuserguide.pdf.

3 FBI Quality Assurance Standards for Forensic DNA Testing Laboratories, at p. 3.

4 Ibid.

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Chapter 4. Quality Assurance, Training, and Accreditation

§ 4:5. Certification of criminalists in the USA

Certification is a voluntary process where a practitioner is recognized as having attained the professional qualifications necessary to practice in one or more disciplines of criminalistics. In the USA, forensic DNA analysts can be certified by the American Board of Criminalists (ABC). The ABC is composed of regional and national organizations that represent forensic scientists. Each organization is entitled to one member on the ABC Examination Committee.[1]

The objectives of the ABC are to set and measure professional levels of knowledge, skills, and abilities, provide guidance in the attainment of levels of competence, provide a means to evaluate competence, and to provide a formal process of recognition for those who meet the professional level of competence.[2]

The ABC offers two levels of certification that can be attained; the Diplomate and the Fellow. The Diplomate is awarded to professionals with a minimum of a baccalaureate degree in a natural science of appropriately related field from an accredited institution, have a minimum of two years of experience, actively working in the Criminalistics, and completed any ABC examination. The Diplomate status is designed for laboratory directors, supervisors, educators, or where specialty examinations have not been planned or developed or for those who are not able to maintain the proficiency test requirements for their Fellow status. The Fellow is awarded to those with a minimum of a baccalaureate degree, two years experience in a specialty area, successful completion of any ABC examination (for forensic DNA professionals, ABC offers a Molecular Biology Exam) and successful participation in an approved proficiency testing program. Although DNA caseworkers are required to take two external proficiency tests per year,[3] the ABC only requires Fellows to report one. Certification is valid for five years. Recertification can be accomplished if the professional has continued participation in the field of forensic science through training, casework, publishing, etc.[4]

Footnotes

1 American Board of Criminalistics www.criminalistics.com.

2 Ibid.

3 FBI Quality Assurance Standard for Testing and Databasing Laboratories, at p. 24.

4 See American Board of Criminalistics www.criminalistics.com.

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Chapter 4. Quality Assurance, Training, and Accreditation

§ 4:6. National academy of sciences report: Strengthening forensic science in the United States

In November of 2005, Congress authorized the National Academy of Sciences (NAS) to conduct a study on forensic science prompted by highly publicized crime laboratory errors. The final report, written and released in 2009 by a committee chaired by Harry Edwards, U.S. District of Columbia Appeals Court Judge, and including other legal scholars, practicing attorneys, scientists, and forensic science practitioners assembled by the NAS, summarized the current state of forensic science in the United States and through recommendations, charted out an agenda for improvement.

While the NAS committee acknowledged the importance of forensic science in the criminal justice system, it pointed out many of the challenges the forensic science community faces. These challenges include the lack of standardized terminology used in reports and testimony, the need for more and better research (studies establishing the scientific basis and validity of forensic methods), administrative separation of forensic science laboratories from law enforcement agencies or prosecutors' offices and improving the overall quality of the work performed and minimizing laboratory errors. The report referenced findings of the Innocence Project that found both unintentional and intentional errors that led to wrongful convictions including; in-laboratory contamination and mislabeling of evidence, in forensic reports, falsified results and misrepresentation of evidence, and in the courtroom, suppression of exculpatory evidence, statistical exaggeration of results of a test conducted, and providing false testimony about test results.[1]

To address the challenges faced by the forensic science community, thirteen recommendations were made by the NAS committee. The first was to establish a National Institute of Forensic Science (NIFS) to promote the development of forensic science into a mature field research and practice. The remaining recommendations dealt with forensic science reports, establishing the scientific basis of forensic methods, independence of forensic laboratories, potential contextual bias, availability of appropriate analytical standards, accreditation, quality assurance, forensic science education, medico-legal death investigation improvement, interoperability of the automated fingerprint systems, and forensic science and homeland security.

Efforts to improve quality in the crime laboratory began long before the release of this report. In the forensic science discipline of DNA, quality standards were established by in the 1990's by the DNA Advisory Board, and ASCLD/LAB began accrediting laboratories in 1982. However, the NAS committee makes the following recommendations to strengthen the oversight of forensic science and points out that in only three states (New York, Oklahoma, and Texas) are accreditation required and certification is not uniformly offered or required.

1) NAS Recommendations

NAS has two relevant recommendations pertaining to quality assurance and accreditation for forensic science laboratories. One recommendation states that:

> “Laboratory accreditation and individual certification of forensic science professionals should be mandatory, and all forensic science professionals should have access to a certification process. In determining appropriate standards for accreditation and certification, the National Institute of Forensic Science (NIFS) should take

> into account established and recognized international standards, such as those published by the International Organization for Standardization (ISO). No person (public or private) should be allowed to practice in a forensic science discipline without certification. Certification requirements should include, at a minimum, written examinations, supervised practice, proficiency testing, continuing education, recertification procedures adherence to a code of ethics, and effective disciplinary procedures. All laboratories and facilities (public or private) should be accredited, and all forensic science professionals should be certified, when eligible, with a time period established by NIFS."[2]

The other relevant recommendation states:

> "Forensic laboratories should establish routine quality assurance and quality control procedures to ensure the accuracy of forensic analyses and the work of forensic practitioners. Quality control procedures should be designed to identify mistakes, fraud, and bias; confirm the continued validity and reliability of standard operating procedures and protocols; ensure that best practices are being followed; and correct procedures and protocols that are found to need improvement."[3]

While the NAS committee called for mandatory accreditation and the use of quality control procedures, it also stated that "accreditation does not mean that the accredited laboratories do not make mistakes, nor does it mean that a laboratory utilizes best practices in every case, but rather, it means that the laboratory adheres to an established set of standards of quality and relies on acceptable practices within these requirements."[4]

In response to the NAS report, the US Department of Justice (DOJ) partnered with the National Institute of Standards and Technology (NIST) in 2013 to establish the National Commission on Forensic Science (NCSF). The objectives of the commission include; enhancing quality assurance and quality control in the forensic laboratory, and identifying and recommending scientific protocols for evidence seizure, testing, analysis, and reporting by forensic science laboratories. The Commission will be comprised of federal, state, and local forensic science service providers, research scientists and academics, law enforcement officials, prosecutors, defense attorneys, judges, and other stakeholders from across the country. In January 2014, the DOJ and NIST announced the appointments to the National Commission on Forensic Science.

The Commission's charter permitted them to establish subcommittees that would report their recommendations and advice to the Commission. The subcommittees established in 2014 were; the Accreditation and Proficiency Testing Subcommittee, the Human Factors Subcommittee, the Interim Solutions Subcommittee, the Medicolegal Death Investigation Subcommittee, the Reporting and Testimony Subcommittee, the Scientific Inquiry and Research Subcommittee, and the Training on Science and Law Subcommittee.

In January, 2015, the Accreditation and Proficiency Testing Subcommittee made a policy recommendation that all Forensic Science Service Providers become accredited. Since accreditation has been voluntary in some jurisdictions and in others it has been mandated by legislation, this policy recommends that the Attorney General take actions to promote and enforce universal accreditation.

The Attorney General's National Commission on Forensic Science's charter expired on April 23, 2017. The Commission's accomplishments and identification of work that still needed to be addressed is summarized in the Commission's business document, Reflecting Back–Looking Toward the Future. The Commission's charter has not been renewed, and no decision by the U.S. Department of Justice has been made whether there will be follow-up to the recommendations made by the commission.

Footnotes

1 National Academy of Sciences, Strengthening Forensic Science in the United States: A Path Forward, 45 (2009).

2 Id. at p. 215.

3 Ibid.

4 Id. at p. 195.

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§ 4:7. California crime laboratory review task force

Forensic science service in California is provided by city, county, State, and Federal Crime Laboratories. This network of laboratories, totaling over 32 (not counting the small police laboratories), face the same challenges identified in the NAS Report, "Strengthening Forensic Science in the United States, A Path Forward." For many of the same reasons that Congress charged the NAS to look at forensic science service in the U.S., in 2007 the California Legislature enacted AB 1079 which established the California Crime Laboratory Review Task Force. This legislative bill directed the task force to make recommendations to best configure, fund, and improve the delivery of state and local crime laboratory services in the future.[1] Issues that the task force addressed included; the organization and management of crime laboratory services, staff and training, crime laboratory funding, performance standards and equipment, and statewide forensic science oversight.

The task force held monthly meetings from December 2007 through September 2009 and in November 2009 released its report; An Examination of Forensic Science in California. This report summarized status of forensic science service in California, addressing such specific issues as adequate staffing levels, employee recruitment and retention, employee salaries, casework production and backlogs, the need for additional funding, equipment needs, and the usefulness of an independent advisory or oversight board. The task force also addressed quality issues, such as training, certification and accreditation. Discussion summaries and recommendations regarding these issues were included in the report.

California is one of the few states to have a forensic science training institute. This institute provides in-service training courses covering most of the forensic science disciplines. Adequate funding is problem for this institute as the demand for training courses is high. The task force recommended the following:

> "Continuing education for criminalists is essential, and the state should fund it accordingly. Crime Laboratories should develop mandatory requirements for continuing education as part of their quality manuals."

- "The State should provide sufficient funding to ensure proper staffing, maintenance, and future expansion of the CCI program."
- "CCI should develop a laboratory management training program."
- "California law schools should incorporate scientific evidence training into their course- work offerings."
- "The state should establish a doctoral program in forensic science at one of its state university campuses."
- "University programs focusing on forensic science should take a more active role in informing students about the scrutiny of pre-employment background checks."[2]

Certification in California is not currently required. Data collected on the number of forensic scientists certified in California indicated that only 17% of the approximately 1100 forensic scientists in California were certified. The task force found only 29 DNA analysts were certified.[3] The task force recommended the following:

- "All persons who practice in a forensic science discipline or testify as a forensic science analyst/examiner should become certified by a reputable certifying body."
- "All laboratories and their parent agencies are strongly encouraged to provide support and incentives to promote individual staff certification. Fiscal-based incentives may include funding the application and sitting fees, as well as offering pay bonuses for certificate holders. Non-fiscal incentives may include on-duty study and test-taking time and the use of certificate status as a promotion factor."
- "All forensic science professionals should have access to a certification process."
- "The state should mandate that the only acceptable certificates are those granted by certification bodies accredited by the Forensic Specialties Accreditation Board, or certification bodies that adhere to requirements equivalent to those set forth by the Forensic Specialties Accreditation Board."[4]

The task force report listed 32 laboratories in California with their specific disciplines that are included in their accreditation. The task force recommended the following:

- "All California public crime laboratories should be accredited through one of the available crime laboratory accreditation programs. The task force does not see a need to establish a parallel or unique forensic laboratory accreditation program in California."
- "The state should further study whether or how forensic science activities that occur outside of accredited crime laboratories (limited service forensic science units most often found in small police departments) could be brought within an accredited organization."[5]

Footnotes

1 California Crime Laboratory Review Task Force, An Examination of Forensic Science in California, 1 (2009), available at ag.ca.gov/publications/crime_labs_report.pdf.

2 Id. at pp. 37–38.

3 Id. at pp. 43–44.

4 Id. at p. 45.

5 Id. at p. 83.

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Chapter 5. Statistics for Autosomal STR Profiles

Introduction

This chapter discusses statistical rarity estimates for autosomal DNA profiles, where "autosomal" refers to the non-sex chromosomes on which the standard forensic testing markers are located.

The evidentiary significance of one DNA profile matching another DNA profile is measured statistically. (See People v. Venegas, 18 Cal. 4th 47, 82, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998); People v. Xiong, 215 Cal. App. 4th 1259, 1269–1270, 155 Cal. Rptr. 3d 877 (5th Dist. 2013), as modified, (May 2, 2013).) Most routinely, the DNA expert offers a statistical expression of the profile's rarity in certain human populations. (See People v. Venegas, 18 Cal. 4th 47, 82, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998).) Additional statistical evaluations of the significance of a DNA profile match can be achieved as well. A variety of approaches to DNA statistics have been suggested and debated in both scientific and judicial forums.

Of course, the significance of DNA evidence will also be a function of its relevance and probative value in view of the totality of case facts. DNA can identify the source of biological material, but not necessarily when or how the DNA was deposited. A Colorado appellate court explained its understanding of this point:

> [W]here, as here, the only direct evidence connecting an accused person to the crime is the presence of DNA at the scene of a crime, the evidence, to be legally sufficient to sustain a conviction, must be coupled with evidence of other circumstances tending to reasonably exclude the hypothesis that the DNA was deposited at a time other than that of the crime. Such other circumstances may include the source material of the DNA and its susceptibility to transfer, the location of the DNA, the character of the place or premises where it was found, the accessibility of that place or premises to the general public, and the object upon which the DNA was found.

(*People v. Clark* (Colo.Ct.App. 2009) 214 P.3d 531, 537-538.) Statistics, therefore, must be considered in context.

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Chapter 5. Statistics for Autosomal STR Profiles

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§ 5:1. Random match probability

The evidentiary significance of a DNA profile match is most often measured by a statistic expressing the rarity of that shared profile, known as the random match probability statistic. (People v. Soto, 21 Cal. 4th 512, 522, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999).) It answers the following question: What is the probability that a person chosen at random from a population of unrelated people will possess a DNA profile that matches the evidence profile? (People v. Nelson, 43 Cal. 4th 1242, 1258, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008).) A random match probability is analogous to the probability printed on the back of a lottery ticket indicating the odd of winning. The latter is the probability that the one winning number, chosen at random by game officials, will match the number on that particular ticket. In a criminal case, then, given the match between the defendant's DNA profile and the perpetrator's DNA profile, the question for the finder of fact is whether the match is a result of coincidence (i.e., the defendant "won"—or "lost," depending upon one's perspective—the lottery), or whether the profiles match because the defendant was in fact the source of DNA at the crime scene.

To return to the lottery analogy, note that the odds of a particular ticket winning differs from the probability that some ticket —any ticket—sold will match the winning number. The chance of this happening will be much higher and will be a function of the number of tickets sold overall, but is of little interest to the holder of any particular ticket. Likewise, the probability that a particular DNA profile will be observed if every person on the planet, or in a city, or in a database is used for comparison purposes will generate a number different from a random match probability estimate. The probability of a match when many profiles are assessed may, in fact, be relevant in a case where a defendant was initially identified in a DNA database search, as will be discussed below. It will not, however, shed light on how unlucky a particular defendant would have to be to share a DNA profile with the perpetrator under the assumption that the defendant was not the perpetrator.

A random match probability statistic will vary depending upon the number of loci available to contribute to the calculation, as well as the rarity of alleles within the profile. The lower the probability of a random match, the more rare the profile in the population. Inferentially, the less probable a coincidental match, the more probable it is that the match was not coincidental, i.e., the two DNA samples have the same source. (People v. Johnson, 139 Cal. App. 4th 1135, 1147, 43 Cal. Rptr. 3d 587 (5th Dist. 2006).)

1) The Product Rule

The random match probability for a DNA profile is calculated by multiplying the genotype (i.e., the observed allele(s)) frequencies (i.e., how often that allele or pair of alleles can be expected to occur at random in a human population) for each locus in an STR profile with the genotype frequency for every other locus in the profile. This process is an application of the "product rule." (See *People v. Soto*, 21 Cal. 4th at 525, 541 [describing the product rule and its general acceptance in the relevant scientific community].) The product rule states that the probability of two separate events occurring simultaneously is the product of their probabilities. For example, the probability of rolling a five on a six-sided die is one in six. The probability of rolling a five again on the same die is also one in six. The first roll happens independently of the second roll, and has no effect on the second roll's outcome. Each subsequent roll of the die will carry the same probability of rolling a five. Because

of the independence of these events, the product rule can be used to calculate the combined probability (P) that a five will be rolled on each of three consecutive rolls. Each individual roll has a probability of (p_n), where n is the roll number:

$P=(p_1)(p_2)(p_3)$

$P=(1/6)^3$

$P=1/216$

There is a one in 216 chance that three separate rolls of the die would produce a five each time. This same principle applies to the markers used for STR testing.

For the product rule to apply to allele frequencies, then, a necessary premise is that the alleles at any one locus are inherited independently of the alleles at any other given locus—like separate rolls of the die. Each of the STR loci commonly used for forensic science testing in the United States was selected in part because the inheritance of alleles at any one locus occurs independently of alleles at any other loci. This means that if an individual inherits a 12 allele from one parent at the D3S1358 locus, he or she still has an equal chance of inheriting any other available combination of alleles from that same parent at each remaining locus. This state of completely independent inheritance is referred to as linkage equilibrium. (See *People v. Soto*, 21 Cal. 4th at 526; People v. Reeves, 91 Cal. App. 4th 14, 33, 109 Cal. Rptr. 2d 728 (1st Dist. 2001), as modified on denial of reh'g, (Aug. 28, 2001).) If it can be demonstrated that a set of loci are in linkage equilibrium, then the product rule may be applied to determine the overall profile frequency in a population.

2) Hardy-Weinberg Equilibrium

While linkage equilibrium is a measure of the independent inheritance of alleles at separate loci, Hardy-Weinberg equilibrium (HWE), is a measure of the independent inheritance of alleles within a single locus. (See *People v. Soto*, 21 Cal. 4th at 525–526; *People v. Reeves*, 91 Cal. App. 4th at 33.) In other words, the allele inherited from the mother is not correlated with the allele from the father. For a population to be in HWE requires certain conditions to be met.

1) The population must be infinitely large.

2) Mating between individuals must be completely random with no restrictions so all alleles have an equal probability of transmission to the next generation.

3) Alleles must not mutate (change).

4) No new alleles can migrate into or out of the population.

Meeting these requirements in human populations is not realistic. Mating among humans is not completely random. A person is much more likely to mate with someone they live in proximity to as opposed to someone who lives across the country.

The inability for the human population to achieve HWE does not, however, mean that allele frequencies depart from HWE to such a significant degree that the product rule does not apply. Studies of allele frequencies at forensic testing loci, from human population databases, do not show a statistically significant departure from HWE. (See, e.g., *People v. Reeves*, 91 Cal. App. 4th at 39–40.) Because of this, the assumption is made that both intra-locus and inter-locus independence applies to alleles in the U.S. population at the loci of interest. Therefore, the product rule is generally accepted as an appropriate method to measure STR profile frequencies in human populations. (*People v. Reeves*, 91 Cal. App. 4th at 39–42 [discussing the "ample evidence" of product rule's general acceptance for calculating the statistical significance of STR profiles].)

To apply the product rule, the genotype frequencies for each locus are multiplied together to calculate an overall expression of the rarity of the profile in a population. Profile frequencies (i.e., the product of each locus's genotype frequency) using the product rule become very rare, very quickly. Using nine STR loci, profile frequency estimates using the U.S. population database routinely demonstrate that the probability of a random appearance of a particular profile is one in billions. For 15-locus profiles, the frequencies of random appearance are routinely one in quadrillions (a one with fifteen zeros) or more.

Based on Hardy-Weinberg equilibrium, the genotype frequencies for heterozygous loci (a genotype with two different alleles) and homozygous loci (a genotype with the same two alleles) can be derived from looking at the genotype combinations possible from a mating of two individuals with the same heterozygous genotype. If two heterozygous genotypes A_1,B_1 and A_2,B_2 are mated, the possible genotypes that could result are A_1,A_2, A_1,B_2, A_2,B_1, and B_1,B_2. The genotype frequency for each outcome is the product of the two allele frequencies. If the sum total of the genotype frequencies in a population is 1 then:

$A^2 + 2AB + B^2 = 1$

A heterozygous locus with alleles a and b, and population frequencies p_a and p_b for each allele respectively, has the overall genotype frequency of:[1]

$P_{ab}=2p_ap_b$

The homozygous genotype a,a has a genotype frequency of:[2]

$P_{aa}=p_a^2$

a) Population substructure

In reality, of course, humans do not mate randomly. Just as some physical traits can become very common in a population (e.g. blond hair and blue eyes in Scandinavia), some alleles may become overrepresented in a population and lead to an excess of homozygous genotypes. To correct for the excess homozygosity of a population, a conservative adjustment is applied to the random match probability formula to protect against an overestimate of rarity given human inbreeding, i.e., non-random mating patterns. (See U.S. v. Trala, 162 F. Supp. 2d 336, 343, 57 Fed. R. Evid. Serv. 1266 (D. Del. 2001).). This correction factor is represented by the Greek letter theta (). A theta correction is applied to the homozygous frequency formula as follows:[3]

$P_{aa}=p_a^2+p_a(1- p_a)$

Generally a theta value of =0.1 is sufficiently conservative for large populations, such as that of the United States. However, a more conservative value of =0.3 may be used for small isolated populations where inbreeding, and therefore excess homozygosity, is more prevalent.

b) Kinship

It should be noted that the random match probability is premised upon an assumption that, if the defendant is not the source of the crime scene DNA, he is not related to the true source. But, if the actual perpetrator is a close relative of the defendant (e.g., a brother), then the probability of a coincidental match is greater. If the defendant's brothers' DNA profiles are not available for exclusion, then the following calculations can be performed to estimate the probability that one or more of a defendant's brothers share his DNA profile.

The probability of a suspect and a relative sharing the same genotype for a homozygous locus is:[4]
$P_a^2 + 4p_a(1-p_a)F$

For a heterozygous locus is:[5]
$2p_ap_b + 2(p_a + p_b - 4p_ap_b)F$

The value of the kinship coefficient F is dependent on the familial relationship and degree off relatedness between the suspect and the relative of interest. "For parent and offspring, F=1/4; for half siblings, 1/8; for uncle and nephew, 1/8; for first cousins, 1/16."[6]

Full siblings require different calculations due to their genetic proximity to the suspect. Brothers are not related linearly (from one generation to the next), but by successive mating of the same two people.

For a homozygous locus:[7]
$(1 + 2p_a + p_a^2)/4$

For a heterozygous locus:[8]
$(1 + p_a + p_b + 2p_ap_b)/4$

Footnotes

1 Formula 4.1b, National Research Council, The Evaluation of Forensic DNA Evidence (NRC II) (1996) 92.

2 Formula 4.1a, NRC II, at p. 92.

3 Formula 4.4a, NRC II, at p. 102.

4 Formula 4.8a, NRC II, at p. 113.

5 Formula 4.8b, NRC II, at p. 113.

6 NRC II, at p. 113.

7 Formula 4.9a, NRC II, at p. 113.

8 Formula 4.9b, NRC II, at p. 113.

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§ 5:2. Fallacies

1) The Prosecutor's Fallacy

Importantly, a random match probability does not represent the statistical probability of guilt. For example, if a random match probability is 1 in 100, it would be incorrect to state that there is a 99% chance that the defendant (who matches) is guilty, or a one percent chance that he is innocent. It would also be incorrect to state that there is only a 1/100 chance that someone (anyone) other than the defendant is the source of the crime scene evidence. To make any of these statements would be to improperly conflate a statistic based on population genetics with a factual issue that depends upon the totality of evidence in the case and not just the DNA evidence. This is known as the "prosecutor's fallacy." In reality, a defendant may have a solid alibi or other affirmative defense that exculpates him in spite of the DNA evidence. (See McDaniel v. Brown, 130 S. Ct. 665, 670, 175 L. Ed. 2d 582 (2010).) Or, the DNA evidence itself may have been generated erroneously. In any case, the probability that the defendant is the source of the DNA evidence must consider all the evidence in the case, not just the DNA evidence.

A more technical explanation of the prosecutor's fallacy is that it confuses random match probability with a source (or guilt) probability statement. (U.S. v. Chischilly, 30 F.3d 1144, 1157, 40 Fed. R. Evid. Serv. 289 (9th Cir. 1994); *McDaniel v. Brown*, 130 S.Ct. at 670.) In other words, instead of viewing a random match probability as providing the probability of a DNA match given an assumption of innocence (a correct question), the fallacy views the random match probability as providing the probability of innocence given the match. This is also known as "transposing the conditional," and switches the hypothesis with the event in the question.

On the other hand, it may not be unreasonable for an expert to extrapolate from statistics and attribute a crime scene DNA profile to a particular person when that person possesses a matching profile that is sufficiently rare. (People v. Nelson, 43 Cal. 4th 1242, 1262, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008); People v. Wilson, 38 Cal. 4th 1237, 1248–49, 45 Cal. Rptr. 3d 73, 136 P.3d 864 (2006); People v. Johnson, 139 Cal. App. 4th 1135, 1146, 43 Cal. Rptr. 3d 587 (5th Dist. 2006).) So-called "source attribution" statements may or may not be permitted by a laboratory's reporting protocols.

2) The Defense Fallacy

Another fallacious statement, sometimes referred to as the "defense fallacy," assumes that the people in a population who could be expected to possess the specific DNA profile in question are just as likely as the defendant to have committed the crime, making the probability that the defendant is guilty a fraction of that number. For example, it would be incorrect to state that, where a profile has a random match probability of 1:1 million, and the relevant population is ten million people, the chance of the defendant being the perpetrator is only 1:10 because ten people in the population are expected to possess the profile. (See *United States v. Chischilly*, 30 F.3d at 1157.)

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§ 5:3. Establishing a population database

Allele frequencies for forensic testing loci appear in published data tables compiled and verified by researchers. (People v. Soto, 21 Cal. 4th 512, 523, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999).) Allele frequencies are determined by compiling allele data from a population of samples. To do this, genotypes are generated from all samples in the test population. All alleles observed in all samples are recorded and counted. For each locus, the number of observations possible is two times the number of samples tested. This is because each sample has two alleles possible for each locus. Homozygous alleles, which are comprised of two copies of an allele, are counted twice. The amount of observances of each allele at the locus is then divided by the total number of alleles tested for the locus to calculate the frequency of each allele in the population.

After all frequency data has been calculated, statistical tests are performed, aided by software programs, to test for independence of loci and alleles within a locus. The database is evaluated to determine if significantly greater occurrence of homozygous genotypes was observed than would be expected from a population in Hardy-Weinberg equilibrium. Testing for locus independence is performed by randomly creating a virtual database of genotypes up to ten times larger than the tested population. Genotype frequencies are then compared between the two databases.

Because human mating is not completely random, allele frequencies vary between racial groups. Rarity estimates are commonly provided for Hispanic, Caucasian, and African-American populations because of differences in allele frequencies between racial groups. (See People v. Wilson, 38 Cal. 4th 1237, 1242, 45 Cal. Rptr. 3d 73, 136 P.3d 864 (2006) [“‘Profile frequencies within the major racial groups in the United States (Caucasian, African-American, Hispanic, East Asian, and Native American) vary to such an extent that separate DNA databases are maintained for the purpose of providing accurate estimates of profile frequency’”].) These three groups comprise the majority of the population of the United States. Estimates for other human population groups may be provided as well, particularly where some evidence exists that the perpetrator of a crime was a member of a particular group. (*People v. Wilson,* 38 Cal. 4th at 1250.) Allele frequency data tables exist for a wide range of racial and geographic populations.

1) Population Size

Allele frequencies for forensic testing loci appear in published data tables compiled and verified by researchers. Frequency estimates exist for all commonly used loci, and for many different racial and ethnic groups. A population size of 100-150 individuals is generally accepted as a sufficient sample from which to estimate allele frequencies. (Chakraborty, *Sample size requirements for addressing the population genetic issues of forensic use of DNA typing*, (1992) 64 Human Biology 141–159.) Several comparisons of data from populations of this size to data from populations numbering in the thousands have show similar allele frequencies between the databases. It is, therefore, neither necessary nor practical to compile a very large database when a much smaller population will provide similar results.

2) Population Sample Sources

Samples for allele frequency databases generally come from blood banks, medical testing facilities, academic institutions and offender databases. Samples from these sources are considered a sufficiently random sampling of the population as a whole.

It is desirable for samples compiled for a frequency databases to come from unrelated people and of known racial or ethnic origin. Compiling large numbers of these ideal samples is often not practical, however. Many times, researchers are dependent on convenience samples-large repositories of previously compiled samples from random individuals. Because of the nature of easily compiled samples for testing, information about ethnic origin and relatedness may be incomplete or all together unknown. Individuals have different ways self-identifying race and ethnicity. A person may identify with more than one racial group yet only list one on an identification form. Other individuals may not know their ancestry. Samples from community sources, such as blood banks may include related individuals. Samples may also be from anonymous sources with no identifying information. These characteristics should not, however, preclude the use of such samples for allele frequency estimates. Repeated comparison of separate databases compiled using different sample selection methods show similar frequencies when compared both to each other and to much larger databases. This consistency provides a basis for confidence in the collection methods and sources.

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§ 5:4. Statistics in DNA Database Cases

The rarity of the DNA profile shared by the perpetrator and defendant, expressed by the random match probability statistic, is always relevant and admissible, even in cold hit cases where the defendant was originally identified in a database search: "'[I]t is relevant for the jury to know that most persons of at least major portions of the general population could not have left the evidence samples.' [Citation.] We agree … that this remains true even when the suspect is first located though a database search." (People v. Nelson, 43 Cal. 4th 1242, 1267, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008); see also People v. Turner (2020) 10 Cal. 5th 786, 805; People v. Xiong, 215 Cal. App. 4th 1259, 1274, 155 Cal. Rptr. 3d 877 (5th Dist. 2013), as modified, (May 2, 2013) ["both the frequency and the random match probability are relevant in cold hit cases. They are, after all, two ways of representing the same thing, the same numbers couched in different concepts"].)

The Court of Appeal in People v. Xiong, 215 Cal. App. 4th 1259, 155 Cal. Rptr. 3d 877 (5th Dist. 2013), as modified, (May 2, 2013) explained in detail why population frequency statistics remain relevant in DNA database "cold hit" cases. "First," noted the court, the statistics

> refer to the *perpetrator's* profile and therefore are unaffected by any particular defendant or suspect. The frequency assesses how few people possess the perpetrator's profile, and the random match probability assesses how unlikely it is that a random person possesses the perpetrator's profile. They have nothing to do with a particular defendant or suspect, or the manner in which he was found, and they can be calculated before any suspect is located. They are fixed and unchanging. When a suspect is located by whatever means, the frequency and probability of the perpetrator's profile remain the same. They give the jury perspective on how few people are likely to have this profile and how incriminating it is that the defendant has it—regardless of how he was found. (Emphasis in original.)

(*Id*. at p. 1274.) Next, the "statistics refer to the rarity of the profile in the *relevant population(s)*. In general, an offender database is not the relevant population. Thus, we think the chance of finding a match *in a database* generally does not matter." (*Ibid*.) "The point is," continued the court, "the rarity of, or the chance of finding, the *perpetrator's* profile in the *perpetrator's* population(s). The chance of finding a particular defendant in an artificially created 'population' of criminals and arrestees is not germane." (*Id*. at pp. 1274–1275.) (Emphasis in original.) And,

> when a particular defendant is found by searching an offender database, that database of criminals and arrestees does not necessarily become the relevant population for gauging the rarity of the profile in a meaningful way. The relevant populations(s) *sic* are generally the major populations in the United States because they provide a jury with the most useful estimates, regardless of the fact that the particular defendant was found as a match by looking through a different population.

(*Id*. at p. 1275.)

Trial court judges retain discretion, however, to permit evidence of another statistic, known as the database probability statistic, if it meets standards of relevance and probative value given the facts of the case. (*People v. Nelson*, 42 Cal. 4th at 1267.) The database probability statistic estimates the chance of a random match to a predetermined profile when searching through a database of a given size. The database probability statistic is a function of both the size of the database searched and the random match probability statistic of the target profile. (See People v. Xiong, 215 Cal. App. 4th 1259, 1276, 155 Cal. Rptr. 3d 877 (5th Dist. 2013), as modified, (May 2, 2013) [describing and discussing database probability statistic].) This statistic was discussed in the National Research Council's 1996 publication *The Evaluation of Forensic DNA Evidence* (NRC II), at pages 7, 40, and 161.

For example, if a degraded crime scene DNA sample has fewer loci available and is characterized by a more common random match probability, then searching for it in a large offender database may result in a significantly greater chance of a coincidental match to a person having nothing to do with the crime. Of course, many, if not most, of the offenders in a database may not be plausible suspects in a given case in view of the age of the crime and/or the appearance of the perpetrator as described by witnesses. Such factors may affect the probative value of the database probability statistic, and should be considered when litigating its admissibility. (See *People v. Xiong*, *supra*, 215 Cal.App.4th at p. 1277 [concluding that exclusion of database probability statistic would be harmless if considered erroneous given the relatively insignificant difference in frequency statistics it would have provided].)

In addition to the random match probability (RMP) calculation and the database probability (DP) calculation, another method of calculating profile frequencies for database matches was proposed by the National Research Council's 1992 report. (*DNA Technology in Forensic Science* ("NRC I").) The report proposes that one set of loci be used to search for a match in a database, and a second, separate set of loci be used to confirm any resulting match. A frequency estimate would then be calculated for the match between the evidence profile and the suspect's profile only at the second set of loci. (NRC I, at p. 124.) Doing so creates a match scenario independent of the database search. By considering the two matches independently of one another, the database match becomes analogous to a suspect being identified through evidence other than DNA.

The NRC I approach differs from the RMP and database probability statistic because it disregards the probability of the initial database match and relies only upon the significance of the second match. It poses potential difficulties, however. For example, suppose the RMP for a database match is one in one billion, and the RMP for the second set of loci is one in one hundred thousand. If the second set of loci used for testing contains fewer loci than the original set, there exists the possibility of undervaluing the significance of the match. Further, use of a significantly smaller group of loci for the initial database search may lead to erroneous matches that would have been avoided had additional comparison points been utilized. The development and use of a sufficient number of "extra" loci with appropriate characteristics (e.g., independent inheritance) may be impractical. Moreover, additional testing may not be possible if the evidence item that generated the original profile was consumed during the initial testing. With no additional sample to test at supplemental loci, the question arises whether the results from the original test could be offered as evidence.

Yet another statistical approach in cold hit cases involves the calculation of a likelihood ratio (LR). This method differs from the previously discussed statistical methods. While the RMP and the database probability estimate the frequency of a profile in a population, the likelihood ratio compares the weight of the evidence given two different hypotheses. For instance, if a match has been found between an evidence profile and a suspect profile from a database search, a likelihood ratio can be calculated to compare the probability of a match occurring from the database search if the suspect is the source of the evidence profile, with the probability of a match occurring from the database search if the suspect is not the source of the evidence profile.

While the database probability calculation weakens the weight of the match found in a database search by the number of profiles in the database, the likelihood ratio does not rely on the probability of finding a matching profile in the particular database. Two mathematicians in the U.K., David Balding and Peter Donnelly, propose that the weight of a match found from a database search does not diminish, but in some cases can increase the weight of the DNA evidence. Part of this increase comes from not only the match between the suspect profile and the evidence profile, but the elimination of all other profiles in the database

as possible contributors of the profile. (*Evaluating DNA Profile Evidence When the Suspect Is Identified Through a Database Search*, (1996) 41 J. Forensic Sciences 603–607)

By using likelihood ratios to calculate the weight of a DNA profile match, there is the opportunity to quantify the effect of the DNA evidence on the overall strength of the case. Bayes's theorem multiplies the odds that the DNA samples came from the same source based on other evidence (prior odds) by the likelihood ratio to obtain the odds that the DNA samples came from the same source including the DNA evidence (posterior odds). In other words, "[t]he posterior odds are the prior odds multiplied by LR." (NRC II, at p. 131.) For example, if the likelihood ratio for a particular match is 10,000, the odds of the DNA from the evidence coming from the suspect are 10,000 times as great as before considering the DNA evidence.

Ultimately, the choice of statistics in a cold hit DNA case is a question of legal relevancy and probative value for trial court judges to resolve, not a question of science for scientists to resolve. (*People v. Nelson*, 43 Cal. 4th at 1264–65.) Thus any ongoing debate over proper statistical evidence does not implicate the foundational requirement of general acceptance of a new scientific technique discussed in People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976).

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§ 5:5. Likelihood ratios

As noted above, an alternative to the random match probability statistic is the likelihood ratio. This calculation weighs the probability that the suspect is the source of the evidence profile (P1), against the probability that the source of the evidence profile is a random individual not related to the suspect (P2). These two probabilities are resented as a likelihood ratio (LR) of the first over the second:
LR = P1 / P2

Assuming the suspect is the source of the evidence profile gives a probability of one for the numerator. The probability that a random individual is the source of the profile is the random match probability (RMP). Therefore the equation becomes:
LR = 1 / RMP

The qualifying statement for the probable association of two profiles with this calculation is given as: “This profile match is 10,000 times more likely if the DNA is from the suspect than if the DNA is from a random individual.”

Because for single-source profiles the likelihood ratio is simply one over the random match probability, generally the RMP is used instead of the LR. For mixtures the likelihood ratio offers a wide range of flexibility in its application. The likelihood ratio sets itself apart from other statistical methods used to estimate profile frequencies because it takes the suspect into account as part of the equation. The LR equation also offers an opportunity to calculate probabilities for multiple scenarios of a crime.

For example, suppose a mixture of DNA from two contributors was detected from a bloodstain at a crime scene. All alleles in the mixture can be accounted for by a combination of the victim and the suspect's profiles. A likelihood ratio can be calculated to explore the probability of several different scenarios for the mixture. Two of these include:

- The probability that the mixture detected was from a combination of DNA from the victim and the suspect, as opposed to a mixture of DNA from two random, unrelated individuals.
- The probability that the mixture detected was from a combination of DNA from the victim and the suspect, as opposed to a mixture of DNA from the victim and a random, unrelated individual.

If the LR for the first scenario is calculated to be 1,000, the conclusion is that the probability of this DNA mixture occurring is 1,000 more likely if it resulted from a combination of DNA from the victim and the suspect than if it resulted from a combination of DNA from two random, unrelated individuals.

A likelihood ratio greater than one favors the numerator of the calculation (i.e., the prosecution hypothesis): the stain is from a combination of DNA from the victim and the suspect. A likelihood ratio less than one favors the denominator of the calculation (i.e., the defense hypothesis): the stain is from a combination of DNA from two random, unrelated individuals. A likelihood ratio equal to one offers an equal probability for either hypothesis.

For discussion of the advent and increasingly widespread usage of probabilistic genotype software to generate likelihood ratios for complex DNA mixtures, see Chapter 11:7, post.

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Chapter 6. DNA Mixtures

Introduction

Biological evidence samples often contain DNA from more than one source. Such evidence presents a “mixed” DNA sample. In order to use information contained in a mixed DNA sample for comparison and possible identification purposes, an analyst must interpret the data to determine to what extent any individual contributor's profile can be distinguished from the mixture.

Historically, DNA mixture interpretation policies and procedures varied greatly between laboratories. For several years, efforts were underway to develop guidelines laboratories could look to when developing their protocols. In January 2010, the Scientific Working Group on DNA Analysis Methods (SWGDAM) released the *SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic Testing Laboratories*. This document expands significantly upon the group's previous guidelines, released in 2000, and provides clear guidance for the development of mixture interpretation policies and procedures. The 2010 SWGDAM guidelines are an effort to bring a level of uniformity to mixture interpretation throughout the forensic DNA community.

This chapter discusses the principles behind DNA mixture interpretation, the statistical methods used to qualify inclusions, and offers examples of calculations used in the interpretation process.

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§ 6:1. Identification and evaluation

Several common scenarios routinely result in DNA mixtures. These include mixtures of semen with vaginal secretions on vaginal swabs, blood mixed with sweat on clothing, blood from multiple contributors on an evidence item, and saliva with skin cells. Mixtures can also result from evidence stains deposited on environmental DNA. This occurs when a biological sample is deposited on a substrate where DNA was already present. Mixtures can also occur as the result of contamination either from the point of collection or at other steps in the analysis process.

DNA mixtures can be identified by the number of allelic peaks detected at each locus in a sample. Because humans have two copies of each autosome (non-sex chromosome), there is an expectation of a maximum of two alleles at each locus. When more than two alleles are detected at more than one locus in a sample, the presence of a mixture is indicated.

The interpretation of test results representing a mixture of DNA from two or more sources is generally accepted in the relevant scientific community as an application of the same essential technique employed for single source samples. (People v. Smith, 107 Cal. App. 4th 646, 665, 132 Cal. Rptr. 2d 230 (2d Dist. 2003); People v. Henderson, 107 Cal. App. 4th 769, 785–789, 132 Cal. Rptr. 2d 255 (4th Dist. 2003); see also People v. Rojas, 181 P.3d 1216, 1222–1223 (Colo. App. 2008) [citing cases from various jurisdictions].)

Ideally, the analyst will be able to differentiate between alleles attributable to a "major" contributor and "minor" contributor(s) to a mixture based on consistently divergent RFU levels. Ambiguity may exist that complicates this task, however, when more than two people contribute to a mixture and/or the peak heights on the electropherogram are too close in magnitude to be clearly attributable to discrete sources. (See State v. Bander, 150 Wash. App. 690, 208 P.3d 1242, 1247–1248 (Div. 1 2009).) Other anomalies, such as "stutter peaks" and "allelic dropout," can complicate mixture interpretation. (*People v. Bander,* 208 P.3d at 1248.) As discussed post, however, the advent and increasingly widespread usage of probabilistic genotype software has dramatically enhanced the ability of laboratories to interpret complex mixtures using likelihood ratios that often produce probative evidence for factfinders in criminal case litigation.

1) Single Source STR Profile Characteristics

To interpret mixture results, an analyst must rely on the properties of single-source short tandem repeat (STR) profiles, using those as tools to determine genotypes for individual contributors. In general, STR profiles attributable to a single source should exhibit similar characteristics. A single source STR profile may exhibit up to two allelic peaks at each locus. Any locus where two peaks are observed is a heterozygous locus, and means that the person has inherited different alleles from each parent. Any locus where one peak is observed is a homozygous locus, and means that the person has inherited the same allele from each parent.

Heterozygous peaks should exhibit balanced peak heights. Because an individual inherits equal amounts of his or her DNA from each parent, each allele at a locus has equal representation in the PCR. The ratio of peaks within a heterozygous locus should be close to 100%. However, peak height ratios for heterozygous loci in single source profiles generally range from 70–100%.

Homozygous peaks are approximately twice the height of heterozygous peaks labeled with the same color. A homozygous peak at a locus is actually comprised of two alleles, one from the individual's mother, and one from his/her father. Because the two alleles are the same size, there is no way to distinguish them from one another, and they are detected by the genetic analyzer as a single peak. This means that the homozygous peak comprised of two alleles should have a peak height approximately double that of a single heterozygote peak of the same color.

2) Number of Contributors To A Mixture

The minimum number of contributors to a mixture can be determined by taking into account the maximum number of alleles present at any one locus. For example, consider an analyzed STR sample that has more than two alleles at several locations, but no more than four alleles at any one locus. If each contributor to the mixture can be represented by two alleles, this mixture must have two contributors. It is possible that the mixture has more than two contributors, but barring a high level of genetic anomalies, there can be no fewer than two. If a mixture were to have any locus with five alleles, it must be concluded that the sample is a mixture of three or more contributors.

Depending on the quality of the mixture data, it may be possible to determine with a high amount of certainty the absolute number of contributors to a mixture. For a sample that exhibits all peaks well above the analysis threshold with no more than four alleles present at any one locus, it is reasonable to assume that there are only two contributors present. For a mixture that shows a high level of allelic dropout (undetected alleles below the analysis threshold) but only three alleles at any one locus, there is a possibility that the true number of contributors may be underestimated. In this situation, an analyst may only be able to make the assumption that the mixture contains DNA from at least two contributors.

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Forensic DNA Evidence: Science and the Law § 6:2

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Chapter 6. DNA Mixtures

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§ 6:2. Interpretation of results

Once a mixture is identified, and the number of potential contributors is determined, the next step is evaluating the sample for possible genotypes. This process is referred to as deconvolution, or mixture interpretation.

1) Deconvolution

The goal of a mixture interpretation is to determine the genotype combinations for any individual who could be included as a contributor to the mixture. The process of deconvolution takes into consideration the properties of a single-source profile and applies them as a logical tool to mathematically determine genotypes for possible contributors. Amplified STR alleles in a mixture, generally, exhibit the same properties as single-source profiles. However, because a mixture is comprised of multiple DNA profiles sharing the total input amount in the PCR, the actual amount of DNA added for each contributor to the mixture is less than that of a single-source profile. Sensitivity studies on single source DNA profiles show a decrease in overall profile quality as DNA template amount decreases. Peak heights (the overall intensity of allelic peaks) and peak balance (the ratio between the peak heights of two alleles at the same locus) decrease. The potential for allelic dropout (failure to detect alleles above the analysis threshold) increases. These effects on STR profile quality can complicate mixture interpretation.

To determine the possible genotypes for a locus, an analyst first considers how many alleles are present, and then how many contributors are assumed to be in the mixture.

a) Four-allele loci

The ability to assume a finite number of contributors to a mixture can greatly affect the amount of genotypes for possible contributors. For a four-allele locus in a mixture of only two contributors, with alleles A, B, C, and D, the possible genotype pairings are:

A,B with C,D
A,C with B,D
A,D with B,C

With only two contributors to a four-allele locus, not only the genotype possibilities, but also the genotype pairs, are limited. Each contributor must be heterozygous and thus responsible for two different alleles. There is no possibility that either contributor could share any of the alleles. This greatly limits the number of individuals in a population who could be included as possible contributors.

For that same locus, assuming at least two and possibly more contributors to the mixture, the possibilities increase to:

A,A A,B A,C A,D B,B B,C B,D C,C C,D D,D

This increase in possible genotypes is due to the acceptance of more than just two contributors to the mixture. Once the possibility for more than two contributors exists, it necessitates the acceptance of the homozygous genotypes A,A; B,B; C,C; and D,D. This also opens the possibility for allele sharing between contributors, increasing the amount of possible genotype pairs.

In addition, if allelic dropout is probable for the mixture, then the potential for lost alleles must also be considered. This allows for the pairing of:

A with any other allele, not B,C, or D
B with any other allele, not A,C, or D
C with any other allele, not A,B, or D
D with any other allele, not A,B, or C

With the assumption of at least two contributors and the possibility for allelic dropout, often no further interpretation of the mixture is possible. However, there are instances where, based on peak heights and relative donor contributions, determination of genotypes for one or more contributors to a mixture may be possible.

b) Three-allele loci

Loci with three alleles introduce the possibility of allele sharing between contributors. It is very common for contributors to a mixture to share several alleles. While it is very unlikely that two random individuals would share more than a few genotypes across an entire profile, shared alleles are expected. It is not uncommon for a fifteen-locus STR mixture of two contributors to have only two or three loci with four alleles. For the following examples, assume a two contributor mixture with all alleles detected:

For a three allele locus with alleles A, B, and C, the possible genotypes are:

A,A A,B A,C B,B B,C C,C

Given the stated assumptions, each contributor must have one of these genotypes. Therefore, it is necessary to consider genotype pairings. This means that if one contributor has a genotype of A,A, the second contributor must have the genotype B,C. Under our stated assumptions, there are only two contributors to this mixture with no allelic dropout. Therefore, all alleles must be accounted for between the two contributor genotypes.

Genotype pairs for a homozygous/heterozygous mixture are:

A,A with B,C
B,B with A,C
C,C with A,B

This scenario of a homozygous/heterozygous pairing is one possibility. For a heterozygote/heterozygote mixture the possibilities are not as absolute. If one contributor is A,B, there still exists the possibility of a C,C second contributor. However, it is also possible that the second contributor is A,C or B,C.

Genotype pairings for a heterozygote/heterozygote mixture are:

A,B with A,C or B,C
A,C with A,B or B,C
B,C with A,B or A,C

c) Two-allele loci

For a two-allele locus the inference of one contributor's type does not narrow the amount of possible genotype pairings. In this situation, there is always the possibility that any of the three genotypes exist for either of the two contributors; with the exception that both contributors cannot both share the same homozygous genotype. If one contributor is A,A, the other must have a B allele.

For a two-allele locus with alleles A and B, the possible genotypes are:

A,A A,B B,B

d) One-allele loci

The possibilities for a one-allele locus with the stated assumptions are narrowed further still. With only one allele present at a locus in a two-contributor mixture, both contributors must share the same homozygous type.

2) Peak Height Ratios

Once all possible genotypes have been determined, the list of genotypes may be narrowed further by considering pairings with respect to peak height ratios (PHR). The PHR for any two alleles is the ratio of the smaller allele to the taller allele, expressed as a percentage. For two peaks A and B, where A=950 RFU and B=1000 RFU, the PHR is calculated as:
PHR = A/B = (950/1000)*100 = 95%

For any good quality single-source STR profile, two alleles within a locus would have a peak height ratio of 100%. However, amplification is a dynamic process, and PHRs will generally fall somewhere between 70 and 100%. However, it is not uncommon to observe PHRs much lower than this in single-source samples, especially those with low amplification input amounts. Because the DNA input for any contributor to a mixed sample may be less than optimum, peak height ratios may be less balanced as well. The threshold for acceptable peak heights is determined by laboratory validation, and may be a single value (e.g., 50%), or may be a sliding scale dependent on peak height of the taller peak in a genotype pair. (e.g., >1000 RFU = 50%, >500 RFU = 40%, >200 RFU = 30%, <200 RFU = any).

Peak height ratios are an extremely useful tool in mixture interpretation. They are the main criteria used for determining the possibility of genotype pairings. PHRs can be calculated to determine if two peaks can pair in a mixture to form a supported genotype pair. For the following four-allele locus with peaks A,B,C, and D, assume a two-person mixture with all alleles detected and a PHR threshold of 50%:

Example 1:
Determine which peaks can pair with allele A.
A=300 RFU B=350 RFU C=975 RFU D=1050 RFU
$PHR_{A,B}$ = 300/350 = 86% $PHR_{A,C}$ = 300/975 = 31% $PHR_{A,D}$ = 300/1050 = 29%
Allele A can only pair with allele B above the PHR threshold.
$PHR_{C,D}$ = 975/1050 = 93%
Genotype C,D is also above the PHR threshold, therefore the only genotype pairing for this locus supported by the assumptions is A,B with C,D.

The use of peak height ratios to determine genotype pairs for four-allele loci is generally straightforward. For loci with three or fewer alleles, the process becomes more involved. A three-allele locus in a two contributor mixture presents the possibility that one of the alleles is shared. Just as with a homozygous peak that is comprised of two separate alleles of the same size, in

a mixture, a single peak may have contributions from more than one source. Peak heights (PH) of shared alleles are additive. The height of a shared peak is simply the peak height attributable to one contributor (C1) plus the peak height attributable to the second contributor (C2). For a shared allele A:

$PHA_{total} = PHA_{C1} + PHA_{C2}$
If two contributors are present in a mixture with the following genotypes:
C1: A=500 RFU and B=500 RFU
C2: A=1000 RFU and C=1000 RFU
It is expected that the alleles in the resulting mixture will be detected as:
A=1500 RFU B=500 RFU C=1000 RFU

When interpreting a mixture, the exact amount of contribution from each individual to a shared peak cannot be absolutely determined, but may be inferred by considering the peak heights of the unshared alleles.

For the next example consider a three-allele locus with alleles A,B, and C in the same two-person mixture as above:

Example 2:
A= 400 RFU B= 750 RFU C= 1200 RFU
All possible genotypes for this locus are:
A,A A,B A,C B,B B,C C,C
The PHR for A,B is:
$PHR_{A,B}$= 400/750 = 53%
A genotype of A,B paired with C,C is supported by the assumptions.
The PHR for B,C is:
$PHR_{B,C}$ = 750/1200 = 63%
A genotype of B,C is supported by the assumptions.
The PHR for A,C is:
$PHR_{A,C}$ = 400/1200 = 33%
A pairing of genotypes A,C with B,B is not supported by the assumptions. Note that this eliminates B,B as a possible genotype. However, if one contributor is A,C and the other is either A,B or B,C, an A,C genotype may be supported by the assumptions.
Could allele C be shared between the two contributors?
A= 400 RFU B= 750 RFU C= 1200 RFU
Shared peak heights are additive, so some division of allele C is needed. Peak height ratios for single source samples should approach 100%. Assume that contributor with type A,C has a PHR of 100%. Contributor A,C represents 400 RFU of the total peak height of peak C. By subtracting the assumed shared portion of peak C:
1200 RFU – 400 RFU = 800 RFU
800 RFU of peak C is assumed to be attributable to contributor B,C.
The PHR for B,C is:
750/800 = 94%
The sharing of allele C is possible.

3) Donor Ratio and Mixture Proportions

In addition to peak height ratios, the amount of DNA donated by each contributor to a mixture relative to the other contributors can be determined and used to assist in deconvolution. If one individual contributes three times as much DNA to a mixture as a second individual, the peak heights attributable to Contributor 1 will be approximately three times as high as those attributable to Contributor 2. To calculate the relative representation of individuals in a two contributor mixture the peak heights of four-allele loci are used. Because in a two-contributor mixture, four-allele loci offer the advantage of non-shared alleles, it is possible to get a clear picture of each donor's relative contribution. An example of two methods used to calculate the relationship between donor contributions are the donor ratio (DR) and mixture proportion (Mx).

a) Donor ratio

A donor ratio is calculated by dividing the sum (Σ) of the peak heights from one contributor (C1) by the sum of the peak heights from a second contributor (C2).

$DR = \Sigma PH_{C1} / \Sigma PH_{C2}$

The ratio is then expressed as a DR:1. For example, "The donor ratio of C1:C2 for this mixture is 4:1." Either contributor can be used as C1, however, using the major contributor (taller) peaks will give a DR >1.

b) Mixture Proportion

A mixture proportion is calculated by dividing the sum of either the peak height or peak area[1] of the minor (smaller) alleles by the sum of all alleles in the locus. This measures the percentage of total peak height attributable to the minor contributor. For a locus with alleles A,B,C, and D where A and B are the minor peaks:
$Mx = (PH_A+PH_B)/(PH_A+PH_B+PH_C+PH_D)$

The proportion is expressed as a decimal that represents the percentage of peak height represented by the minor contributor in the mixture. For example, an Mx of 0.25 means that 25% of the total peak height for a locus is represented by the minor contributor. As the Mx increases, the difference between the peak heights of major and minor contributors decreases. Where both contributors are equal in a mixture, the Mx will equal 0.5. In other words, each contributor shares 50% of the peak height for the locus.

For each of these methods, determining which alleles are likely to pair for minor and major contributors is relatively straightforward for DR of 3:1 and higher and Mx of .25 and lower. At these levels it is likely that pairings between taller and smaller peaks would not be supported by an assumed PHR threshold, and would therefore be eliminated. It is when these two values begin to favor a more balanced ratio between contributors that clear major and minor pairings do not exist.

Both donor ratios and mixture proportions can be used to test if a genotype pairing is supported for either a major or minor contributor. Consider a three-allele locus assuming a two-contributor mixture with a PHR threshold of >50% and a DR of 3:1:

Example 3:
A=900 B=1300 C=1200
Is it possible that a major contributor to this mixture could be A,A?
First, check to see if a B,C pairing is possible given the PHR threshold:
$PHR_{B,C} = 1200/1300 = 92\%$
A,A and B,C airing is supported by the PHR assumption.
Next, check to see if, given the DR assumption, A,A could be the major contributor:
DR= 900/(1300+1200) = 0.36
The DR of 0.36 is much less than 3, therefore, it is not possible for A,A to be a type for the major contributor to this mixture. However, the major contributor could be a B,C with a minor A,A:
DR=(1300+1200)/900 = 2.7
How would this calculation look using an Mx of 0.25?
To check if, given the Mx assumption, A,A could be the major contributor, the minor contributor's proposed type B,C becomes the numerator of the calculation:
Mx=(1300+1200)/(900+1300+1200) = 0.74
The Mx of 0.73 is much more than 0.24 therefore, it is not possible for A,A to be a type for the major contributor to this mixture. However, the major contributor could be a B,C with a minor A,A:
Mx=(900)/(900+1300+1200) = 0.26

Donor ratios and mixture proportions can vary from locus to locus across a mixture. This variability tends to be dependent on the quality of the mixture and peak heights. In order to allow for this variability, laboratories may establish a range of acceptable DR or Mx values. For example, a donor ratio of 3:1 with a threefold range would support donor ratios from 1:1 up to 9:1. A mixture proportion of 0.4 with a ±0.20 range would allow for mixture proportions from 0.20 to 0.60.

c) Stutter

When performing mixture interpretation calculations an analyst must be conscious of peaks in stutter positions. Stutter peaks are DNA peaks that occur four bases in size away from an allelic peak. Peaks that are four bases smaller than an allelic peak are said to be in an N-4 stutter position. Peaks that are four bases larger than the allelic peak are said to be in an N+4 stutter position. Stutter is a result of dynamic effects of the polymerase chain reaction, and is a well-documented phenomenon. A more detailed discussion on stutter can be found in § 3:4.

Genetic analysis software may be set to filter all peaks in an N-4 stutter position that are below a set peak height percentage. A filter will leave N-4 stutter peaks unlabeled, even if it is above the analysis threshold. This essentially renders the stutter peaks “undetected” to the analyst.

In mixtures with a major component that is significantly higher than a minor component, it is possible that allelic peaks attributable to a minor contributor heterozygote pair may be filtered out as stutter. If the minor contributor's allele that is not in the stutter position is above the laboratory's homozygote threshold (the peak height at which it is acceptable to consider a peak a homozygote), interpretation without consideration of filtered peaks in stutter positions may lead to the incorrect exclusion of a genotype pairing between the minor allele and the stutter peak.

4) Assumed Donors

Some forensic DNA samples have an expectation that a particular donor is present. For example, a victim is expected to be a contributor to DNA detected from her own vaginal swab. Samples such as this are referred to as intimate samples. Any item that has been collected directly from an individual's body is considered intimate.

An assumed donor's profile can be an extremely useful tool for mixture deconvolution. With the ability to attribute a genotype to one contributor, the amount of possible foreign contributor genotypes may be greatly decreased. For example, consider a four-allele locus in a two contributor mixture with alleles A, B, C, and D. With no assumed donor, the possible genotype combinations are:

Contributor 1	Contributor 2
A,B	C,D
A,C	B,D
A,D	B,C
B,C	A,D
B,D	A,C
C,D	A,B

If an assumed contributor (Contributor 1) to this mixture has a genotype of A,C the only possible genotype for a foreign contributor is B,D. The B and D alleles are referred to as obligate foreign alleles. The same benefit can also be seen in three- and two-allele loci, although it may not be possible to narrow the foreign contributor types to just one possibility. For example, in a three-allele locus with alleles A, B, and C, possible genotype combinations for a two-contributor mixture are:

Contributor 1	Contributor 2
A,A	B,C
A,B	A,C or B,C or C,C

A,C	A,B or B,C or B,B
B,B	A,C
B,C	A,A or A,B or A,C
C,C	A,B

If Contributor 1 has the genotype A,B then a foreign contributor could have either an A,C or B,C or C,C genotype. A reference profile with any of these genotypes would be included as a possible foreign contributor to the mixture at this locus. In this example it is helpful to note that all possible foreign contributor genotype possibilities include a C allele.

a) Obligate alleles

Obligate alleles are peaks that can definitively be attributed to one contributor. Most often that occurs when assuming a donor. As with the above example, because the assumed donor is an A,B, it means that any foreign contributor to the mixture must have a C allele. Obligate alleles can be specified during database searches. For example for this three-allele locus, a search without an obligate allele specified would return candidate profiles with all possible genotype combinations for the locus, including A,B; B,B; and A,A even though under the stated assumptions, those genotypes are not supported. When the C allele is designated as an obligate for the search, only candidate profiles with the genotypes A,C; B,C; and C,C will be included in the search results.

5) Special Considerations

Just as with single-source DNA profiles, mixtures are susceptible to effects from environmental factors. However, these effects can be either amplified or masked in mixture samples. Patterns specific to inhibition (interference with amplification) and degradation (deterioration of DNA in a sample) seen in single-source samples can act as a guide to recognizing and interpreting these effects in mixtures. The effects should be treated with even more caution in mixed samples.

a) Inhibition

Inhibition can be caused by chemical components in a DNA sample that prevent the polymerase chain reaction (PCR) from working completely. DNA extraction procedures generally include steps to remove any inhibitors that may be present; however, some may persist and be introduced to the PCR. Inhibition can lead to non-amplification of a few to several loci as well as affect peak height balance and donor proportion. Inhibited mixtures often are unsuitable for interpretation.

b) Degredation

Degraded samples may offer challenges for interpretation regarding peak height balance, allelic dropout, and donor proportions. A degraded DNA sample can be identified by a pattern of sharply decreasing peak heights. This drop-off in peak intensity is referred to as a "ski-slope effect," due to its resemblance to a ramp. In a degraded sample, low molecular weight (smaller) STR fragments have high peak heights. A sharp steady decrease in peak heights is observed as molecular weight (size) of the fragments increases, resulting in very small peaks at larger molecular weight loci. Often times, peaks at the largest molecular weight loci are not detected above the analysis threshold. Degraded samples in general may offer more opportunity for interpretation than an inhibited sample. But caution must be exercised when interpreting a degraded mixture.

c) Differential degradation

One particular concern in degraded mixtures is the effect of differential degradation. A fresh evidentiary stain that has been deposited on a surface where DNA is already present is a common scenario. As DNA is exposed to environmental conditions, it begins to degrade. Therefore, if partially degraded DNA is present on a surface where a new, fresh DNA sample is placed, when

the stain is sampled, a mixture of both DNA stains will be collected. When the sample is analyzed, the fresh DNA should exhibit balanced peak heights across all loci while the degraded DNA will most likely show a pattern of decreasing peak heights. This overlay effect can cause a major, degraded contributor at the smaller molecular weight loci to appear as the minor component at the larger molecular weight loci. In the absence of an assumed contributor, this can lead to incorrect attribution of possible genotypes.

6) Inclusion and Exclusion

If a mixture has been evaluated as suitable for comparison, and once all possible genotypes have been determined, it is appropriate to compare reference samples for inclusion or exclusion as possible contributors to the mixture.

a) Inclusion

If a reference sample possess genotypes that are included as possible contributor types at all loci tested, the profile can be included as a possible contributor to the mixture. An inclusionary statement may read: "A DNA mixture was detected from item X. Assuming the presence of two contributors in this mixture, John Doe is included as a possible contributor to DNA detected from this item." The phrase "cannot be excluded" may also be used to convey the same association.

These statements should not be interpreted as meaning that because John Doe can be included as a possible contributor that his DNA is in fact part of the mixture. The statement simply means that John Doe's STR profile includes a genotype at each locus that is also included as a possible genotype for a contributor to the mixture at the corresponding locus. A statistical estimation of the probability of inclusion must be offered with any inclusion statement.

b) Exclusion

If a profile does not possess a genotype that can be included as a possible contributor at all loci tested, then the profile is excluded as a possible contributor. An exclusionary statement may read: "A DNA mixture was detected from item X. Assuming the presence of two contributors in this mixture, John Doe is excluded as a possible contributor to DNA detected from this item." The phrase "cannot be included" may also be used to convey the same association. A statistic for the probability of inclusion for the mixture is not required to qualify exclusion.

As the complexity of a mixture increases, it is possible that data may not be available at all loci, or that the information at an individual locus is not suitable for comparison. The ability to conclusively include or exclude a possible contributor from a mixture becomes more complex. It is essential that the criteria used to include or exclude contributors is clearly stated in the case notes and decided upon prior to the comparison of the interpreted mixture profile with any reference samples. The criteria for inclusions, exclusions and inconclusive results are guided by polices established by the testing laboratory.

Footnotes

1 For examples given here, all calculations are performed using peak heights.

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§ 6:3. Mixture statistics

Any inclusion of a reference profile as a potential contributor to a mixture must be qualified by a statement of the significance of the inclusion. If a single-source profile is determined from a mixture, the random match probability (RMP) can be applied just as with non-mixed samples. When a mixture interpretation includes more than a single profile as a potential contributor, a different calculation is appropriate. This may be a modified version of the RMP, the likelihood ration (LR), or the combined probability of exclusion/inclusion (CPE/CPI). The appropriate calculation can be selected based on the stated assumptions used for interpretation. (Scientific Working Group on DNA Analysis Methods, *SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories* (2010).)

1) Random Match Probability (RMP)

The random match probability applies the product rule to determine the estimated frequency of a profile in a population. The calculated frequency for each allele in a genotype at a locus is multiplied by the frequency of each of the other loci. The resulting frequency is a measure of the probability that an unrelated individual, at random would by chance possess the profile.

When this calculation is used on an interpreted mixture profile it is referred to as a modified RMP. At each locus, the probability for each possible interpreted genotype is added together. The resulting sums are then multiplied together to calculate an overall probability that a random unrelated individual would, by chance, be included as a contributor to the mixture.

The main distinguishing feature of this calculation is that it assumes the number of contributors present in a mixture. If the modified RMP is calculated assuming a number of donors to the mixture, but considering all genotype combinations for the assumed contributors, it is an unrestricted calculation. If peak height ratio and donor proportion information is used to refine the list of possible genotypes, the calculation is referred to as restricted.

2) Likelihood Ratio (LR)

The likelihood ratio is a ratio of the probability of the same event happening given two different sets of assumptions. For a single-source profile, the numerator assumes that the evidence profile came directly from the suspect. The denominator assumes that the evidence profile came from a random individual with the same profile. This calculation becomes LR=1/RMP.

For mixture profiles, the likelihood ratio can be calculated as either restricted or unrestricted depending on the consideration given to peak heights and donor proportions. For an interpreted mixture profile, the likelihood ratio numerator becomes the probability that the suspect and another contributor with an included genotype are contributors to the mixture. The denominator is the probability of two random included individuals.

The likelihood ratio distinguishes itself from the RMP and CPE/CPI in that it is the only calculation of the three that assumes the presence of the suspect. It also can be calculated using multiple different scenarios, each one with a separate likelihood of occurrence.

3) Combined Probability of Exclusion/Inclusion (CPE/CPI)

In a case where two or more people contributed DNA to a mixture, and not every allele in the mixture can be attributed to a separate source, the expert witness may be able to offer a statistic expressing the percentage of the population that could have contributed to the mixture (or stated differently, the percentage of the population not excluded as a potential contributor). This is known as a combined probability of inclusion, and reflects the sum of the frequencies of all genotypes contained within the mixture. (See National Research Council, *The Evaluation of Forensic DNA Evidence* 127 (1996); George v. Almager, 674 F. Supp. 2d 1160, 1189–1190 (S.D. Cal. 2009), aff'd, 432 Fed. Appx. 683 (9th Cir. 2011), petition for cert. filed (U.S. July 26, 2011).)

The combined probability of exclusion/inclusion (CPE/CPI) calculation differs from the RMP and LR because it does not allow for the assumption of a number of donors to a mixture. For this calculation, all genotype combinations are considered. Because of this provision, an unrestricted CPE/CPI is not appropriate for mixtures with allelic dropout. This calculation is only used for mixtures where all alleles are detected. It is possible to calculate an unrestricted CPI for a mixture where allelic dropout is present in perhaps one locus only. In this instance, the locus with allelic dropout would be excluded from the calculation.

For mixtures with clear major donors and perhaps a low-level contributor with a few trace alleles detected near the analysis threshold, a restricted CPI may be calculated using all possible combinations of just the major alleles.

The probability of inclusion (PI) is calculated as the sum of the allele frequencies squared for a locus. The PI for each locus is then multiplied by all other PI to calculate the CPI for the profile. The CPE is then 1-CPI.

Any of these calculations may be applied to any or all of the loci in a mixture to qualify the inclusion of an individual to a mixture. However, only one type of calculation can be used per mixed sample. If RMP is used, it must be used on all loci. A CPI cannot be calculated for some loci in the mixture and RMP for others.

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§ 6:4. Interpretation software

1) Overview

The process of mixture interpretation represents a significant portion of the total analyst hours required to produce a reportable DNA result. In order to aid the interpretation process, several software tools are available to perform the calculations necessary for mixture deconvolution. The programs are structured to use analyst and laboratory established parameters and assumptions to evaluate, interpret, and determine possible contributor profiles from DNA mixture data.

For example, an analyst may use a software tool to determine possible major and minor contributor genotypes from a two-person mixture. The analyst will input the allelic peak data (*e.g.* allele designations and peak heights) into the software. The software will then use the mixture data to perform calculations for several genotype combinations for each contributor at every locus. Potential genotype combinations are then accepted or rejected based either on their adherence to established mixture analysis parameters or by how probable it is that a specific genotype pairing would occur. The analyst can then use these results to perform comparisons to reference samples and draw conclusions about an individual's inclusion or exclusion as a contributor to the mixture.

Interpretation software tools are not meant to replace the analyst's evaluation of the data, but simply to streamline the mixture deconvolution process and assist the analyst in forming his or her conclusions.

2) Probabilistic Genotype Software

Beginning in 2016, forensic DNA laboratories began using probabilistic genotype software to assist in the qualitative interpretation of DNA mixtures. The software generates statistical models of observed allele combinations. The results of such modeling are likelihood ratios that compare competing theories in a case.

In June 2015, the Scientific Working Group on DNA Analysis Methods (SWGDAM) issued a document entitled *Guidelines for the Validation of Probabilistic Genotyping Systems*. (Available at www.swgdam.org/publications.) It includes the following general description of the technology at pages two-three:

> A probabilistic genotyping system is comprised of software, or software and hardware, with analytical and statistical functions that entail complex formulae and algorithms. Particularly useful for low-level DNA samples (i.e., those in which the quantity of DNA for individuals is such that stochastic effects may be observed) and complex mixtures (i.e., multi-contributor samples, particularly those exhibiting allele sharing and/or stochastic effects), probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results. Historical methods of mixture interpretation consider all interpreted genotype combinations to be equally probable, whereas probabilistic approaches provide a statistical weighting to the different genotype combinations. Probabilistic genotyping does not utilize a stochastic threshold. Instead, it incorporates a probability of alleles dropping out or in. In making use of more genotyping

> information when performing statistical calculations and evaluating potential DNA contributors, probabilistic genotyping enhances the ability to distinguish true contributors and non-contributors. A higher LR [likelihood ratio] is typically obtained when evaluating a person of interest (POI) who is a true contributor to the evidence profile, and a lower LR is typically obtained when the POI is not a true contributor. While the absence of an allele or the presence of additional allele(s) relative to a reference sample may support an exclusion, probabilistic genotyping approaches allow inclusion and exclusion hypotheses to be considered by calculating a LR in which allele drop-out and drop-in may be incorporated.

(See Moss, Note, The Admissibility of TrueAllele: A Computerized DNA Interpretation System (2015) 72 Wash. & Lee L. Rev. 1033, 1061 ["TrueAllele relies on a class of algorithms derived from a Bayesian statistical analysis called Monte Carlo-Markov Chain (MCMC) modeling. The MCMC statistical approach has been used in a variety of situations to successfully model many complex data sets"].)
(Footnote omitted.) The two principle software packages utilizing a probabilistic genotype approach are TrueAllele® and STRmix®.

Case law and academic commentary addressing the admissibility of probabilistic genotype software has begun to emerge. One 2017 journal article, based on the author's research into the issue, asserted that "[c]ourts have nearly universally admitted the results of these programs over objection in *Frye/Daubert* litigation, [fn] and in at least one case, a defendant used results to convince prosecutors to support vacating his conviction [fn]." (Roth, Machine Testimony (2017) 126 Yale L.J. 1972, 2019 & fn. 247; see *United States v. Gissantaner* (6th Cir. 2021) __ F.3d __ [2021 U.S.App. Lexis 6465, *17-*18 [STRmix "has garnered wide use in forensic laboratories across the country. More than 45 laboratories use it, including the FBI and many state law enforcement agencies. At this point, STRmix is the 'market leader in probabilistic genotyping software.' [Citation.] [¶] Consistent with this reality, numerous courts have admitted STRmix over challenges to its general acceptance in the relevant scientific community"] United States v. Tucker (E.D.N.Y. 2020, 18 CR 0119) 2020 U.S. Dist. Lexis 3055, *8-*13 [discussing STRmix® admissibility and reviewing related decisions across jurisdictions]; United States v. Lewis (D.Minn. 2020, 18-cr-194) 2020 U.S. Dist. Lexis 38705 [extensive discussion of probabilistic genotyping software and related admissibility issues]; State v. Simmer (Neb. 2019) 935 N.W.2d 167 [same]; United States v. Gissantaner (W.D. Mich. 2019) 417 F.Supp.3d 857 [STRmix® results not admissible under Daubert analysis]; People v. Bullard-Daniel, 54 Misc. 3d 177, 42 N.Y.S.3d 714 (County Ct. 2016) [STRmix software admissible under *Frye* test]; Note: The Admissibility of TrueAllele: A Computerized DNA Interpretation System (2015) 72 Wash. & Lee L. Rev. 1033; State v. Wakefield, 47 Misc. 3d 850, 9 N.Y.S.3d 540 (Sup 2015) [TrueAllele software admissible under *Frye* test].)

Courts and commentators have also devoted attention to questions of discovery related to this kind of interpretive software; in particular, whether the manufacturer's "source code" and other programming details must be provided to the opponent of the evidence in order to provide a sufficient basis on which to understand and potentially challenge the reliability of results. (See Imwinkelried, Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques (2016) 66 DePaul L. Rev. 97.) For a discussion of California case authority addressing the prosecution's discovery obligations related to commercial mixture interpretation software, see Chapter 10:1, subsection 4, ante.

Note, however, that courts continue to carefully scrutinize proffered mixture interpretation evidence, and may exclude it in cases where laboratories become overly aggressive and interpret complex mixtures in ways not supported by their own validated protocols. An example of this is found in United States v. Williams (N.D. Cal. 2019) 382 F.Supp.3d 928. Williams involved a pretrial defense motion to exclude prosecution evidence that a defendant contributed DNA to a mixed sample. The sample had been interpreted with a probabilistic genotyping program called Bullet. The question presented to the court was "whether Bullet was validated to analyze the mixture at issue here." (*Id.* at p. 929.) The court concluded that it was not, because the mixture in the case may have consisted of more than four contributors, while the Bullet program had been validated by the laboratory only for mixtures of up to four contributors. (*Id.* at pp. 929, 931.) Ultimately, the question was one of reliability under Rule 702 of

the Federal Rules of Evidence. (*Id.* at p. 935.) Based on the body of evidence presented, the court found that the DNA analyst "did not reliably conclude that only four individuals contributed DNA to the mixture at issue." (*Id.* at p. 936.) Of significance to the court was evidence that SERI, the laboratory in question, "demonstrated an inability to distinguish five-person mixtures from four-person mixtures. During the GlobalFiler validation study, it did not correctly identify a single five-person mixture. [The analyst] asserted that these errors occurred because 'by coincidence,' the individuals who contributed DNA to the study shared alleles. But a 100% rate of error gives no confidence in SERI's ability to be accurate if faced with the same coincidence in the real world." (*Id.* at p. 937.)

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Forensic DNA Evidence: Science and the Law Ch. 7 Introduction

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Chapter 7. Alternate DNA Testing Methods

Introduction

Short tandem repeat (STR) testing is currently the most widely used method for forensic human identification. However, in cases where STR testing has either been unsuccessful or has failed to answer the question of interest, other testing methods exist that scientists can utilize.

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§ 7:1. Y chromosome short tandem repeats

The Y chromosome is one of the smallest chromosomes in the human genome. It is passed from one generation to the next from father to son. The presence of a Y chromosome at conception triggers a chemical chain reaction of events that, barring any anomalies along the way, will result in the development of a male individual. Y chromosome short tandem repeats, or "Y-STRs," are short tandem repeat regions that occur only on the Y chromosome.

1) Inheritance

DNA contained inside the nucleus of a cell is packaged into tightly coiled segments called chromosomes. Each human cell, with the exception of the sex cells (i.e., egg and sperm), contains one pair of sex chromosomes (i.e., X and Y) and twenty-three pairs of autosomes (i.e., non-sex chromosomes). Each autosome pair is made up of two versions of the same chromosome; one inherited from the mother and one from the father. The sex chromosomes are two different chromosomes. A female inherits an X chromosome from each parent. A male inherits an X chromosome from his mother and a Y chromosome from his father.

During the production of sex cells, a copy of one half of each of the mother's chromosome pairs goes into each egg. A copy of one half of each of the father's chromosome pairs goes into each sperm. Half of all sperm cells produced by a male individual thus contain a Y chromosome, and half contain an X chromosome. At conception an egg can be fertilized by either a sperm containing an X chromosome, or a sperm containing a Y chromosome.

At just 60 million base pairs in size, the Y chromosome is almost one-third the size of its partner, the X chromosome. During sex cell production, autosomes trade sections of DNA that represent specific traits (i.e., genes). This ensures continued genetic variation in a population. The process is facilitated by the similarity between each chromosome of an autosomal pair. The X and Y chromosomes, however, vary not only in size, but also gene content. Because of these differences, the gene trading, or recombination, that takes place routinely with autosomes occurs only on a very small scale between the X and Y chromosomes.

Barring mutations, 95% of the genetic information on the Y chromosome is left unchanged from one generation to the next. Because of this conservation, all male relatives from the same paternal line will have the same genetic information in the non-recombinant region of their Y chromosomes. There is also a large portion of the Y chromosome that is comprised of regions that are not represented on the X chromosome. This means that genetic testing in these regions produces results that are specific to male individuals only. In other words, Y chromosome specific genetic testing of DNA from female individuals produces no result.

2) Typing Methods

Despite its small size, the Y chromosome is rich in STR regions. Over 300 Y-STR regions appropriate for human identification have been characterized. The typing method for Y-STRs is the same as for autosomal STRs, namely, polymerase chain reaction (PCR) multiplex amplification followed by capillary electrophoresis. However, the STR profile generated from Y-STR amplification has different characteristics from that of an autosomal STR amplification. Because each male individual has only

one Y chromosome, the Y-STR profile generated should have only one allele present at each locus, as opposed to two with autosomal STRs. Thus a Y-STR profile is referred to as a haplotype, as it contains half of the gene compliment of a somatic (i.e., non-sex) cell. This means that, unlike autosomal STR loci that are inherited independently of one another, Y-STR loci are inherited in tandem. This is why all the males from a genetic lineage will have the same Y-STR type.

Just as with autosomal STRs, the Scientific Working Group on DNA Analysis Methods (SWGDAM) Y-STR subcommittee selected core loci for Y-STR testing in the United States. Selection of a core set of loci for Y-STR testing allows direct comparison of haplotypes generated by different laboratories.

3) Evidentiary Significance

Whereas autosomal STRs can determine the source of a DNA profile with a high degree of certainty, a Y-STR haplotype can, at best, match a questioned haplotype to that of a male lineage. If a match is made between an evidence Y-STR profile and a suspect Y-STR profile, the match must be qualified by a statement such as: "The Y-STR haplotype detected from item X matches the Y-STR haplotype detected from the reference from suspect Z. Therefore, neither suspect Z, nor any of his paternally related male relatives can be excluded as a possible source of the male DNA detected from item X." An association of this kind does not offer the specificity of an autosomal STR match.

a) Statistics

Because all Y-STR loci are located on one chromosome with no recombination, the product rule may not be used to estimate the rarity of a profile in a population. Instead, rarity estimates are calculated with the counting method.

As the name implies, the counting method estimates the frequency of the Y-STR profile as the number of times the haplotype has been observed in the searched database. For example, in a database of 2,000 haplotypes, if the searched haplotype is found once in the database, it is said to have a frequency of one in 2,000. Because this estimate is dependent on the size of the database, the frequency estimate will change with the sample size of the database and the number of observances with each search. It is imperative when reporting a frequency estimate for a haplotype search that the results specify the database searched, number of profiles searched, number of matches found, and the loci searched.

In addition to the haplotype frequency, an estimation of the rarity of the haplotype frequency may be applied. This estimation, called a confidence interval gives, with a specified degree of certainty (e.g., 95%), the maximum percentage of a population that would be expected to have the haplotype of interest. The estimation of the maximum frequency is referred to as an upper bound limit. The calculation takes into account the number of observances of the haplotype in the database being searched as well as the size of the database.

b) Haplotype databases

As researchers have developed techniques for analyzing Y-STRs, they have also compiled databases of haplotypes from their test samples; however, these databases are all individual entities. The statistical significance of a search performed in a database is dependent on the specific database searched. As Y-STR testing has become more widely used in the forensic community efforts have been made to create a U.S. Y-STR database. A centralized database for Y-STRs does exist in Europe; however, it includes only a small number of core loci. An effort is underway in the U.S. by scientists at the University of Central Florida to compile a national Y-STR database comprised of a 49-locus haplotype. The hope is to eventually consolidate all individual databases into a centralized database with the ability to calculate frequencies for haplotypes at 49 loci and within specific racial groups.

4) Forensic Science Applications

Although Y-STR data may not be able to offer identification to the degree that autosomal STRs do, there are useful applications for Y-STR typing in forensics.

a) Sexual assault

In sexual assault cases where evidence often is comprised of a large quantity of female DNA mixed with a low amount of male DNA, Y-STRs can offer a chance to identify a suspect who may have remained undetectable with autosomal STR testing. A labia swab from an assault with reported oral copulation of the victim by the suspect may contain saliva from the perpetrator. In this case, a differential extraction is not appropriate, as there is no way to separate the male non-sperm cells from the female cells. It is likely that the female's DNA will overshadow the male DNA, leaving the possibility that the male's information may be lost. By amplifying only Y-STRs, the female DNA in the sample is undetected, thereby allowing any male DNA in the sample to be analyzed. If a suspect reference is available for comparison, Y-STRs may be able to confirm a match between the suspect's haplotype and the haplotype from the evidence.

Y-STR analysis can also be very helpful in sexual assault cases with vasectomized male perpetrators, where differential extraction will not be able to partition male from female DNA. Y-STR analysis offers a method by which the perpetrator's DNA can be detected even in the presence of high amounts of female DNA.

b) Familial searches

For cases where a database search has produced a pool of candidate matches for possible relatives of a perpetrator, Y-STRs can be used to eliminate any offender who does not share the perpetrator's paternal lineage. Moreover, a Y-STR match increases the confidence that an actual familial relationship exists between a known database offender and the questioned evidence profile.

c) Limitations

Even with the existence of reference databases for the estimation of haplotypes frequencies, no offender Y-STR database is available for searches of suspectless cases. At present, the usefulness of Y-STR typing extends only to cases with a suspect reference with which to compare haplotypes.

5) Y-STR Admissibility

In 2012, for the first time, a California appellate court concluded that the results of Y-STR analysis were admissible. In People v. Stevey, 209 Cal. App. 4th 1400, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013), the defendant was convicted of various sex crimes. Y-STR testing with the "Yfiler kit" was performed on pubic hairs collected during the investigation. (209 Cal. App. 4th at 1407–1408.) A prosecution expert testified that the Y-chromosome haplotype matched the defendant's, and a statistical rarity estimate was given. (*Id*. at 1408.) The trial court denied a defense request to hold a hearing under People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976), to determine whether the Y-STR testing was a generally accepted technique in the relevant scientific community. (*Id*. at 1410.)

The Court of Appeal affirmed, holding that "Y-STR testing does not embrace new scientific techniques" and thus is not subject to a first-prong *Kelly* determination. (*Id*. at 1412.) The *Stevey* court described how the methods and technologies involved in Y-STR analysis are analogous to those used in conventional STR typing, and it cited a number of cases from other jurisdictions affirming the fundamental reliability of the technique. (*Id*. at 1412–1415.) It further held that "use of the counting method and the confidence factor as a conservative adjustment to the statistical probability of a match is also generally accepted within the scientific community." (*Id*. at 1415.) A number of cases from other jurisdictions have reached similar conclusions about Y-

STR typing. (See, *e.g.*, State v. Calleia, 414 N.J. Super. 125, 148–149, 997 A.2d 1051 (App. Div. 2010), judgment rev'd, 206 N.J. 274, 20 A.3d 402 (2011); Shabazz v. State, 265 Ga. App. 64, 592 S.E.2d 876, 879 (2004); Curtis v. State, 205 S.W.3d 656, 661 (Tex. App. Fort Worth 2006), petition for discretionary review refused, (Feb. 28, 2007); State v. Russell, 141 Wash. App. 733, 172 P.3d 361, 365 (Div. 2 2007).)

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§ 7:2. Mitochondrial DNA

Not all DNA found in the human body is located within the 23 pairs of nuclear chromosomes. Structures within each cell called mitochondria contain a separate, complete genome. Mitochondria are considered the power centers of the cell. Their function is to convert food into a cell's energy source, adenosine triphosphate. A single cell may contain anywhere from a few, up to ten thousand mitochondria. “Mitochondrial DNA in inherited only from the mother. It is, therefore, shared with siblings, the mother, the mother's siblings, and anyone else related in the maternal line. Nevertheless, mitochondrial DNA is extremely useful in analyzing items of evidence that contain little nuclear DNA, such as hair that does not have the hair root attached.” (People v. Westerfield, 6 Cal. 5th 632, 648, fn. 4, 243 Cal. Rptr. 3d 18, 433 P.3d 914 (Cal. 2019).)

1) Location and Structure

The mitochondrial DNA molecule (i.e., genome) is found inside each mitochondrion. Each mitochondria contains approximately two to ten full copies of the genome. While genomic (nuclear) DNA contains approximately three billion bases, the mitochondrial DNA (mtDNA) genome is much smaller-approximately 16 thousand bases long. The mtDNA molecule is circular and double stranded. It is comprised of a coding region that comprises most of the genome, and two hypervariable regions (HVI and HV2). These two hypervariable regions contain the most variation between individuals and are the most commonly sequenced areas for forensic mitochondrial typing.

2) Inheritance

Like Y-STRs, mtDNA is inherited as a single copy, or haplotype, through only one parental line; in this case the mother's. All maternally related relatives in a lineage will share the same mtDNA type. Unlike Y-STRs, males as well as females have mtDNA in their cells. However, only females can transmit their mtDNA to the next generation. At conception, when a sperm cell enters an egg, any mitochondrial DNA from the sperm that may enter the egg is inactivated. This means that only the female mtDNA is transmitted to the next generation. For example, if a mother has a male child and a female child, they both will share the mother's mtDNA type. When those children then reproduce, the offspring of the female child will share the same mtDNA type with his or her mother and grandmother. The offspring of the male child will have a different type from his or her aunt and grandmother. The male child's offspring will have inherited his or her mtDNA type from his or her mother, continuing on a separate lineage.

Because mtDNA is found in all humans, it has been widely used for studying human migration patterns from early humans to modern day populations. The changes that have taken place in the genome over long periods of time can be traced and analyzed to help understand the history of human migration and the formation of specific population groups.

3) Typing Methods

Mitochondrial DNA typing methods rely on the changes that occur in single bases of a mtDNA sequence. By comparing a mtDNA sequence from a questioned sample to a standard reference sequence and recording the differences between the two,

a mtDNA haplotype is developed. This reference sequence used for comparison is called the revised Cambridge Reference Sequence or rCRS. The original Cambridge Reference Sequence (CRS), published in 1981 was developed from a single person of European descent. After publication, errors were discovered in the sequence. The errors were corrected and the revised Cambridge Reference Sequence (rCRS) was published in 1999.

Over time, with the collection and typing of greater numbers of samples, certain common haplotype groups have emerged. These haplogroups follow a geographic distribution. Specific haplogroups are associated with Africans, Europeans, Asians, and Native Americans.

a) Sequencing

In order to fully investigate the sequence differences and develop a mtDNA type for an individual or evidence item, the hypervariable regions of the mitochondrial genome must be sequenced. In other words, each base along the DNA strand in a specific region of the mtDNA genome must be read. In order to sequence the regions of interest several amplification reactions must be performed that include specialized nucleotides, called dideoxynucleotides (ddNTPs). These nucleotides differ from the deoxynuclotides (dNTPs) used in conventional PCR because once a ddNTP is added to an elongating DNA strand, its structure will prevent any further nucleotides from being added to the fragment. This stops the amplification process for the fragment.

A sample prepared for sequencing will be divided into four portions, one for each base (A, C, G, or T). Each ddNTP is labeled with a separate color dye. The amplification proceeds with labeled ddNTPs being added randomly to the ends of the amplifying fragments. At the end of the amplification reaction, each reaction tube is filled with labeled fragments of varying length. The contents of the tubes are then combined for capillary electrophoresis. The samples are injected and detected by the genetic analyzer. The analyzed data is represented as a sequence of colored peaks all one base length difference with each color corresponding to a different letter. The order in which the letters are detected is the sequence of the mtDNA region. The sequence of the sample is then compared to the rCRS, the differences noted, and the haplotype determined. This process is laborious and time consuming, involving several amplification reactions as well as specialized software for sequencing and analysis.

b) Linear array typing

An alternative to sequencing is linear array typing. This technique can be utilized as a screening tool in laboratories that use mtDNA analysis for casework applications. The process involves attracting mtDNA sequences that have differences from the revised Cambridge Reference Sequence (rCRS) at specific locations to a membrane (thin piece of paper). Chemicals are then added that identify where DNA has attached to the membrane. A pattern of bands appears and reveals where a questioned sample's sequence differs from the rCRS. Comparisons between references and evidence samples are easily made and only the samples that matched with strip typing need go on to sequencing. If an evidence sample is submitted for testing with reference samples, array testing may be able to limit the number of samples that ultimately need sequencing.

4) Statistics

Like Y-STRs, mtDNA statistics are based on haplotypes and not on allele frequencies. Using the counting method, haplotype frequencies are given as the number of times a haplotype occurs in a reference database. Specialized software such as the mtDNA Population Database Project facilitates haplotype searches, calculates frequency estimates, and perform searches including nuclear STR profiles and active case files through the COmbined DNA Index System-mitochondrial DNA (CODIS^{mt}).

Also, as with Y-STRs, a confidence interval can be applied to the frequency estimate that calculates with a percent certainty the percentage of the population that would be expected to have the haplotype of interest. For example, a haplotype search of an evidence profile in a database of 1000 profiles may yield zero matches with a 95% upper bound confidence interval of 0.25%. This means that only one quarter of one percent of the population would be expected to possess that haplotype.

5) Forensic Applications

Mitochondrial DNA testing is used routinely in missing persons DNA programs. It is particularly useful as an analysis method when dealing with severely compromised samples commonly handled by analysts in these programs, such as charred remains, very old or degraded samples, or hair without roots. Often, probable identifications of found remains are made through mtDNA testing after autosomal STR testing has failed. Mitochondrial DNA testing of hair evidence can be especially useful in cases where nuclear DNA typing opportunities have been exhausted with no probative results. A bone from human remains that has produced no autosomal STR results for comparison may undergo mtDNA typing. If a haplotype is determined from the bone it can then be compared to a database of haplotypes from reference samples of relatives of missing persons to look for maternal relatedness.

6) Admissibility

The reliability of mitochondrial DNA testing, including evidence of the statistical significance of test results, has been considered by a number of courts holding that such evidence is admissible. (See, e.g., People v. Stevey, 209 Cal. App. 4th 1400, 1414–1415, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013) [holding, in part, that mitochondrial DNA testing and its statistical methods are generally accepted as reliable by the scientific community]; Wagner v. State, 160 Md. App. 531, 864 A.2d 1037, 1046 (2005) [citing cases]; see also U.S. v. Beverly, 369 F.3d 516, 531, 64 Fed. R. Evid. Serv. 357, 2004 FED App. 0136P (6th Cir. 2004); U.S. v. Coleman, 202 F. Supp. 2d 962, 970 (E.D. Mo. 2002); State v. Pappas, 256 Conn. 854, 776 A.2d 1091, 1105 (2001); Magaletti v. State, 847 So. 2d 523, 528 (Fla. Dist. Ct. App. 2d Dist. 2003); Lewis v. State, 889 So. 2d 623, 673 (Ala. Crim. App. 2003).)

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§ 7:3. Single nucleotide polymorphisms

Single nucleotide polymorphisms (SNPs) are differences of one base at a particular location between two different DNA sequences. SNPs are not a new technology, but have been utilized for many years, especially to study genetically based diseases. There are several forensic-based applications for SNPs as well. The single-base variations found in the mtDNA genome are SNPs. Much of the variation in the once widely used method of Restriction Fragment Length Polymorphism (RFLP) is due to SNPs.

SNPs offer advantages for forensic testing such as being able to identify racial or ethnic background and physical traits such as eye color of evidence samples. Because SNPs are changes in one base pair at a specific location in the genome, there are two possibilities, or alleles, for each SNP. This is different than the multi-allele model of short tandem repeats. With so few genotype possibilities at any location, the number of loci tested to achieve discrimination between individuals needs to be much greater than that of STRs. It has been estimated that SNP multiplexes of 50 to 100 loci would be required to achieve the discrimination power of STR multiplexes with 10–16 loci. (Butler, *Advanced Topics in Forensic DNA Typing: Methodology* 347–349 (2012).)

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§ 7:4. Low copy number analysis

1) Description and Concerns

When a low amount of DNA is added to a polymerase chain reaction, the resulting STR data may exhibit characteristics not commonly seen in amplified samples with higher template input amounts. This is known as low copy number, or LCN, testing. (See, e.g., U.S. v. Davis, 602 F. Supp. 2d 658, 669 (D. Md. 2009) [noting that experts for both the prosecution and defense agreed that, "at a minimum, LCN testing involves testing minuscule amounts of DNA that fall below the (somewhat amorphous) stochastic threshold—around 100 picograms or less"]; People v. Megnath, 27 Misc. 3d 405, 898 N.Y.S.2d 408, 411 (Sup 2010) [Office of the Chief Medical Examiner of the City of New York "can perform LCN DNA testing on evidence samples of less than 200 picograms of DNA evidence," which is the equivalent of approximately 33 cells' worth of DNA].) Low copy number testing can result in:

1) Severe peak height imbalances

2) Allelic drop out/in: Peaks may not be reproducible from one genetic analyzer injection to the next

3) Increased stutter peaks

Implications of the amplification of low, or "trace" amounts of DNA are currently being investigated. Low amounts of template DNA are routinely analyzed in cases with touch evidence. For example a swab from a gun grip may be analyzed for DNA from a possible shooter. The neckband of a t-shirt found at a crime scene may be analyzed to determine a profile for the wearer. A swab of the steering wheel of a car may be analyzed to determine who may have been driving the car at the scene of a crime. These are all examples of typical evidence items that often yield very low amounts of DNA.

There are techniques used for enhancing the quality of low copy number samples including increasing PCR cycle number and "clean-up" of amplified product after the PCR. PCR typically amplifies STRs with 25–30 cycles. Increasing the amount of cycles performed (i.e., over 30) in the PCR is one way to increase the amount of DNA produced for analysis. By letting the reaction continue longer, more product is produced. However, the increased cycle number can increase the instance of the above effects.

Purification of amplified PCR product has been shown to improve overall STR results. At the end of a PCR, a reaction tube contains not only amplified DNA but also residual chemicals from the amplification mixture. These residual chemicals are co-injected into the capillary of the genetic analyzer for electrophoresis. The presence of these components can interfere with the injection (uptake) of amplified DNA into the capillary, and the quality of the data generated by the genetic analyzer. Similar to purifying a DNA extract after organic extraction, the removal of these residual chemicals by filtration can greatly increase the quality of the STR data generated by the genetic analyzer.

2) Admissibility

Few courts in the United States have considered the admissibility of low copy number (LCN) DNA analysis. In U.S. v. McCluskey, 954 F. Supp. 2d 1224 (D.N.M. 2013), the district court considered the admissibility of LCN evidence, and held that the government had not met its burden under *Daubert*. (*Id*. at p. 1288.) Five factors influenced this conclusion:

> PCR/STR analysis of low-level DNA has been tested, and has been found to exhibit stochastic effects rendering the DNA profiles unreliable; indeed, the empirical testing by the NMDPS [New Mexico Department of Public Safety] Lab itself caused the Lab to declare testing of less than 250 pg resulted in stochastic effects. The Lab set its own threshold for reliability. It has not been demonstrated to this Court that the NMDPS Lab is able to obtain reliable DNA profiles from samples below 250 pg, or to reliably interpret such profiles. *See Daubert*, 509 U.S. at 593–94 (factors to consider include whether the theory or technique can be and has been tested). Second, peer review and publications have raised serious questions about the reliability of testing low amounts of DNA and accounting for stochastic effects. The Court has not been referred to any publications supporting the reliability of the NMDPS Lab's LCN testing. Third, the recognition of stochastic effects constitutes acknowledgment of a significant risk of error. Fourth, there are standards controlling LCN testing, to the extent that each laboratory is required to empirically establish its own stochastic threshold. Fifth, the reliability of LCN testing is not "generally accepted in the relevant scientific community." *Daubert*, 509 U.S. at 593–94.

(954 F.Supp.2d at p. 1288.) Notably, it was the lack of internal validated standards in the testing laboratory, and shortcomings of the government's expert witness, that informed much of the court's reasoning. (See, e.g., *id*. at pp. 1277–1288.) Thus, the court did not hold LCN testing inadmissible under all circumstances as a matter of law. (See *id*. at p. 1279, "the question before this Court is not whether it is possible to perform LCN testing reliably—but instead whether the LCN testing performed in this case, by the NMDPS Lab, is reliable.")

Other cases, however, involve the distinct factual premise of laboratories that do incorporate previously validated specialized techniques for low quantity samples into their technical procedures. (See, e.g., U.S. v. Morgan, 53 F. Supp. 3d 732, 735–39, 741-742, 95 Fed. R. Evid. Serv. 770 (S.D. N.Y. 2014), aff'd, 2017 WL 129902 (2d Cir. 2017) [low copy number analysis and test results admissible under *Daubert* test]; Phillips v. State, 226 Md. App. 1, 126 A.3d 739, 748–751 (2015), cert. granted, 446 Md. 704, 133 A.3d 1110 (2016) and aff'd on other grounds, 2017 WL 253652 (Md. 2017) [low copy number DNA testing admissible under *Frye* test in view of validated and generally accepted lab procedures].) In fact, in deciding *Morgan* the court explained that *McCluskey* "contrasted [the lab in *McCluskey*] with [the lab in *Morgan*], noting that [the latter] 'has done extensive internal validation of its [low copy number] testing and has received certification and approval for it ….'" (53 F.Supp.3d at 736, fn. 2, citation omitted).

In People v. Megnath, 27 Misc. 3d 405, 898 N.Y.S.2d 408 (Sup 2010), a New York trial court concluded that LCN evidence satisfied the general acceptance admissibility standard set forth in Frye v. U.S., 293 F. 1013, 34 A.L.R. 145 (App. D.C. 1923). (898 N.Y.S.2d at 413–414.) The court was influenced by the fact that LCN analysis "is basically the same method of DNA testing that occurs with [high copy number] DNA testing. The only difference between the testing methods is that the LCN method can test smaller amounts of DNA by increasing the amplification cycles." (898 N.Y.S.2d at 413.) "In HCN and LCN DNA testing, the same four steps for analysis are used," stated the court. "They are extraction, quantitation, amplification, and electrophoresis. In addition, many of the same scientific issues that arise in HCN DNA testing, such as stutter, allelic or locus drop-out, and allelic drop-in also occur in LCN DNA testing." (*Ibid*.) For this reason, held the court, LCN analysis is not a novel scientific technique that need be subjected to a Frye admissibility hearing. (898 N.Y.S.2d at 414.)

Nonetheless, the court addressed the scientific merits, observing that the laboratory's LCN testing method had been validated in both peer-reviewed literature and internal laboratory validation studies, and is thus "reproducible and reliable." (898 N.Y.S.2d at 414.) Finally, held the court, defense concerns "such as transference, the increased incidence of allelic drop-out, drop-in, and stutter, as well as other alleged interpretation issues" associated with LCN analysis bear on the weight of the evidence, not its admissibility. (*Ibid*; but see Roth, *Safety in Numbers? Deciding When DNA Alone IS Enough to Convict*, (2010) 85 N.Y.U. L. Rev. 1130, 1137 [citing California trial court ruling excluding LCN evidence for "lack of consensus in scientific community"].)

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Chapter 7. Alternate DNA Testing Methods

§ 7:5. Forensic Genetic Genealogy

A relatively new (circa 2018) DNA-based investigative tool is known as Forensic Investigative Genetic Genealogy (FIGG), or Forensic Genetic Genealogy (FGG), or Investigative Genetic Genealogy (IGG). However labeled, the method seeks to capitalize, for law enforcement purposes, on the existence of public genealogy databases serving consumers who typically use them to conduct ancestry research. The databases contain collections of DNA profiles generated with testing kits that identify genetic data points useful for making kinship associations between people, as well as data about physical and medical/health characteristics.

DNA markers used for FIGG purposes are Single Nucleotide Polymorphisms (SNPs) rather than short tandem repeats (STRs). Direct to consumer companies provide ancestry DNA testing kits that target more than or equal to 500,000 SNPs. Law enforcement, given the evidentiary nature of the samples, often targets a smaller number of SNPs (~10,000). Once an unknown perpetrator's SNP profile is searched within a genealogy database, law enforcement or contract researchers assess various kinship probabilities and associations based on shared DNA. They typically attempt to construct a family tree based on both the genetic data and available metadata such as birth and death records, geography, and other relevant facts that could yield useful investigative information about the identity of the source of the unknown DNA sample. If and when FIGG yields the identity of the likely perpetrator, investigators will seek to legally obtain a known DNA reference sample from that person to conduct a direct STR comparison and confirm or dispel the hypothesis that that person is the source of unknown DNA from the crime scene. (See State v. Hartman, 27 Wash. App. 2d 952, 534 P.3d 423, 427–429 (Div. 2 2023) [describing the details of an investigation that employed genealogy methods to solve a decades-old rape/murder of a young girl].)

Since the "Golden State Killer" was identified using FGG in 2018, the technique has become increasingly common as a supplement to using casework and database STR profiles to identify perpetrators. FIGG leads can be cited as probable cause in support of search or arrest warrants. In People v. Lepere, 91 Cal. App. 5th 727, 308 Cal. Rptr. 3d 558 (4th Dist. 2023), as modified, (June 2, 2023) and review denied, (July 19, 2023), the California Court of Appeal described how investigators used FGG to solve a 1980 murder/sexual assault: "In 2020, the cold case investigation was assigned to Anaheim Police Detective Julissa Trapp, who sought assistance from the FBI. The unknown DNA profile was sent to a company that was able to generate a single nucleotide polymorphism (SNP) profile. The digitized genetic data was uploaded to a genealogy website. [¶] In 2021, the FBI notified Trapp that Lepere had been identified as a person of interest." (91 Cal.App.5th at p. 731.) The FGG lead was included as probable cause in an application for a search warrant of Lepere's property. A magistrate issued the warrant, and DNA from a beer can collected from the suspect's trash matched the perpetrator's profile. (*Ibid*.) In response to an appellate claim that the warrant was invalid for lack of probable cause, the Court of Appeal held that "the genealogical investigation by the Orange County Crime Lab and the FBI established a possible DNA connection between Lepere and the 1980 murder. Further, there was corroborating evidence that Lepere may have been near the victim's apartment in Anaheim, California, at about the time of the 1980 murder. In short, we find there was 'a fair probability … that a search' of Lepere's outside trash can 'would uncover' circumstantial DNA evidence linking Lepere to the commission of the 1980 Anaheim murder. [Citation.] Thus, … the New Mexico magistrate had a reasonable basis for issuing the search warrant, and the trial court properly denied Lepere's pretrial motion to suppress the DNA evidence." (*Id*. at p. 734.)

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Chapter 8. California's DNA Data Bank Program

§ 8:1. Overview

1) Summary

Routine searches of state and federal DNA databases are identifying perpetrators of formerly unsolved, or "cold," crimes at an ever-increasing rate. DNA databases operate on a theory of recidivism, namely, that many criminal offenders commit more than one crime. See People v. King, 82 Cal. App. 4th 1363, 1376, 99 Cal. Rptr. 2d 220 (1st Dist. 2000) ("It also is an unfortunate truth that many offenders commit more than one crime, and recidivism is common"); cf. Samson v. California, 547 U.S. 843, 853–854, 126 S. Ct. 2193, 165 L. Ed. 2d 250 (2006) ([noting 68–70% recidivism rate among California parolees].)

A DNA database is analogous to a series of spreadsheets in a computer, with each spreadsheet containing DNA profiles in electronic format. Databases function by comparing DNA profiles generated from biological crime scene evidence (e.g., blood, hair, sperm) against known reference DNA profiles collected from criminal arrestees and/or convicted offenders in a given state, or in the federal criminal justice system. The crime scene DNA profiles must be attributable to the perpetrator(s) of the crimes to be eligible for upload into a database. When two profiles match, a "cold hit" may be declared and the offender's identity disclosed by the state to law enforcement as an investigative lead. A match may be between an offender and an unknown evidence profile, or between two unknown evidence profiles from different cases. (See, e.g., U.S. v. Jenkins, 887 A.2d 1013, 1017 (D.C. 2005) [a cold hit is a "match of a crime scene sample with a suspect identified through a database search"].) A match between two DNA profiles generated from crime scene evidence is known as a "case-to-case" hit.

While this chapter will describe features of DNA database programs in general, the primary focus will be on California's program, and the corresponding law and practices that have developed in the state.

2) Legal Authority for California's Program

The governing authority for California's state-level DNA database is California Penal Code sections 295 to 300.4. (See People v. Robinson, 47 Cal. 4th 1104, 1116–1118, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010) [describing legislative history and function of California's DNA Data Bank Program]; People v. Lowe, 221 Cal. App. 4th 1276, 1288–1291, 165 Cal. Rptr. 3d 107 (4th Dist. 2013), as modified, (Dec. 4, 2013) [same]; People v. Xiong, 215 Cal. App. 4th 1259, 1266, 155 Cal. Rptr. 3d 877 (5th Dist. 2013), as modified, (May 2, 2013), fn. 4 [same].) California has, by far, the largest DNA database in the country, and one of the largest in the world when considered on a standalone basis. As of February 2023, California's SDIS contained over 3,196,000 searchable offender DNA profiles and over 155,800 forensic (crime scene) DNA profiles, and had reported over 101,800 hits to law enforcement as investigative leads. As will be discussed in more detail, California law authorizes collection of reference DNA profiles for database purposes from all newly convicted or adjudicated felons, from all those newly convicted or adjudicated of misdemeanors who have a prior felony conviction or adjudication of record, and adults arrested for felony offenses.

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§ 8:2. LDIS, SDIS, NDIS, and CODIS

1) Local DNA Index System (LDIS)

The local, public, laboratories that develop DNA profiles from crime scenes evidence and upload them into state DNA databases are known as LDIS (Local DNA Index System) labs. These labs must satisfy the FBI's requirements to participate in the national DNA database system. LDIS labs are typically affiliated with a municipal police agency, a county sheriff or medical examiner, a district attorney's office, or a state department of justice.

2) State DNA Index System (SDIS)

The state-level DNA databases that receive the crime scene profiles of unknown origin from LDIS labs are known as SDIS (State DNA Index System) programs. All 50 states have a SDIS, the parameters and functions of which are defined by individual state laws. In particular, each state determines the classifications of criminal offenders who can lawfully be required to provide known reference DNA samples to the state for processing and upload into the state database, and subsequent comparison against crime scene evidence profiles. In California, the laboratory housing the SDIS program also is responsible for processing the high volume of known offender DNA samples that are submitted for comparison against crime scene DNA evidence.

3) National DNA Index System (NDIS)

In addition to comparing known offender profiles against unknown crime scene profiles at the state level, SDIS programs upload the majority of their contents into the NDIS, (National DNA Index System). NDIS is the United States national-level database, administered by the Federal Bureau of Investigation at its Quantico, Virginia laboratory. It conducts national level comparisons and reports interstate cold hits—both offender-to-case hits and case-to-case matches. NDIS is governed by federal statutory authority and associated regulations. (42 U.S.C.A. § 14132; 28 C.F.R. §§ 28.1 et seq.)

4) Combined DNA Index System (CODIS)

The acronym CODIS (Combined DNA Index System) is commonly used as an umbrella label for DNA database programs in general. More specifically, CODIS refers to the DNA database software developed by the FBI and licensed to state (SDIS) and local (LDIS) laboratories, thus forming a national network.

In U.S. v. Kincade, 379 F.3d 813, 845 (9th Cir. 2004), the court described the CODIS network as follows: "CODIS is a three-tired hierarchical system of information sharing. The FBI's National DNA Index System (NDIS) constitutes the highest level in the CODIS hierarchy, all participating laboratories at the local and state level have access to the NDIS database. All DNA profiles in the CODIS system are collected at the local level (LDIS) before flowing to operative state databases (SDIS). SDIS 'allows laboratories within states to exchange DNA profiles.' See CODIS Mission Statement and Background, available at http://www.fbi.gov/hq/lab/codis/program.htm (last visited June 20, 2004) [hereinafter CODIS Mission Statement and Background].

'The tiered approach allows state and local agencies to operate their databases according to their specific legislative or legal requirements.' *Id*."

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§ 8:3. History and purpose of California's program

1) Chronology

The State of California has collected biological samples for forensic identification purposes from statutorily enumerated criminal offenders since 1984. (Former Pen. Code, § 290.2, added by Stats. 1983, ch. 700; former Pen. Code, §§ 295 to 303.3, added by Stats. 1998, ch. 696, § 2 (*The DNA and Forensic Identification Data Base and Data Bank Act of 1998*), amended by Prop. 69, Gen. Elec. (Nov. 2, 2004).) The historical evolution of California's DNA Data Bank Program is described in both People v. Robinson, 47 Cal. 4th 1104, 1116–1118, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010) and Alfaro v. Terhune, 98 Cal. App. 4th 492, 497–498, 120 Cal. Rptr. 2d 197 (3d Dist. 2002). (See also People v. Buza, 4 Cal. 5th 658, 665-666, 230 Cal. Rptr. 3d 681, 413 P.3d 1132 (Cal. 2018).) The following is a brief summary of the statutory evolution of California's DNA Data Bank Program:

1984–1987:	Sex registrants (Pen. Code, § 290) paroled from state prison must provide blood sample to Department of Justice laboratory "for analysis and categorizing into blood groupings" for law enforcement purposes. (Pen. Code, § 290.2.)
1988:	Law expands to include collection to felony sex registrants released on probation or from county jail. (Pen Code, § 290.2.)
1989–1992:	Law expands to include those convicted of enumerated felony assault and battery crimes as well as felony sex offenders; provides for DNA testing "and other genetic typing analysis" instead of blood type; describes computerized DNA database; sets forth use and disclosure restrictions. (Pen. Code, § 290.2.)
1993–1997:	Law expands to include those convicted of murder; provides for coordination between Department of Justice and local public DNA laboratories. (Pen. Code, § 290.2.)
1998–2004:	Penal Code section 290.2 is repealed and replaced by Section 295 et seq., known as the "DNA and Forensic Identification Data Base and Data Bank Act of 1998;" describes the operation, requirements, and limitations of the DNA Data Bank Program in

2004-present:	comprehensive detail; expands the list of qualifying offenses to include many serious and violent crimes; precursor to current law. (Pen. Code, §§ 295 et seq.) Proposition 69 passed by voters in November 2004; expands and clarifies existing law; provides for DNA collection from all existing felons and adult felony arrestees; includes additional detail on program operation and parameters; provides for funding. (Pen. Code, §§ 295 et seq.)

The technology applied to these samples has changed over time as the science underlying genetic-based forensic identification has evolved from ABO blood typing systems, to RFLP analysis, to contemporary Short Tandem Repeat profiles generated using Polymerase Chain Reaction technology.

2) Proposition 69 (2004)

Following the 2004 general election, a voter initiative titled—and still referred to colloquially as—"Proposition 69" became the governing authority for the State's DNA Data Bank Program. It is located in sections 295 to 300.3 of the Penal Code. (Pen. Code, §§ 295 et seq.) Proposition 69 expanded and clarified existing law, most notably to mandate DNA collection from all convicted or adjudicated felons, as well as adult felony arrestees and other categories of offenders. By law, the DNA Data Bank Program is designed to "assist federal, state, and local criminal justice and law enforcement agencies within and outside California in the expeditious and accurate detection and prosecution of individuals responsible for sex offenses and other crimes, the exclusion of suspects who are being investigated for these crimes, and the identification of missing and unidentified persons, particularly abducted children." (Pen. Code § 295, subd. (c).) More specifically, the State's program is required to analyze, store, correlate, and compare DNA identification samples for use in criminal investigations. (Pen. Code, § 295.1, subd. (c); see People v. King, 82 Cal. App. 4th 1363, 1369–1378, 99 Cal. Rptr. 2d 220 (1st Dist. 2000).)

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§ 8:4. Funding California's DNA Data Bank Program

1) Funding Statutes

Proposition 69 added Government Code section 76104.6, which provides a funding mechanism for the DNA Data Bank Program based on the allocation of additional fines, penalties, and forfeitures imposed in criminal cases. (Gov. Code, § 76104.6; see People v. Castellanos, 175 Cal. App. 4th 1524, 1529–1530, 98 Cal. Rptr. 3d 1 (2d Dist. 2009); People v. Valencia, 166 Cal. App. 4th 1392, 1394, 83 Cal. Rptr. 3d 455 (2d Dist. 2008).) Section 76104.6, subdivision (a), states in part that, "[F]or the purpose of implementing the DNA Fingerprint, Unsolved Crime and Innocence Protection Act, there shall be levied an additional penalty of one dollar for every ten dollars ($10), or part of ten dollars ($10), in each county upon every fine, penalty, or forfeiture imposed and collected by the courts for all criminal offenses … ."

Subsequent enactment of Government Code section 76104.7 created additional penalties in criminal cases in order to provide further funding of the State's forensic laboratories and DNA Data Bank Program. (Cal. Gov. Code, § 76104.7.) Section 76104.7, subdivision (a), states in part that, "[I]n addition to the penalty levied pursuant to Section 76104.6, there shall be levied an additional state-only penalty of four dollars ($4) for every ten dollars ($10), or part of ten dollars ($10), in each county upon every fine, penalty, or forfeiture imposed and collected by the courts for all criminal offenses … ." (See People v. Hamed, 221 Cal. App. 4th 928, 933, 164 Cal. Rptr. 3d 829 (6th Dist. 2013), fn. 2 [describing successive amendments to section 76104.7 between 2006 and 2012, increasing DNA penalty from $2 to $3 to $4]; People v. Villegas, 97 Cal. App. 5th 253, 284–285, 315 Cal. Rptr. 3d 346 (1st Dist. 2023) [describing the statutory framework of DNA penalties].) The money collected "shall be used to fund the operations of the Department of Justice forensic laboratories, including the operation of the DNA Fingerprint, Unsolved Crime and Innocence Protection Act, and to facilitate compliance with the requirements of subdivision (e) of Section 299.5 of the Penal Code." (Gov. Code, § 76104.7, subd. (b).)

2) Ex Post Facto Implications

In People v. Batman, 159 Cal. App. 4th 587, 71 Cal. Rptr. 3d 591 (3d Dist. 2008), the court held that imposition of the DNA penalty assessment pursuant to section 76104.6 violated state and federal constitutional ex post facto protections when it was imposed for a criminal act committed before the funding provision was enacted into law. (*People v. Batman*, 159 Cal. App. 4th at 591.) Central to this conclusion was the court's determination that the section 76104.6 assessment is, in fact, punitive. (*Ibid.*)

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§ 8:5. Management of DNA Data Bank Program

By law, the California Department of Justice's DNA Laboratory is "responsible for the management and administration of the state's DNA and Forensic Identification Database and Data Bank Program … ." (Pen. Code, § 295, subd. (g).) The California Department of Justice also coordinates the State's participation in the National DNA Index System (NDIS), the national DNA database administered by the Federal Bureau of Investigation. (*Ibid*.) The California Department of Justice likewise is charged with adopting policies, regulations, and procedures for the operation of the DNA Data Bank Program. (Pen. Code, §§ 295, subd. (h), 298, subd. (b)(6); see People v. Dial, 130 Cal. App. 4th 657, 661, 30 Cal. Rptr. 3d 252 (1st Dist. 2005) [describing management of DNA Data Bank Program].)

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§ 8:6. Collection and processing of offender reference samples

1) Buccal Swab Collection, Testing, and Upload

Under Proposition 69, correctional institutions, probation departments, and local law enforcement agencies collect buccal swab samples from offenders who fall within the parameters set forth in Penal Code Section 296. (Pen. Code, §§ 295, subd. (e), 296.1.) A number of courts have described the DNA collection protocols and mandates set forth by California law, including People v. Robinson, 47 Cal. 4th 1104, 1116–1118, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010); People v. King, 82 Cal. App. 4th 1363, 99 Cal. Rptr. 2d 220 (1st Dist. 2000); Alfaro v. Terhune, 98 Cal. App. 4th 492, 497–98, 505–506, 120 Cal. Rptr. 2d 197 (3d Dist. 2002); People v. Adams, 115 Cal. App. 4th 243, 255–259, 9 Cal. Rptr. 3d 170 (6th Dist. 2004), as modified, (Feb. 5, 2004); People v. Dial, 130 Cal. App. 4th 657, 661, 30 Cal. Rptr. 3d 252 (1st Dist. 2005); and U.S. v. Kincade, 379 F.3d 813, 835 (9th Cir. 2004).

Statutory DNA collection requirements are "'self-executing' in that they are mandatory and arise with or without a trial court advisement or order to that effect." (*People v. Dial*, 130 Cal. App. 4th at 661–662; People v. Brewer, 87 Cal. App. 4th 1298, 1302, 105 Cal. Rptr. 2d 293 (1st Dist. 2001); see Pen. Code, § 296, subd. (d).) The law permits no discretion on the part of law enforcement in collecting database samples. (*People v. King*, 82 Cal. App. 4th at 1363, 1373.) The submission of samples is "mandatory and appl[ies] whether or not the court advises a person … that he or she must provide the data bank and database specimens, samples, and print impressions." (Pen. Code, § 296, subd. (d); People v. Travis, 139 Cal. App. 4th 1271, 44 Cal. Rptr. 3d 177 (1st Dist. 2006) ["The provisions of the act are mandatory and automatic upon conviction of a felony."].)

The buccal swab consists of "gently scraping the inner cheek repeatedly with a small stick." (Haskell v. Brown, 677 F. Supp. 2d 1187, 1190 (N.D. Cal. 2009); see also Balding v. State, 812 N.E.2d 169, 173 (Ind. Ct. App. 2004) ["'A buccal swab is a specialized applicator with a sponge or foam tip, which is rubbed on the inside of the cheek to collect epithelial cells. This procedure is noninvasive and pain free.' [Citation.]"].)

The use of buccal swabs instead of blood samples has constitutional significance to courts determining the intrusiveness of the search pursuant to a Fourth Amendment reasonableness analysis. Collecting a DNA sample by a buccal swab rubbed against the subject's inner cheek is less invasive than penetrating the skin with a needle and withdrawing a blood sample. (See, e.g., Friedman v. Boucher, 580 F.3d 847, 863 (9th Cir. 2009) ["The state's use of a buccal swab to collect DNA cells from the inside of a pretrial detainee's mouth is undeniably far less intrusive than drawing blood and a relatively minor intrusion upon Friedman's expectation of bodily privacy"]; U.S. v. Amerson, 483 F.3d 73, 84 (2d Cir. 2007) ["If instead [of a blood sample], the DNA were to be collected by cheek swab, there would be a lesser invasion of privacy because a cheek swab can be taken in seconds without any discomfort"]; U.S. v. Davis, 657 F. Supp. 2d 630, 655 (D. Md. 2009) ["many courts have recognized that the intrusion inherent in the drawing of blood or the swabbing of one's mouth is 'minimal'"]; Com. v. Maxwell, 441 Mass. 773, 808 N.E.2d 806, 810 (2004) ["Unlike a blood sample extracted by needle, a buccal swab does not involve an 'intrusion below the skin,' and is arguably more akin to a saliva sample, as it involves obtaining bodily material from inside the mouth"].)

Once collected, offender DNA samples are sent to the Department of Justice's Richmond DNA Laboratory. (Pen. Code, §§ 295, subd. (i)(1)(C), 298, subd. (a).) There, laboratory staff process the samples in high volumes, often as many as 20,000 each

month, in order to generate DNA profiles and upload them into the searchable computer database. (See Pen. Code, § 297, subd. (a)(3).) All offender samples in California are typed using the 15-locus Identifiler® testing kit employing PCR-STR technology. Some other states, as well as the federal government, continue to use 13-locus offender profiles generated with Profiler Plus® and COfiler® testing kits. As DNA databases grow, additional loci will likely be validated and added to the CODIS standard to provide enhanced powers of discrimination.

By law, only Department of Justice laboratories may upload offender and arrestee reference samples into the state DNA Database. (Pen. Code, § 297, subd. (a)(3).)

2) Mandated Classes of Offenders

Pursuant to California law, known reference DNA samples are collected by state and local law enforcement and custodial officials from the following persons:

a) All adults convicted, or juveniles adjudicated, of a felony offense (Pen. Code, § 296, subd. (a)(1)). This includes those defendants not guilty by reason of insanity. (*Ibid*.)

b) All adults convicted, or juveniles adjudicated, of a misdemeanor offense with a prior felony of record. (Pen. Code, §§ 296, subd. (a), 296.1, subds. (a)(2), (a)(3), (a)(4).) The prior felony conviction or adjudication may be from California or an out-of-state jurisdiction, as long as the latter is the equivalent of a California felony.

c) All adults arrested for or charged with a California felony (including a wobbler) offense (Pen. Code, § 296, subd. (a)(2)(C)). This provision became effective on January 1, 2009, and is not retroactive to arrests occurring before that date. Between November 2004 and January 1, 2009, only adult felony arrests for murder, manslaughter, felony sex offenses, and attempts to commit those crimes qualified an arrestee for DNA collection. (§ 296, subd. (a)(2).)

d) All adults and juveniles required to register as a sex offender under Penal Code section 290, regardless of the conviction date. (Pen. Code, § 296, subd. (a)(3).) The predicate offense could be either a felony or misdemeanor. This requirement includes those offenders whose predicate sex offense was a misdemeanor committed before Proposition 69 took effect in 2004. (Good v. Superior Court, 158 Cal. App. 4th 1494, 71 Cal. Rptr. 3d 125 (1st Dist. 2008), as modified, (Feb. 1, 2008).)

e) All adults and juveniles required to register as an arson offender under Penal Code section 457.1. (Pen. Code, § 296, subd. (a)(3).) The predicate offense could be either a felony or misdemeanor.

f) All adults and juveniles charged with a felony offense, but then referred to and housed in a sex offender treatment program or mental health facility, e.g., because a defendant is incompetent to stand trial pursuant to Penal Code section 1368/1370. (Pen. Code, § 296(a)(3).) This group includes defendants classified as mentally disordered sex offenders and sexually violent predators. (Pen. Code, § 296, subds. (c)(1), (c)(3).)

3) Definition of "Conviction"

An adult felony conviction occurs upon entry of a plea or verdict, without respect to the sentence imposed or disposition rendered. (Pen. Code, § 296, subd. (b).) Neither expungement of a conviction pursuant to Penal Code section 1203.4, nor the postconviction reduction of a felony to a misdemeanor pursuant to Penal Code section 17, subdivision (b), affects the classification of a current or prior felony conviction or adjudication for DNA collection purposes. (Pen. Code, § 299, subd. (f); Coffey v. Superior Court, 129 Cal. App. 4th 809, 821–822, 29 Cal. Rptr. 3d 59 (1st Dist. 2005), as modified on denial of reh'g, (June 16, 2005)).

4) Juvenile Adjudications

A juvenile adjudication is a felony only when the court determines it to be such at the disposition hearing described in Welfare and Institutions Code section 702. (In re Nancy C., 133 Cal. App. 4th 508, 512, 34 Cal. Rptr. 3d 871 (3d Dist. 2005).) Noted the In re Nancy C. court, "a minor's admission of a wobbler offense charged as a felony is not an 'adjudication' of the misdemeanor or felony status of that offense." (*Ibid*.)

5) Verification of Qualifying Status

The law enforcement agencies and custodial institutions conducting DNA sample collections are responsible for verifying that those persons providing samples are qualifying offenders as described by state law. (Pen. Code, § 298, subd. (b)(5).)

6) Timing of Sample Collections

Penal Code section 296.1 sets forth the circumstances under which DNA database samples can be lawfully collected by law enforcement and custodial officials.

a) Arrestees

Arrestee samples must be given "immediately following arrest, or during the booking or intake or prison reception center process or as soon as administratively practicable after arrest, but, in any case, prior to release on bail or pending trial or any physical release from confinement or custody." (Pen. Code, § 296.1, subds. (a)(1)(A).) If that does not happen, however, following the filing of charges the trial court can order the arrestee to report to a jail or other facility to provide the required sample. (§ 296.1, subd. (a)(1)(B).)

b) Convicted offenders

Samples may be taken from convicted felons as long as the convicted defendant remains incarcerated, on probation, in a residential treatment facility, or on parole for the offense. (Pen. Code, § 296.1, subds. (a)(2), (a)(3), (a)(4).) Both supervised and unsupervised probationers are included in this group. Samples may be taken from those convicted of misdemeanors under the same circumstances, provided that the convicted defendant has a prior felony conviction or adjudication of record. (§ 296.1, subds. (a)(2)(A)(i), (a)(3)(A)(i), (a)(4)(A)(i).) Once the convicted defendant is discharged from the jurisdiction (custodial or otherwise) of the criminal justice system, the authority to collect a nonconsensual DNA database sample ends as well.

c) Sex registrants

The required DNA sample may be collected from a registered sex offender (see Pen. Code, § 290) either:

a) At the time of or immediately following the conviction resulting in registration status;

b) At the time the person registers in California following transfer from another state;

c) At the time of his or her annual registration update; or

d) Before his or her annual registration update, following notification by a law enforcement, probation, parole, or court officer. (Pen. Code, § 296.2, subd. (c).) The notice may be either verbal or in writing.

With any of the options for collecting DNA from registered sex offenders, the offender may be provided with an appointment to report to his or her local county jail or other approved facility to accomplish the collection. If the notification to the offender is provided before the annual registration update, the offender must report to the designated collection facility "within 10 calendar days" to provide the sample. (§ 296.2, subd. (c).)

7) Retroactivity

Unlike the law governing arrestee sample collection, the statutory provisions related to DNA collection from convicted and adjudicated offenders are fully retroactive. (Pen. Code, § 296.1, subd. (b); see Good v. Superior Court, 158 Cal. App. 4th 1494, 1504, 71 Cal. Rptr. 3d 125 (1st Dist. 2008), as modified, (Feb. 1, 2008).) Accordingly, all adults convicted, or juveniles adjudicated, of a misdemeanor offense with a prior felony conviction or adjudication from California or another jurisdiction must provide a sample for the Database during their term of incarceration or probation for the misdemeanor. (Pen. Code, § 296.1, subds. (a)(2), (a)(3).)

8) Deceased Inmates

When a state prison inmate dies in custody, the county coroner with jurisdiction over the postmortem investigation may obtain a DNA sample for state database purposes if the inmate was mandated by law to provide one at the time he died. (93 Ops.Cal.Atty.Gen. 78 (2010). The coroner need not notify the inmate's next of kin before providing a DNA sample to the state Department of Justice. (*Ibid*.)

9) Suspect Samples

California law permits law enforcement agencies to upload into the state database DNA profiles of suspects not yet arrested. (Pen. Code, § 297, subd. (c).) Unlike other statutorily mandated DNA samples, however, a suspect sample must be legally obtained without reliance on the DNA Data Bank Program law. In other words, and most commonly, the suspect sample will have been obtained with free, knowing, and voluntary consent of the suspect, or by valid warrant. Whether the profile for an "abandoned" DNA sample surreptitiously collected by law enforcement is eligible for upload into the DNA Database is an open question. At the very least, the agency that collects such a sample should be able to verify its origin with sufficient confidence.

Significantly, suspect samples may only be submitted when an investigation is active and ongoing, and must be removed within two years of upload if (1) the person has been eliminated as a suspect, or (2) the investigation is no longer active and ongoing. (Pen. Code, § 297, subd. (c)(2).) The Department of Justice monitors the status of suspect samples to ensure compliance with the two-year inclusion rule.

10) Legally Obtained and Plea Bargain Samples

The DNA Database Act broadly contemplates that any "legally obtained" DNA sample may be uploaded and searched at the state level. (Pen. Code, § 295.1, subd. (c)(5).) On its face, this would authorize upload of reference DNA samples obtained by consent, or samples that have been "abandoned" such that the subject retains no legitimate expectation of privacy in them. (See, e.g., People v. Gallego, 190 Cal. App. 4th 388, 395–396, 117 Cal. Rptr. 3d 907 (3d Dist. 2010), review denied, (Mar. 16, 2011) [DNA from cigarette butt tossed by suspect onto sidewalk was abandoned for Fourth Amendment purposes, thus permitting law enforcement to seize and analyze it without a warrant].) To date, there has been no systematic attempt to collect abandoned or consensual DNA samples for inclusion in California's DNA Database.

More specifically, state law permits conditioning a plea bargain to an otherwise non-qualifying offense upon the defendant providing a DNA sample for database purposes: "Nothing in this chapter shall be construed as prohibiting collection and analysis of specimens, samples, or print impressions as a condition of a plea for a non-qualifying offense." (Pen. Code, § 296, subd. (a)(5).) This provision would typically operate where a defendant with no prior felony conviction or adjudication pleads guilty or no contest to a misdemeanor offense, with an element of the plea bargain requiring him to provide a DNA sample to the state for permanent inclusion in the DNA Database. In fact, in People v. Willis, 222 Cal. App. 4th 141, 165 Cal. Rptr. 3d 600 (2d Dist. 2013), the court emphasized that imposition of DNA collection, pursuant to Penal Code section 296, as a condition of

summary probation does not necessarily indicate that the court intended the underlying offense to be a felony. (*Id*. at p. 146.) In *Willis*, the offense was a misdemeanor and the trial court was authorized to require DNA collection as a consequence of the defendant's guilty plea.

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§ 8:7. Use of force in collections

California law authorizes law enforcement, custodial, and corrections personnel to use "reasonable force" to effect DNA database sample collection from offenders required by law to provide a sample. (Pen. Code, § 298.1, subd. (b).) "Reasonable force" is "force that an objective, trained, and competent correctional employee, faced with similar facts and circumstances, would consider necessary and reasonable to gain compliance … ." (§ 298.1, subd. (c)(1)(A).) Use of force must be preceded by written or verbal request from the custodial officer involved, and may occur only upon written authorization by the supervising officer at the custodial facility. (§ 298.1, subds. (b)(1), (c)(1)(B).) In addition, authorities must make "efforts to secure voluntary compliance" before employing reasonable force. (15 Cal. Code Regs., § 3025, subd. (k).)

In Hamilton v. Brown, 630 F.3d 889 (9th Cir. 2011), the Ninth Circuit concluded that forcible collection of DNA from a state prison inmate mandated to provide a sample pursuant to Penal Code section 296 did not violate the Fourth, Eighth, or Fourteenth Amendments to the United States Constitution. (See also Sanders v. Coman, 864 F. Supp. 496, 499–501 (E.D. N.C. 1994) [no Eighth Amendment violation where prison officials used reasonable force to collect DNA samples from unwilling prisoners pursuant to North Carolina statute]; Ryncarz v. Eikenberry, 824 F. Supp. 1493, 1502 (E.D. Wash. 1993).)

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§ 8:8. Crimes related to DNA sample collection

1) Refusal to Provide Sample

With the passage of proposition 69 in 2004, it became a misdemeanor offense for a qualifying convicted offender or arrestee to refuse to provide a mandated DNA sample following written notice from the collecting agency. (Pen. Code, § 298.1, subd. (a).)

2) Providing a Misattributed Sample; Sample tampering

Proposition 69 also made it a non-reducible felony offense punishable by two, three, or four years in state prison to provide an intentionally misattributed DNA sample to the state for database purposes. (Pen. Code, § 298.2.) Two variations of this crime are described: First, knowingly facilitating the collection of a sample attributed to the wrong person, with the intent that the government be deceived as to the origin of the sample. (§ 298.2, subd. (a)(1).) Second, knowingly tampering with a DNA sample or collection kit with the intent that the government be deceived as to the origin of the sample. (§ 298.2, subd. (a)(2).)

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§ 8:9. Erroneous collection of database samples: suppression of evidence and liability

The high volume of DNA database sample collections in California results, inevitably, in occasional mistaken collections from persons under no mandate to provide a sample. Several provisions of state law address this circumstance, and preclude mistaken collections from becoming a basis to challenge a subsequent conviction. Additional provisions preempt liability for mistaken collections.

1) Constitutionality of Collection From Non-Qualifying Offenders

Penal Code section 297, subdivision (g), provides that, "The detention, arrest, wardship, adjudication, or conviction of a person based upon a databank match or database information is not invalidated if it is determined that the specimens, samples, or print impressions were obtained or placed or retained in a databank or database by mistake." Similarly, section 298, subdivision (c)(3), states that, "The failure of the Department of Justice or local law enforcement to comply with Article 4 or any other provision of this chapter shall not invalidate an arrest, plea, conviction, or disposition."

The California Supreme Court considered the constitutional implications of mistaken DNA sample collection in People v. Robinson, 47 Cal. 4th 1104, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010). In that case, the defendant's DNA sample had been collected for databases purposes based on the mistaken impression that his prior misdemeanor domestic violence conviction qualified him for collection. (*People v. Robinson,* 47 Cal. 4th at 1118.) It did not, however; only felony domestic violence would have mandated collection. Following a database cold hit identifying defendant as the perpetrator of a rape, he brought a motion to suppress under Penal Code section 1538.5. (*People v. Robinson,* 47 Cal. 4th at 1115, 1119.) The court held that the sample collection, although in violation of the state statute, did not violate the Fourth Amendment for the same reasons that statutorily permissible collections from convicted offenders do not. (*People v. Robinson,* 47 Cal. 4th at 1119–1123.) In brief, the state interest in preventing and solving crime expeditiously and accurately outweighs the minimal privacy intrusion occasioned by the suspicionless seizure of DNA for limited identification purposes. (*Ibid*.)

Moreover, the Robinson court held that, even if the DNA collection had violated the Fourth Amendment, the trial court correctly declined to suppress the evidence because the collection was an unintentional mistake that resulted from "negligence, 'rather than systemic error or reckless disregard of constitutional requirements' … ." (*People v. Robinson,* 47 Cal. 4th at 1129.) This conclusion implies, conversely, that intentional, reckless, or systemic disregard of statutory limitations on DNA collection may well justify the suppression remedy.

2) Collection-Related Liability

There is no civil or criminal liability for those persons performing DNA collections required by law "when done in accordance with medically accepted procedures" and/or "when performed in accordance with standard professional practices." (Pen. Code, § 298, subd. (c)(1).) Nor can the Department of Justice or its employees incur civil or criminal liability for mistaken processing and upload of database samples and profiles. (§ 298, subd. (c)(2).)

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§ 8:10. Expungement and retention of offender DNA profiles

1) Expungement Mechanisms: Statutory and Non-Statutory

Offender DNA profiles that do not, or no longer, qualify for inclusion may be expunged from California's searchable DNA database under the following circumstances:

a) Following the felony arrest, no felony charges were or will be filed within the applicable statute of limitations (Pen. Code, § 299, subd. (b)(1));

b) Following the felony arrest, felony charges were filed but subsequently dismissed (Pen. Code, § 299, subd. (b)(1));

c) Following a felony arrest and filing of felony charges, the defendant was acquitted at trial (Pen. Code, § 299, subd. (b)(4));

d) The qualifying felony conviction was reversed on appeal, and the case was dismissed (Pen. Code, § 299, subd. (c)(1));

e) The person was found factually innocent of the qualifying felony offense (Pen. Code, § 299, subd. (b)(3)).

Under Proposition 69, courts have no independent statutory obligation to order expungement of DNA information for those who qualify, nor does the Department of Justice have a duty to affirmatively review and purge profiles and samples meeting expungement criteria. (In re C.B., 6 Cal. 5th 118, 127, 237 Cal. Rptr. 3d 471, 425 P.3d 40 (Cal. 2018).) Instead, an expungement request is made by means of a petition to the superior court. It must be accompanied by documentation of the circumstance that allegedly justifies expungement, e.g., a court docket indicating dismissal of charges, a letter from the county District Attorney stating that office's intent not to file charges, etc. (Pen. Code, § 299, subd. (c).) A model expungement petition and a corresponding order for expungement are available on the website of the California Judicial Council. (Http://www.courtinfo.ca.gov/forms/documents/cr185.pdf; http://www.courtinfo.ca.gov/forms/documents/cr186.pd.) Notice of the expungement request must be provided to the Department of Justice and the prosecuting attorney. (Pen. Code, § 299, subd. (c).)

According to state law, "The denial of a request for expungement is a nonappealable order and shall not be reviewed by petition for writ." (Pen. Code, § 299, subd. (c)(1).) (See https://oag.ca.gov/bfs/prop69.)

In the alternative, an expungement request may be made directly to the Department of Justice's DNA Data Bank Program, if supported by sufficient documentation of one or more of the criteria set forth above. (See Pen. Code, § 299, subd. (c)(2)(B) [listing documentation options].) The latter option is non-statutory, and additional information is available from the Department of Justice's DNA Data Bank Program.

Statutory authority governing the federal DNA database program incorporates a similar expungement provision. (42 U.S.C.A. § 14132, subd. (d)(1)(A).)

2) Propositions 47 and 64, and DNA Database Expungement

In November 2014, the California electorate passed Proposition 47, which reclassified certain nonserious, nonviolent felony criminal offenses to misdemeanors. Part of Proposition 47 was codified as Penal Code section 1170.18. That provision permits convicted felons to petition the superior court to reclassify their felony convictions as misdemeanors, and impose corresponding misdemeanor sentences. The Legislature employed broad language: "A felony conviction that is recalled and resentenced under subdivision (b) or designated as a misdemeanor under subdivision (g) shall be considered a misdemeanor for all purposes …." (Pen. Code, § 1170.18, subd. (k).) The question arose whether reclassification of a felony to a misdemeanor under this new law also entitled the offender to expungement of the DNA sample that had been submitted to the state pursuant to Penal Code section 296. The California Supreme Court addressed the issue in In re C.B., 6 Cal. 5th 118, 237 Cal. Rptr. 3d 471, 425 P.3d 40 (Cal. 2018).

In re C.B. consolidated and reviewed two decisions from the Court of Appeal: In re C.H., 2 Cal. App. 5th 1139, 206 Cal. Rptr. 3d 775 (1st Dist. 2016), and In re C.B., 2 Cal. App. 5th 1112, 206 Cal. Rptr. 3d 785 (1st Dist. 2016). In both cases, juveniles were adjudicated of theft-related felonies and declared wards of the court. Both provided a mandated DNA sample for state and federal DNA database purposes, pursuant to Penal Code sections 296 and 296.1. In 2015, each juvenile successfully petitioned to have his felony offense redesignated as a misdemeanor under Proposition 47. The question for the Supreme Court was whether those reclassifications should also have entailed expungement of DNA samples and profiles, particularly in view of the statutory language directing that a reclassified violation would be a misdemeanor "for all purposes …."

The court focused its statutory analysis on Penal Code section 299, the provision governing retention (or expungement) of DNA database samples and profiles. (*C.B.*, *supra*, 6 Cal.5th at p. 126.) Importantly, observed the court, "the current scheme operates as it has since the databank's inception: a showing of changed circumstances eliminating a duty to *submit* a sample is an insufficient basis for *expungement* of a sample already submitted." (*Id*. at p. 128.) Thus, concluded the court, even though C.B. and C.H. no longer possessed felony adjudications of record, "they cannot meet the additional expungement requirements of [Penal Code] section 299, subdivision (b): lack of charges, acquittal, appellate reversal, or a finding of factual innocence. On the face of the statute, eligibility for expungement is confined to these circumstances. Nothing in section 299 authorizes expungement on the ground that conduct previously deemed a felony is now punished only as a misdemeanor." (*Ibid.*; see People v. Foster (2019) 7 Cal.5th 1202, 1209 [discussing and summarizing holding in *C.B.*].)

The fact that Proposition 47 permitted reclassification of a felony offense "for all purposes" did not alter this analysis. Of significance to the *C.B.* court was that Proposition 69 expressly distinguished the obligation to provide DNA upon arrest (or conviction) from the criteria that permit post-submission expungement of a database sample and associated profile. (6 Cal.5th at p. 129.) Thus, even when reduction of a felony to a misdemeanor under Proposition 47 means that the offender need not submit a DNA sample for database purposes, nothing in Proposition 69 indicates that the new status changes access to the specific, enumerated, prerequisites for expungement. (*Ibid*.) The drafters of Proposition 47 could have provided a statutory exception to this structure, but did not. (*Ibid*.) Proposition 47 cannot be read as providing an implied basis for expungement of DNA samples and profiles, above and beyond the express terms of Penal Code section 299. (*Id*. at p. 130.) "There is no inconsistency," opined the court, "between treating a redesignated offense as a misdemeanor for all purposes and declining to expunge a previously submitted DNA sample." (*Ibid*.)

The court in *C.B.* further held that retention of DNA database samples following redesignation of a felony to a misdemeanor under Proposition 47 was not inconsistent with the overall policy goals of either statutory scheme: "In short, no purpose underlying Proposition 47 or 69 requires expungement here. Proposition 69 expands the state's databank to advance the compelling interests in public safety and appropriate exoneration through more accurate identification of criminals. The retention of existing samples is consistent with that goal. Proposition 47 reduces punishments for certain crimes as a means of refocusing prison and prosecutorial resources on other crimes judged more serious. Nothing in the retention of samples hinders those aims." (6 Cal.5th at p. 133.)

Nor, finally, did state or federal equal protection guarantees require that those who saw their felonies reduced to misdemeanors under Proposition 47 be treated identically to those merely arrested for or charged with a misdemeanor from the outset. (*Id.* at pp. 134-135.)

In People v. Harris, 15 Cal. App. 5th 47, 222 Cal. Rptr. 3d 781 (4th Dist. 2017), review granted, see cal. rules of court 8.1105 and 8.1115, 225 Cal. Rptr. 3d 503, 405 P.3d 1075 (Cal. 2017), the court likewise affirmed the denial of a defendant's motion to expunge her DNA database sample and profile after her felony theft conviction was reduced to a misdemeanor. The court analyzed the statutory language of the state's DNA databank law, and reasoned that the subsequent reduction of a felony conviction to a misdemeanor was not an actionable event:

> Under the plain meaning of subdivisions (b) and (f) of [Penal Code] section 299, Harris is not entitled to DNA expungement because she has a past qualifying offense under section 296, subdivision (a)—i.e., she was convicted of an offense that qualified her for inclusion in the DNA database when her DNA sample was collected. The subsequent reclassification of her offense to a nonqualifying offense does not change the fact that at the time her DNA sample was taken, the taking was lawful because it was based on an offense that qualified for DNA submission. As noted in *In re C.B.* (2016) 2 Cal.App.5th 1112, 206 Cal.Rptr.3d 785 (C.B.), "the DNA sample submission requirement under the DNA Database Act does not necessarily hinge on whether a person is convicted of a felony or misdemeanor. Rather, under the relevant statutory language, the act's triggering point is when '[a]ny person, . . . is convicted of or *pleads guilty or no contest to any felony offense*.' (§ 296, subd. (a)(1), italics added.)" [*Citation*.]

(*People v. Harris, supra*, 15 Cal.App.5th at pp. 55-56.) *Harris* further held that AB 1492 did not amend Proposition 47 "because Proposition 47 'neither requires nor prohibits the expungement of DNA records. . . .' [Citation.]" (*Id.* at p. 59.) The court also affirmed the trial court's rejection of Harris's related equal protection claim and argument that the state's retention of her DNA sample violated state and federal constitutional privacy rights. (*Id.* at pp. 62, 65.)

A legislative enactment effective January 1, 2016, spoke directly to the issue of DNA sample retention following reclassification of a felony to a misdemeanor under Proposition 47. That law, designated AB 1492, amended Penal Code sections 298 and 299. (Stats 2015, ch. 487, § 4.) The Legislature clarified that the Proposition 47 reduction of a felony conviction or adjudication to a misdemeanor does not relieve the offender of the duty to provide a database sample. Otherwise it mirrors current law.

The passage of Proposition 64 in November 2016 similarly gave rise to questions about DNA sample retention and expungement. That voter initiative provided for reduction of marijuana felonies to misdemeanors or infractions, and resentencing, where a court determines that the defendant poses no threat to public safety. (See People v. Rascon, 10 Cal. App. 5th 388392–393, 216 Cal. Rptr. 3d 385 (2d Dist. 2017).) More broadly, "Proposition 64 was intended to decriminalize certain marijuana offenses by reducing sentences, dismissing marijuana-related offenses from criminal records, and prohibiting refiling of charges after prior marijuana-related convictions are reduced." (People v. Laird, 27 Cal. App. 5th 458, 465, 238 Cal. Rptr. 3d 313 (4th Dist. 2018).) The *Laird* court noted the similarity of statutory language animating the central provisions of Proposition 64 and Proposition 47: "The language of redesignation in Propositions 47 and 64 is nearly identical; Proposition 64 states that a conviction that is recalled and resentenced 'shall be considered a misdemeanor or infraction for all purposes.' (Health & Saf. Code, § 11361.8, subd. (h).)" (27 Cal.App.5th at p. 464.) But, *Laird* concluded, resdesignating a former felony offense "does not change the character of the original charge for administrative actions occurring before the redesignation, and the original felony guilty plea is a proper basis for collecting a DNA sample." (*Ibid*.)

Laird also pointed to the absence of language in Proposition 47 addressing DNA retention, and declined to infer content in an otherwise comprehensive statute. (*Laird*, *supra*, 27 Cal.App.5th at p. 465.) Moreover, noted the court, DNA collection was not thematically included in the overall scheme of reducing marijuana sentences, because DNA collection was nothing more than an administrative consequence of conviction: "DNA collection 'is not punitive, does not involve concepts of retroactivity or ex post facto implications, but is confined to a simple administrative identifying procedure akin to fingerprinting or keeping

one's whereabouts known to law enforcement.' (*Good v. Superior Court*, 158 Cal. App. 4th 1494, 1508, 71 Cal. Rptr. 3d 125 (1st Dist. 2008); see [Pen. Code,] § 299, subd. (f) [referencing the DNA sample as a 'separate administrative duty'].)" (*Laird*, *supra*, 27 Cal.App.5th at p. 465; see also *id*. at p. 467 ["DNA collection and retention is not punitive"].) Nor does reduction of a marijuana offense "for all purposes" imply that an offender "has 'no past or present offense or pending charge which qualifies [him] for inclusion within' the database. ([Pen. Code,] § 299, subd. (a))." (*Laird*, *supra*, 27 Cal.App.5th at p. 467.)

Finally, constitutional equal protection principles do not demand a different conclusion. "Laird pleaded guilty to and was convicted of a felony, which places him in a class distinct from post-Proposition 64 individuals who do not plead guilty to and are not convicted of a felony at any point in time. The distinction is reasonable because the collection of DNA is administrative and satisfies a legitimate purpose …." (*Id*. at p. 469.)

3) Circumstances Under Which Expungement Not Authorized

Postconviction relief under Penal Code sections 1203.4, 1203.4a, and/or 17, subdivision (b), is not a ground for expungement of a properly collected offender DNA profile. (Pen. Code, § 299, subd. (f).) Penal Code section 296, subdivision (b), provides that the "sentence imposed" and the disposition rendered" are immaterial in determining whether a DNA sample collection mandate exists.

In Coffey v. Superior Court, 129 Cal. App. 4th 809, 29 Cal. Rptr. 3d 59 (1st Dist. 2005), as modified on denial of reh'g, (June 16, 2005), the defendant pleaded guilty to a felony wobbler offense, and a DNA sample was collected pursuant to Penal Code section 296. Pursuant to a plea bargain, however, sentencing was deferred for one year, after which the trial court reduced the offense to a misdemeanor under Penal Code section 17, subdivision (b). The trial court denied the defendant's motion to expunge his DNA profile. The appellate court affirmed, holding that the plain language of the DNA database statute defines a plea to the felony version of a wobbler as a conviction for DNA collection purposes. (*Coffey v. Superior Court*, 129 Cal. App. 4th at 821–822, citing Pen. Code, § 296, subds. (a), (d), (f).) The subsequent reduction to a misdemeanor was immaterial. (*Ibid*.; see also Doe v. Brown, 177 Cal. App. 4th 408, 425, 99 Cal. Rptr. 3d 209 (4th Dist. 2009) ["a trial judge may not relieve a sex offender of the obligation to comply with the requirements mandated under the DNA Act by providing relief pursuant to section 1203.4].)

Nor did the defendant in *Coffey* have a constitutional right to return of the previously collected DNA sample, which in any event was collected in compliance with the Fourth Amendment. (*Coffey v. Superior Court*, 129 Cal. App. 4th at 817, 823; see also People v. Baylor, 97 Cal. App. 4th 504, 507–508, 118 Cal. Rptr. 2d 518 (4th Dist. 2002), opinion modified on denial of reh'g, (May 6, 2002) [no constitutional mandate to expunge or return DNA database sample collection in compliance with the Fourth Amendment, even if subsequently enacted expungement statute enacted].)

If an offender meets one of the expungement criteria set forth in section 299, no expungement need occur if the offender is subsequently required to provide a sample for an independent reason. In People v. Espana, 137 Cal. App. 4th 549, 40 Cal. Rptr. 3d 258 (4th Dist. 2006), the defendant was erroneously ordered in 2003 to provide a DNA sample despite being convicted of a then-non-qualifying offense. In the course of the appellate litigation, however, Proposition 69 took effect and redefined the defendant's conviction as a qualifying offense. The court noted that "if defendant's original DNA sample were expunged, he would be required to submit a new sample as either an inmate or a parolee." But it would be an idle act, observed the court "to remove defendant's DNA from the data bank if the state could turn around and compel a new DNA sample and then again place it in the data bank." (*People v. Espana*, 137 Cal. App. 4th at 553.) Accordingly, the defendant's request for expungement was properly denied. (*Ibid*.)

4) Retention and Ongoing Use of Profile and Samples

The California Department of Justice retains offender DNA samples and profiles that are not expunged. Retention of the physical sample permits confirmation retesting in the event of a database match. It also allows testing of additional forensic identification markers in the event that two or more offender profiles can only be distinguished from each other through further analysis of

different genetic markers. Finally, retaining DNA samples makes it possible to update forensic profiles as new or additional identification kits and technologies become available. For example, when forensic DNA technology transitioned from RFLP-based systems to PCR-based systems, the State retested all retained database samples using the new technology and was able to modernize its database accordingly.

Several courts have considered the question of whether the retention and indefinite use of offender DNA samples and profiles in a database implicates Fourth Amendment interests beyond those informing the initial seizure of the DNA samples. The First Circuit Court of Appeals, for example, held that the continued database searching of a DNA profile lawfully possessed by the government does not constitute a separate search implicating a convicted offender's legitimate expectation of privacy. (Boroian v. Mueller, 616 F.3d 60, 67–68 (1st Cir. 2010).) In reaching this conclusion, the court noted that "identification records of convicted felons, such as fingerprints or mugshots, are routinely retained by the government after their sentences are complete and may be expunged only in narrowly defined circumstances." (*Boroian v. Mueller*, 616 F.3d at 67.) Moreover, the use of those retained records to compare "against other records in [the government's] lawful possession does not infringe on an individual's legitimate expectation of privacy." (*Ibid*.)

Other case law is in accord. (See Johnson v. Quander, 440 F.3d 489, 499 (D.C. Cir. 2006) [like searching lawfully retained fingerprints, the continuing comparison of DNA profiles in a CODIS database "does not independently implicate the Fourth Amendment"]; Wilson v. Collins, 517 F.3d 421, 428 (6th Cir. 2008) [claim based on the government's retention and use of DNA profile "does not implicate the Fourth Amendment"]; U.S. v. Amerson, 483 F.3d 73, 86 (2d Cir. 2007); Smith v. State, 744 N.E.2d 437, 440 (Ind. 2001).)

In People v. Roberts (2021) 68 Cal.App.5th 64, the California Court of Appeal considered "whether using a DNA sample taken from a defendant who is validly arrested for a felony on probable cause but never formally charged, violates the defendant's federal or state constitutional rights against unreasonable search and seizure or his state constitutional right to privacy." (68 Cal.App.5th at p. 67.) In other words, whether the Fourth Amendment permits government use of an arrestee's DNA sample as a CODIS-generated investigative lead in an unrelated case when that sample was eligible for expungement, but the arrestee never sought to have it removed from state and national DNA databases. The issue arose when the California Department of Justice reported a DNA database "cold hit" match between the defendant's DNA profile and DNA left at the scene of the brutal murder of a 13-year-old girl. (*People v. Roberts* (2021) 68 Cal.App.5th at 67, 74.) The defendant's known DNA profile had been seized, processed, and searched pursuant to the DNA Database Act (Pen. Code, § 295 et seq.) following his lawful arrest on probable cause for an unrelated criminal offense. (People v. Roberts (2021) 68 Cal.App.5th at 77-78.) He was not prosecuted for that crime. (*People v. Roberts* (2021) 68 Cal.App.5th at 78.) The *Roberts* court held that, because seizure of the defendant's arrestee DNA sample had been constitutional (citing Maryland v. King (2013) 569 U.S. 435 and People v. Buza (2018) 4 Cal.5th 658), the fact that "he was neither formally charged nor subject to a probable cause determination by a neutral magistrate" did not alter "the Fourth Amendment calculus" in any meaningful way. (*People v. Roberts* (2021) 68 Cal.App.5th at 102.)

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§ 8:11. Collection and processing of crime scene samples

Crime scene DNA samples are collected by investigating law enforcement agencies and submitted to their local forensic DNA service provider laboratories for processing. Crime scene DNA samples are referred to as "forensic unknown samples," with their corresponding DNA profiles known as "forensic unknown profiles."

1) Prerequisites For Source Laboratories

Municipal, county, and state law enforcement crime laboratories in California that meet accreditation requirements (Pen. Code, § 297, subds. (a)(1) & (2), (d)) may upload DNA profiles into the State's DNA Database. State law does not permit private laboratories to upload profiles directly into SDIS, regardless of accreditation status. Nor can public laboratories not affiliated with a law enforcement organization upload profiles into SDIS.

Those public law enforcement labs that participate in CODIS must be designated as such by the California Department of Justice, and "meet state and federal requirements, including the FBI Quality Assurance Standards, and [be] accredited by an organization approved by the NDIS Procedures Board." (§ 297, subd. (a)(2).) The "state … requirements" include approval by the Department of Justice administrators of the DNA Data Bank Program; a process that includes a site inspection. The NDIS Procedures Board is chaired by the FBI, and sets policies and practices that all state and local laboratories participating in CODIS must follow. Most commonly, laboratory accreditation satisfying this provision is achieved through the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB), using either the "Legacy" or "International" (ISO) standards employed by that body. Accreditation through Forensic Quality Services, Inc. (FQS) is also acceptable.

2) Private Laboratories

Private laboratories may not upload crime scene DNA profiles directly into the state's database. Private labs may, however, contract with authorized public labs to process DNA samples and provide the resulting profiles for quality review and approval by, and upload through, the public lab. (Pen. Code, § 297, subd. (b).) Private labs must be inspected and approved by their contracting public law enforcement laboratory, however, and, like public participating labs, must be accredited by an acceptable organization and comply with the FBI Quality Assurance Standards. In essence, the public lab that uploads data generated by a private lab must adopt the data as its own.

3) The "Putative Perpetrator" Requirement

State and federal regulations require that unknown crime scene evidence profiles be attributable to the putative perpetrator of the crime under investigation. (FBI, DNA Acceptance Standards (2005) at p. 3 ["A laboratory submitting a DNA profile to the Forensic Index at NDIS that is derived from forensic evidence, shall only offer those alleles that are attributed to the putative perpetrator(s)"].) This requirement ensures that if and when a direct database match is reported, it will be an investigative lead

of value to law enforcement and will preclude to the extent possible needless contact between law enforcement and innocent third parties.

4) Technical Requirements

Forensic unknown profiles must also meet certain technical standards to be eligible for upload into the state database. A minimum of seven loci of data must be available for searching the California database. The FBI requires a minimum of ten loci for upload of an unknown profile into the National DNA Index System. In addition, the "four-by-four" rule enforced by the California Department of Justice mandates that, for any forensic unknown profile uploaded into the state database, no more than four loci may have "extra" alleles (i.e., more than two), and there may not be more than four alleles at any locus.

5) Upload Into National DNA Database

California's DNA Data Bank program is part of the FBI's national Combined DNA Index System (CODIS) network that is designed to enable "federal, state, and local crime labs to exchange and compare DNA profiles electronically," thereby linking crimes to each other and to criminal offenders on an interstate basis. (Pen. Code §§ 295(g) & (h)(4); see http://www.fbi.gov/hq/lab/codis/brochures.htm; see also U.S. v. Kincade, 379 F.3d 813, 818–820 (9th Cir. 2004) [describing function and interoperability of DNA databases].)

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§ 8:12. Use restrictions on Data Bank samples and profiles

State law requires that the Department of Justice use the DNA samples and profiles in its database for "identification purposes" only. (Pen. Code, § 295.1; § 297, subd. (a) [laboratories participating in Database Program authorized to analyze specimens and samples "in order to establish identity and origin of samples for identification purposes."]; see Alfaro v. Terhune, 98 Cal. App. 4th 492, 508, 120 Cal. Rptr. 2d 197 (3d Dist. 2002).) More specifically, California's DNA Data Bank Program exists to "assist federal, state, and local criminal justice and law enforcement agencies within and outside California in the expeditious and accurate detection and prosecution of individuals responsible for sex offenses and other violent crimes, the exclusion of suspects who are being investigated for these crimes, and the identification of missing and unidentified persons … ." (Pen. Code, § 295, subd. (c).)

Various other provisions of the DNA database law reference limitations on the permissible uses of DNA samples and profiles possessed by the State. (Pen. Code § 295, subd. (a) [DNA … "analysis is a useful law enforcement tool for identifying and prosecuting criminal offenders and exonerating the innocent"]; § 295, subd. (b)(3) ["It is necessary to enact this act … in order to … enable the state's DNA and Forensic Identification Database and Data Bank Program to become a more effective law enforcement tool"]; § 295, subd. (d) ["the collection of DNA samples pursuant to this chapter is an administrative requirement to assist in the accurate identification of criminal offenders"]; § 295.1, subd. (a) ["The Department of Justice shall perform DNA analysis … pursuant to this chapter only for identification purposes"]; § 297, subd. (a) [limiting the laboratories that may process DNA samples which are permitted to "upload and compare those profiles against available state and national DNA and forensic identification databanks and databases in order to establish identity and origin of samples for forensic identification purposes"]; § 299.5, subd. (i) [providing for severe criminal and civil penalties if a DNA Database sample or profile is used "for other than criminal identification or exclusion purposes or for the identification of missing persons"].)

Such use restrictions have been cited by courts in conducting a Fourth Amendment balance of the state's interest in seizing DNA database samples against the invasion of privacy those seizures entail. (See People v. King, 82 Cal. App. 4th 1363, 1377, 1375, 99 Cal. Rptr. 2d 220 (1st Dist. 2000) [discussing the database's use limitations as part of the constitutional balancing analysis]; Alfaro v. Terhune, 98 Cal. App. 4th 492, 507–508, 120 Cal. Rptr. 2d 197 (3d Dist. 2002) ["The extent of the [data bank] intrusion is measured by reference to express limitations on the uses to which the specimens and samples may be put … ."].)

In Hamilton v. Brown, 630 F.3d 889 (9th Cir. 2011), the Ninth Circuit similarly relied on the use limitations built into the California DNA database law in affirming the constitutionality of collections from convicted offenders: "Here, DNA testing under the California DNA Act, like the federal law, is limited to the collection of identifying information. Cal. Pen. Code § 299.5 (limiting use of samples to criminal identification, exclusion of suspects, and identification of missing persons and imposing penalties for misuse). Having been convicted and incarcerated, Hamilton has no legitimate expectation of privacy in the identifying information derived from his DNA." (*Hamilton v. Brown*, 630 F.3d at 895.)

Conversely, some courts have warned that use of DNA samples and profiles beyond what was authorized to justify their original collection and retention, in ways that reveal "more intimate or private information about the profile's owner," could implicate privacy rights in new ways that give rise to Fourth Amendment violations. (Boroian v. Mueller, 616 F.3d 60, 69 (1st Cir. 2010).)

To the extent that DNA database samples possibly may be put to unauthorized or overly invasive use in the future, however, there is no cognizable Fourth Amendment violation. (U.S. v. Karo, 468 U.S. 705, 712, 104 S. Ct. 3296, 82 L. Ed. 2d 530 (1984) ["[W]e have never held that potential, as opposed to actual, invasions of privacy constitute searches for purposes of the Fourth Amendment."].)

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§ 8:13. Disclosure restrictions

Under California law, a criminal defendant is entitled to discovery of his or her own DNA Database profile and associated information. (Pen. Code, § 299.5, subd. (g).) All other DNA profiles are confidential, as set forth in Penal Code section 299.5(h):

> Except as provided in subdivision (g) and in order to protect the confidentiality and privacy of database and data bank information, the Department of Justice and local public DNA laboratories shall not otherwise be compelled in a criminal or civil proceeding to provide any DNA profile or forensic identification database or data bank information or its computer database program software or structures to any person or party seeking such records or information whether by subpoena or discovery, or other procedural device or inquiry.

(See also § 299.5, subd. (a) ["All DNA and forensic identification profiles and other identification information retained by the Department of Justice pursuant to this chapter are exempt from any law requiring disclosure of information to the public and shall be confidential except as otherwise provided in this chapter."]; People v. McCray, 144 Cal. App. 4th 258, 266–267, 50 Cal. Rptr. 3d 343 (2d Dist. 2006) [describing Database Act's disclosure limitations].) Other provisions of the law limit disclosure of database samples, profiles, and associated information to law enforcement. (See, e.g., Pen. Code, § 299.5, subd. (f).)

At least one court had described statutory confidentiality provisions as protecting DNA database information against attempts to use it for scientific research purposes. (U.S. v. Kincade, 379 F.3d 813, 837 (9th Cir. 2004) [observing that statutory confidentiality protections counter defense claim that "soon, if not already, scientists will request access to what would serve as [a] preexisting goldmine of DNA data for their research"].)

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§ 8:14. Penalties for violating use or disclosure restrictions

Violations of use and disclosure restrictions carry with them criminal and civil penalties. (Pen. Code, § 299.5, subd. (i).) Any individual who uses a sample or DNA profile for any purpose other than criminal identification, or the identification of missing persons, or who discloses the sample or DNA profile to an unauthorized person, faces "imprisonment in the state prison." (§ 299.5, subd. (i)(1)(A).) In addition, any Department of Justice employee who misuses or improperly discloses a sample or DNA profile is subject to a fine of up to $50,000 plus attorney's fees and costs. (§ 299.5, subd. (i)(2)(A).)

By virtue of its participation in CODIS at a national level, California is potentially subject to federal penalties as well for violating federal use and disclosure standards set forth by law. (See 42 U.S.C.A. §§ 14132 et seq.; see also 61 Fed. Reg. 37497 (July 18, 1996) ["[C]riminal justice agencies with direct access to CODIS must agree to … restrict access to DNA samples and data."].) In addition, law enforcement access to CODIS may be canceled for failure to meet the quality control and privacy requirements of federal law: "Access to the index established by this section is subject to cancellation if the quality control and privacy requirements described in subsection (b) [of Section 14132] are not met." (42 U.S.C.A. § 14132, subd. (c); see also Privacy Act of 1974; New System of Records, 61 Fed. Reg. 37497 (July 18, 1996) ["[C]riminal justice agencies with direct access to NDIS must agree to adhere to national quality assurance standards for DNA testing, undergo semi-annual external proficiency testing, and restrict access to DNA samples and data. The NDIS will not accept DNA analyses from those agencies and/or DNA personnel who fail to comply with these standards and restrictions; and the NDIS Custodian is authorized to restrict access to and delete any DNA records previously entered into the system."].)

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§ 8:15. Confirming and reporting a cold hit to law enforcement

Following the observation of a "candidate match" between an offender reference DNA profile and an unknown crime scene profile, the California Department of Justice will notify the law enforcement laboratory that uploaded the evidence profile. Once the source laboratory has "dispositioned" the candidate profile as a match based on a scientific assessment of the genetic data, the Department of Justice will re-analyze the offender reference sample in its possession to confirm the validity of the original profile. The Department of Justice also will confirm the identity of the offender based on thumbprints submitted with the original sample. When this confirmation process is complete, the Department of Justice will provide the offender's name and other available identification information to the source laboratory.

California's DNA Data Bank Program is designed to provide an investigative lead to law enforcement. The cold hit identification of an offender is commonly used as probable cause for a subsequent arrest warrant. Law enforcement will normally obtain a new known reference DNA sample from the suspect pursuant to a search warrant, whose probable cause is again based, at least in part, on the DNA Database match. The same crime laboratory that analyzed the original case evidence will test the new reference sample and conduct the casework comparison. The results of that comparison, and not the database match, will be identification evidence for purposes of trial.

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Forensic DNA Evidence: Science and the Law § 8:16

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§ 8:16. Constitutionality of DNA database collections and searches under the Fourth Amendment

1) Sample Collection From Convicted and Adjudicated Offenders

The constitutionality, under the Fourth Amendment, of the warrantless, suspicionless collection of DNA Database samples from the classes of qualifying offenders enumerated in state law has been the subject of much litigation. Compelled sampling of biological material for database purposes is a search subject to the Fourth Amendment. (See Skinner v. Railway Labor Executives' Ass'n, 489 U.S. 602, 616, 109 S. Ct. 1402, 103 L. Ed. 2d 639 (1989); Banks v. U.S., 490 F.3d 1178 (10th Cir. 2007).)

California case law affirms that database collections from convicted adult felons, regardless of the nature of the felony offense, are constitutional under the Fourth Amendment's reasonableness balancing test. (See, e.g., People v. Robinson, 47 Cal. 4th 1104, 1120–1122, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010); People v. Travis, 139 Cal. App. 4th 1271, 1289–1290, 44 Cal. Rptr. 3d 177 (1st Dist. 2006); People v. Johnson, 139 Cal. App. 4th 1135, 1168, 43 Cal. Rptr. 3d 587 (5th Dist. 2006); People v. Adams, 115 Cal. App. 4th 243, 259, 9 Cal. Rptr. 3d 170 (6th Dist. 2004), as modified, (Feb. 5, 2004); Alfaro v. Terhune, 98 Cal. App. 4th 492, 505–506, 120 Cal. Rptr. 2d 197 (3d Dist. 2002); People v. King, 82 Cal. App. 4th 1363, 1371–1378, 99 Cal. Rptr. 2d 220 (1st Dist. 2000).)

The rationale underlying this body of authority was summarized by the California Supreme Court in People v. Robinson, 47 Cal. 4th 1104, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010), as follows:

> [T]he "nonconsensual extraction of biological samples for identification purposes does implicate [federal] constitutional interests" [citation], but … such nonconsensual extraction of biological samples from adult felons is reasonable because "those convicted of serious crimes have a diminished expectation of privacy and the intrusions authorized by the Act are minimal" while "the Act serves compelling governmental interests," including "'the overwhelming public interest in prosecuting crimes accurately.' [Citation.] A minimally intrusive methodology that can serve to avoid erroneous convictions and to bring to light and rectify erroneous convictions that have occurred manifestly serves a compelling public interest. [Citation]"

(*People v. Robinson*, 47 Cal. 4th at 1121; see also People v. McCray, 144 Cal. App. 4th 258, 266–267, 50 Cal. Rptr. 3d 343 (2d Dist. 2006) [summarizing California decisional authority on this issue].)

The constitutional collection of statutorily mandated DNA samples from convicted and adjudicated offenders is not limited to those who have committed serious, violent, or sex offenses. Rather, the utility of maintaining a permanent, reliable, and accurate identification record for all convicted and adjudicated felons outweighs the minor intrusion on the minimal privacy interests those people maintain in their identities. (*People v. Travis*, 139 Cal. App. 4th at 1289–1290; see also Jones v. Murray, 962 F.2d 302 (4th Cir. 1992), as amended, (Apr. 27, 1992) [collection from all convicted felons pursuant to Virginia law constitutional].)

So too is collection of DNA from a juvenile adjudicated of a felony offense constitutional. (In re Calvin S., 150 Cal. App. 4th 443, 449, 58 Cal. Rptr. 3d 559 (3d Dist. 2007), as modified on denial of reh'g, (May 30, 2007).)

Federal courts as well have consistently upheld the constitutionality, under the Fourth Amendment, of collecting DNA database samples from convicted felons. (See, e.g., Hamilton v. Brown, 630 F.3d 889 (9th Cir. 2011); U.S. v. Kriesel, 508 F.3d 941, 946 (9th Cir. 2007); U.S. v. Kraklio, 451 F.3d 922, 924–25 (8th Cir. 2006); Johnson v. Quander, 440 F.3d 489, 496 (D.C. Cir. 2006); U.S. v. Sczubelek, 402 F.3d 175, 184 (3d Cir. 2005); Padgett v. Donald, 401 F.3d 1273, 1280 (11th Cir. 2005); U.S. v. Kincade, 379 F.3d 813 (9th Cir. 2004); U.S. v. Hugs, 384 F.3d 762, 769 (9th Cir. 2004); Green v. Berge, 354 F.3d 675, 679 (7th Cir. 2004); Groceman v. U.S. Dept. of Justice, 354 F.3d 411, 413 (5th Cir. 2004); U.S. v. Kimler, 335 F.3d 1132, 1146, 61 Fed. R. Evid. Serv. 1024, 7 A.L.R. Fed. 2d 583 (10th Cir. 2003); Boling v. Romer, 101 F.3d 1336, 1340 (10th Cir. 1996); Rise v. State of Or., 59 F.3d 1556, 1562 (9th Cir. 1995); Roe v. Marcotte, 193 F.3d 72, 74 (2d Cir. 1999); Jones v. Murray, 962 F.2d 302, 308 (4th Cir. 1992), as amended, (Apr. 27, 1992).)

2) Sample Collection From Arrestees: *Maryland v. King*

As of 2014, 30 states and the federal government collect DNA samples from those arrested, but not yet convicted, of a criminal offense. The scope of these laws varies, with different classifications of arrestees targeted in different jurisdictions. The constitutionality, under the Fourth Amendment, of collection from arrestee samples continues to be the subject of litigation as of early 2014. Yet, in a 2013 decision the United States Supreme Court addressed the issue in what Justice Alito called during oral argument "perhaps the most important criminal procedure case this Court has heard in decades." The case was Maryland v. King, 133 S. Ct. 1958, 186 L. Ed. 2d 1 (2013).

King involved a Maryland man arrested in 2009 on assault charges who provided a DNA sample upon arrest. Maryland law required that individuals arrested for commission or attempted commission of certain serious violent and sex crimes provide a buccal swab DNA sample at the time of arrest. (133 S.Ct. at p. 1967.) Unlike California's arrestee DNA law, Maryland prohibits processing the sample to generate a searchable DNA profile until the arrestee is arraigned and a judge makes a formal finding of probable cause to detain the arrestee for that serious qualifying offense. (*Ibid*.) Maryland law also requires automatic expungement of arrestee DNA samples in cases not resulting in conviction, and prohibits familial searching using DNA database profiles. (*Ibid*.) It should be noted that California offers both statutory and non-statutory expungement mechanisms for DNA database samples (see *supra* § 8:10), and does not engage in familial searching using its SDIS arrestee index.

A five-Justice majority of the Supreme Court upheld Maryland's practice, concluding that "DNA identification of arrestees is a reasonable search that can be considered part of a routine booking procedure." (133 S.Ct. at p. 1980.) The Court conducted its Fourth Amendment analysis of DNA collection at arrest by employing a totality of the circumstances balance, weighing "'legitimate governmental interests' against 'the degree to which [the search] intrudes upon an individual's privacy.'" (*Id*. at p. 1970, quoting Wyoming v. Houghton, 526 U.S. 295, 300, 119 S. Ct. 1297, 143 L. Ed. 2d 408 (1999).) The government interests in arrestee collections were framed around the search being "'a routine administrative procedure[ ] at a police station house incident to booking and jailing the suspect.'" (*Id*. at p. 1971.) The purposes and benefits of that routine procedure include identifying the person under arrest, ascertaining that person's criminal history as a component of identification, providing information useful to classifying and safely housing the arrestee in jail, providing information relevant to decisions on setting—or revoking—bail and thus enhancing public safety and ensuring appearance for trial. (*Id*. at pp. 1972–1974.) The Court analogized the purposes and benefits of arrestee sampling to those associated with the routine and accepted practice of fingerprinting arrestees—with the exception that DNA-based identification "is an advanced technique superior to fingerprinting in many ways." (*Id*. at p. 1976.) It thus assigned "great weight both to the significant government interest at stake in the identification of arrestees and to the unmatched potential of DNA identification to serve that interest." (*Id*. at p. 1977.)

The *King* majority found the counterweight of arrestee privacy interests insufficient to sway the balance. It pointed to arrestees' diminished expectations of privacy, and distinguished arrestee DNA collections from programmatic searches assessed under the "special needs" doctrine. (133 S.Ct. at p. 1978.) And, while DNA collection does implicate the Fourth Amendment, the "brief intrusion of an arrestee's person" resulting from collection of the DNA sample with a buccal swab is insignificant in the context of an arrest. (*Id*. at p. 1979.) The Court observed that use of "non-coding alleles" for CODIS purposes is a scientific safeguard

that mitigates privacy concerns, as does the "undisputed" fact that DNA collected for database searching is used exclusively for identification. (*Ibid*.) As to the latter, the Court cited several Maryland statutes imposing use and disclosure restrictions upon DNA database collections and operation. (*Id*. at pp. 1979–80.)

Justice Scalia, in a vigorous dissent, argued that the majority's reasoning was disingenuous; namely, that the real purpose behind arrestee DNA collections was to solve prior crimes, for which involuntary biological samples cannot be seized without a warrant. (*King*, *supra*, 133 S.Ct. 1958, 1982–86 (Scalia, J., dissenting).) But, Justice Scalia also acknowledged the breadth of the Court's ruling as one extending well beyond the parameters of Maryland law: "As an entirely predictable consequence of today's decision, your DNA can be taken and entered into a national DNA database if you are ever arrested, rightly or wrongly, and for whatever reason." (*Id*. at p. 1989.)

3) Sample Collection From Arrestees: *People v. Buza*

After nearly a decade of litigation in the state's lower courts—and one previous grant of review—in 2018 the California Supreme Court issued its long-awaited opinion in People v. Buza, 4 Cal. 5th 658, 230 Cal. Rptr. 3d 681, 413 P.3d 1132 (Cal. 2018). The question presented in *Buza* was whether the DNA collection requirement in California's DNA Database Program legislation "is valid as applied to an individual who, like defendant, was validly arrested on 'probable cause to hold for a serious offense'—here, the felony arson charge for which defendant was ultimately convicted—and who was required to swab his cheek as 'part of a routine booking procedure' at county jail. [Citation.]" (*Buza*, *supra*, 4 Cal.5th at p. 664, quoting Maryland v. King, 569 U.S. 435, 456–466, 133 S. Ct. 1958, 186 L. Ed. 2d 1 (2013).) The California Supreme Court held that, with respect to that class of arrestees, collection of DNA at booking is permissible under both state and federal Constitutions. (4 Cal.4th at p. 665.) The majority took pains to clarify that it did not consider the case a "facial constitutional review of the DNA Act as it might be applied to other arrestees." (*Id*. at p. 693.)

Defendant Buza had been arrested in 2009 after setting fire to a police car. At booking on suspicion of felony arson, he refused to provide the DNA sample mandated under Penal Code section 296, subdivision (a)(2)(C) and section 296.1, subdivision (a)(1)(A). The district attorney charged Buza with, among other offenses, a violation of Penal Code section 298.1, subdivision (a)—the misdemeanor of refusing to provide a DNA sample. A jury convicted Buza on all counts. Buza argued on appeal that California's statutory DNA collection requirement violated both the Fourth Amendment of the United States Constitution and article I, section 13, of the California Constitution. (*Buza*, *supra*, 4 Cal.5th at pp. 668–669.)

The *Buza* court considered the Fourth Amendment aspect of the case through the lens of *Maryland v. King*, *supra*, 569 U.S. 435. It observed that *King* confirmed that "DNA identification of arrestees is reasonable on booking following an arrest supported by probable cause to believe the arrestee has committed a serious offense." (*Buza*, *supra*, 4 Cal.5th at p. 673.) It rejected appellant Buza's argument that differences between Maryland's and California's DNA collection laws demanded a different outcome: "[N]one of the differences to which defendant points meaningfully alters the constitutional balance struck in *King*." (*Id*. at p. 674; see also *id*. at p. 683.) The distinctions Buza had sought to rely upon were (1) California's collection of arrestee DNA from a broader spectrum of offenses; (2) California's authorization of collection and testing of DNA before an arrestee is charged and before a magistrate's determination of the validity of those charges; and (3) the absence of automatic expungement of DNA samples for those not charged with, or convicted of, a felony. (*Ibid*.)

As for the nature of the offense for which a person is arrested, the California Supreme Court observed that *King*'s holding applied broadly to all felony offenses, and noted that any felony is considered a "serious" offense. (*Ibid*.) The *Buza* court did not consider whether collection from non-felony arrestees would be permissible.

On the question of timing of DNA sample collection and processing, the California Supreme Court deferred to *King*'s determination that arrestee DNA collection is "a 'legitimate police *booking* procedure,' like fingerprinting or photographing, that enables jail officials to know whom they have taken into custody. (*King*, *supra*, 569 U.S. at p. 466, italics added.)" (*Buza*, *supra*, 4 Cal.5th at p. 676.) Nor, wrote the *Buza* court, did *King* premise its holding on Maryland's statutory requirement of

a judicial finding of probable cause before an arrestee DNA sample could be typed and uploaded into CODIS databases. (*Id.* at p. 677.) Instead, the key government interest influencing the Fourth Amendment balance in *King* was that arrestee DNA collection at booking "enables law enforcement to know whom they have in custody"—an interest that attaches as soon as the arrestee is taken into custody rather than possibly days later when a magistrate reviews the charges. (4 Cal.5th at p. 677.) This interest remains tethered to the booking process even if the arrestee's DNA sample is not immediately processed and searched against state and national DNA databases. (*Id.* at p. 678.) The court also noted that a magistrate's formal determination of the lawfulness of an arrest is not an element of a lawful arrest, and does not contribute to the reasonableness of an arrest after the fact. (*Id.* at p. 679.)

In response to Buza's argument about the adequacy of California's DNA expungement procedures, the court declared it to be "a question we must leave for another day" because Buza was validly arrested and convicted of a felony offense, and never sought expungement, thus depriving him of any entitlement to litigate the hypothetical constitutional implications of contrasting approaches to DNA expungement. (*Buza*, *supra*, 4 Cal.5th at pp. 681, 683.) For that matter, added the court, the record in the case was factually undeveloped on how California's expungement procedures functioned in practice under various scenarios. (*Id.* at pp. 681–682.) "This court ordinarily does not issue constitutional rulings based on speculation, and we will not do so here," the court reasoned. (*Id.* at p. 683.) That being said, the court did offer a guide to the structure such litigation might take. On one hand, based on longstanding precedent, "the retention of an arrestee's fingerprints, photographs, and other identifying information in law enforcement files generally has not been thought to raise constitutional concerns, even though the arrestee may later be exonerated." (*Id.* at p. 680.) On the other hand, one could ask whether "a different rule should apply" "given the uniquely sensitive nature of DNA information …." (*Ibid.*)

Turning to the legality of the state's statutory arrestee DNA collection provisions under article I, section 13 of the California Constitution, the *Buza* court necessarily engaged in the same reasonableness balancing test analysis prescribed for determining search and seizure questions under the federal Constitution. (*Buza*, *supra*, 4 Cal.5th at p. 684.) In fact, under 1982's Proposition 8, "the exclusionary rule does not apply to a search or seizure that violates California Constitution, article I, section 13, but does not violate the Fourth Amendment, and the fruits of such a search or seizure are admissible in a criminal trial. This means that in California criminal proceedings, issues related to the suppression of evidence seized by police are, in effect, governed by federal constitutional standards." (*Id.* at p. 685.) Accordingly, the question in *Buza* was "whether adequate reasons are present here to conclude, despite *King*, that California voters exceeded constitutional bounds in mandating the collection of a DNA sample from an individual arrested and booked on probable cause to believe he had committed a serious offense." (*Id.* at p. 687.) The court concluded that no such conclusion was merited, for several reasons.

First, the court acknowledged that DNA sampling could both "provide accurate and reliable identification of criminal offenders" *and* "establish a suspect's involvement in crimes." (*Buza*, *supra*, 4 Cal.5th at p. 687.) Thus, collection at arrest serves the state's interest in identifying the person in custody in order to "inform[] decisions about how to proceed with the arrestee" just as law enforcement would use the arrestee's facial mug shot, tattoos, or fingerprints to both identify the arrestee and potentially generate investigative leads. (*Id.* at p. 688.) Nor does the timing of the DNA results impact the analysis: "Even if a DNA profile is not generated until weeks or months after the initial booking, the information it yields about the arrestee and his criminal history can still have an 'important bearing' on the processing of the arrestee—whether, for example, to revisit an initial determination to release the arrestee or to impose new release conditions. [Citation.] Information obtained after initial booking may also influence the jailer's decision about where to house the arrestee." (*Id.* at p. 689.) And, the functionality of fingerprint-based identification protocols complement, but are not substitutes for, the distinct utility offered by DNA-based identification methods. (*Ibid.*)

Second, the court rejected Buza's argument that the potently sensitive personal information genetically encoded in a person's DNA should be a significant factor in the privacy aspect of a balancing test. (*Buza*, *supra*, 4 Cal.5th at pp. 689–690.) The court noted *King*'s assessment that "CODIS testing is designed to reveal nothing more about the arrestee than his or her identity, and that state law forbade the use of DNA information for nonidentification purposes." (*Id.* at p. 689.) In dismissing privacy concerns, however, *Buza* ultimately relied upon the use and disclosure provisions integrated into California's DNA Database law: "[T]he DNA Act makes the misuse of a DNA sample a felony, punishable by years of imprisonment and criminal fines. (Pen. Code, §

299.5.) These strong sanctions substantially reduce the likelihood of an unjustified intrusion on the suspect's privacy." (4 Cal.5th at p. 690.) Later in the opinion, the court provided additional detail about those aspects of California's law weighing in favor of constitutionality, describing them as "safeguards built into the DNA Act: the limited nature of the information stored in databases on an arrestee (specifically, a numerical profile describing noncoding parts of the arrestee's DNA); the legal protections against possible misuse of the profile or the sample (including felony sanctions for knowing improper use or dissemination); and the availability of procedures for removing the profile from the database and destroying the sample should the basis for the arrestee's inclusion dissipate." (*Id*. at p. 692.) The court declined to speculate about future advances in science or other developments that could alter the privacy calculus. (*Id*. at p. 690.)

Third, *Buza* disclaimed the applicability of California case authority extending broader state privacy protections than those afforded by the federal Constitution to searches conducted in the field and before the actual booking process commences. (4 Cal.5th at pp. 690–601.) DNA seizures, in contrast, are part of the booking process itself, and are thus "justified by an interest in accurate identification that applies to all persons who are taken into police custody following a valid arrest for a serious offense. Cases concluding that full booking searches are inappropriate for arrestees who will never be booked into jail are thus of limited relevance here." (*Id*. at p. 691.)

Finally, the California Supreme Court emphasized that its holding in *Buza* was "limited," and would not necessarily apply to "other categories of arrestees." (4 Cal.5th at p. 691.) The latter could include those "wrongly or pretextually arrested," those never charged with a crime, or those "ultimately acquitted of any charged offenses." (*Id* at p. 692.) The court hypothesized that some other arrestee "might reasonably anticipate that charges will never be brought and any attempted prosecution will inevitably fail" if he or she is arrested in the absence of probable cause, and thus "may, at least in some circumstances, have a valid as-applied challenge to the adequacy of the DNA Act's expungement procedures or to application of the Act's other operative provisions, in addition to the other remedies available for unlawful arrest. (*Id*. at pp. 692–693.) But, the *Buza* court offered no insight on the merits of such a challenge.

In People v. Marquez, 31 Cal. App. 5th 402, 242 Cal. Rptr. 3d 530 (4th Dist. 2019), the Court of Appeal referenced *Buza* in reviewing a suppression motion based on the defendant's assertion that he had not been validly arrested, and thus should not have had his DNA sample collected at arrest. (31 Cal.App.5th at pp. 410–411.) The court wrote that "the prosecution failed to prove by a preponderance of the evidence that Marquez was validly arrested in 2006. We are presented with the very situation that our Supreme Court declined to address in *Buza*; that is, there is nothing in the record to indicate that Marquez's 2006 arrest was supported by probable cause." (*Id*. at p. 410.) The court opined that "it is a reasonable inference that at the time of his arrest in 2006, there were no reasonable grounds to believe that he was guilty of any 'serious' or 'jailable' crimes." (*Id*. at p. 411.) It did not explain why this inference was reasonable, but merely pointed out that no charges were ever filed. (*Id*. at p. 410–411.) The court even acknowledged that there may have been reasons for the absence of charges having nothing to do with the circumstances of the arrest. (*Id*. at pp. 410–411 ["There may be variety of reasons for this; perhaps the police did not file the case with the district attorney, or perhaps the district attorney chose not to file charges"].) In the end, however, *Marquez* held that the prosecution bore the burden of demonstrating that the statutorily-mandated DNA collection properly occurred, and, at least in this case, failed to meet that burden. (*Id*. at p. 411.)

4) Sample Collection From Arrestees: Other State And Federal Litigation

In People v. Roberts (2021) 68 Cal.App.5th 64, the California Court of Appeal conducted an extensive review of state and federal authority addressing the constitutionality of arrestee DNA collections under the DNA Database Act. (68 Cal.App.5th at 97-102.) That analysis formed the basis for the court's consideration "whether using a DNA sample taken from a defendant who is validly arrested for a felony on probable cause but never formally charged, violates the defendant's federal or state constitutional rights against unreasonable search and seizure or his state constitutional right to privacy." (*People v. Roberts*, 68 Cal.App.5th at 67.) The issue arose when the California Department of Justice reported a DNA database "cold hit" match between the defendant's DNA profile and DNA left at the scene of the brutal murder of a 13-year-old girl. (*People v. Roberts*, 68 Cal.App.5th at 67, 74.) The defendant's known DNA profile had been seized, processed, and searched pursuant to the DNA

Database Act (Pen. Code, § 295 et seq.) following his lawful arrest on probable cause for an unrelated criminal offense. (*People v. Roberts*, 68 Cal.App.5th at 77-78.) He was not prosecuted for that crime. (*People v. Roberts*, 68 Cal.App.5th at 78.) The *Roberts* court held that, because seizure of the defendant's arrestee DNA sample had been constitutional (citing Maryland v. King (2013) 569 U.S. 435 and People v. Buza (2018) 4 Cal.5th 658), the fact that "he was neither formally charged nor subject to a probable cause determination by a neutral magistrate" did not alter "the Fourth Amendment calculus" in any meaningful way. (*People v. Roberts*, 68 Cal.App.5th at 102.)

In People v. Lowe (2013) 221 Cal.App.4th 1276, the California Court of Appeal addressed the constitutionality of arrestee DNA collections. In *Lowe*, the defendant was convicted of a series of sex crimes, burglaries, and robberies committed between 2003 and 2006. He was identified as the perpetrator by a DNA database match to an arrestee sample he provided upon his arrest in 2006 for commission of one of the sex crimes. The trial court denied his motion to suppress evidence, which had claimed that the involuntary arrestee DNA sampling he was subject to violated the Fourth Amendment to the United States Constitution. The Court of Appeal affirmed, holding that "the 2004 Amendment [to California's DNA Data Bank Act] authorizing the mandatory and warrantless collection and analysis of buccal swab DNA samples from felony arrestees does not violate the Fourth Amendment, and, thus, the court properly denied Lowe's suppression motion …." (221 Cal.App.4th at p. 1281.) The court further held that this conclusion was consistent with Maryland v. King, 133 S. Ct. 1958, 186 L. Ed. 2d 1 (2013). (221 Cal.App.4th at p. 1281.)

As in *King*, the Court of Appeal in *Lowe* subjected California's arrestee DNA program to a reasonableness balancing analysis. Its findings on the use, and privacy implications, of arrestee DNA mirrored those set forth in *King*. (221 Cal.App.4th at pp. 1292–1296.) In addition, however, the *Lowe* court included governmental interests in solving past crimes and preventing future crimes as factors weighing in favorable of reasonableness. (*Id*. at pp. 1295–1296.) It summarized its rationale as follows:

> We conclude that the legitimate governmental interests promoted by the warrantless collection of buccal swab DNA samples from felony arrestees who are taken into custody upon probable cause far outweigh the arrestees' privacy concerns. Our conclusion is based on the following five reasons: The felony arrestee's diminished privacy interests; the de minimis nature of the physical intrusion involved in the collection of a buccal swab DNA sample; the carefully limited scope of the DNA information that is extracted; the strict limits on the range of permissible uses of the DNA information obtained and the significant criminal penalties imposed upon those who violate those limitations; and the strong law enforcement interests in obtaining arrestees' identifying information, solving past and future crimes, deterring future criminal acts, and exonerating the innocent.

(*Id*. at pp. 1296–1207.)

Finally, *Lowe* considered *Maryland v. King*. It opined that *King*'s reasoning applied to California's DNA database law just as it did to Maryland's. (221 Cal.App.4th at p. 1298.) "Here, as in *King*," concluded the *Lowe* court, "the minimal intrusion of the buccal swab into the arrestee's diminished right to privacy is outweighed by the important governmental interests served by the challenged statute. Here, as in *King*, scientific and statutory safeguards (discussed, *ante*) are provided by the 2004 Amendment such that the analysis of the collected DNA sample 'd[oes] not amount to a significant invasion of privacy that would render the DNA identification impermissible under the Fourth Amendment.' (*King*, *supra*, 133 S.Ct. at p. 1980.)" (221 Cal.App.4th at p.1298.)

In Haskell v. Harris, 745 F.3d 1269 (9th Cir. 2014), the Ninth Circuit addressed the constitutionality of arrestee collection. It framed the question as: "Is California's DNA collection scheme constitutional as applied to *anyone* 'arrested for, or charged with, a felony offense by California state or local officials?'" (Emphasis in opinion.) In response, held the court, "[a]fter *Maryland v. King* … the answer is clearly yes." (*Id*. at p. 1271.) *Haskell* grew out of the United States District Court's ruling in Haskell v. Brown, 677 F. Supp. 2d 1187 (N.D. Cal. 2009), aff'd, 669 F.3d 1049 (9th Cir. 2012), reh'g en banc granted, 686 F.3d 1121 (9th

Cir. 2012). There, the district court considered a constitutional challenge to collection of arrestee DNA samples under California law, and denied the plaintiff's request for a preliminary injunction on collection of arrestee samples by state authorities. (*Haskell v. Brown*, 677 F.Supp.2d at 1203.) In so doing, the court concluded that, while "[a]rrestees undoubtedly have a greater privacy interest than convicted felons, … Plaintiffs have not shown that that interest outweighs the government's compelling interest in identifying arrestees, and its interest in using arrestees' DNA to solve past crimes." (*Haskell v. Brown*, 677 F.Supp.2d at 1201.)

The district court's ruling in *Haskell* was appealed to the Ninth Circuit, which affirmed and held that California's statutory scheme permitting warrantless DNA collection from felony arrestees for database purposes did not violate the Fourth Amendment. (Haskell v. Harris, 669 F.3d 1049 (9th Cir. 2012), reh'g en banc granted, 686 F.3d 1121 (9th Cir. 2012).) In July 2012, however, the Ninth Circuit vacated the panel opinion and granted an *en banc* rehearing of the case, in Haskell v. Harris, 686 F.3d 1121 (9th Cir. 2012). The result was its clear affirmation of California's arrestee program pursuant to the United States Supreme Court's decision in *Maryland v. King*, as discussed above.

In Friedman v. Boucher, 580 F.3d 847 (9th Cir. 2009), the Ninth Circuit held that the forcible seizure of DNA from a Nevada arrestee "simply because the deputy district attorney wanted to put Friedman's DNA sample in a cold case data bank" violated the Fourth Amendment. (*Friedman v. Boucher*, 580 F.3d at 850, 858.) The seizure was unrelated to the charges upon which Friedman was arrested, and not authorized by any Nevada statute. (*Friedman v. Boucher*, 580 F.3d at 854.) Although Friedman had a prior (23 years earlier) sex crime conviction in the State of Montana, that state's DNA database law did not authorize DNA sample collection by Nevada law enforcement. (*Friedman v. Boucher*, 580 F.3d at 854–856.) The Ninth Circuit also considered but rejected the argument that the DNA seizure could be justified as an administrative search conducted for security reasons at the detention facility. (*Friedman v. Boucher*, 580 F.3d at 857.) Finally, the court observed that "neither the Supreme Court nor this Court has ever ruled that law enforcement officers may conduct suspicionless searches on pretrial detainees for reasons other than prison security," and opined that case law addressing seizure from convicted offenders was factually dissimilar and thus unpersuasive. (*Friedman v. Boucher*, 580 F.3d at 856–858.)

In the United States Court of Appeals for the Third Circuit, an en banc rehearing has been granted of a panel decision holding collection of arrestee DNA samples constitutional under a Fourth Amendment "totality of the circumstances" analysis. (U.S. v. Mitchell, 652 F.3d 387 (3d Cir. 2011), petition for cert. filed (U.S. Nov. 22, 2011).)

In the Ninth Circuit, the court granted an en banc rehearing (U.S. v. Pool, 646 F.3d 659 (9th Cir. 2011)) of a panel decision (U.S. v. Pool, 621 F.3d 1213 (9th Cir. 2010), reh'g en banc granted, 646 F.3d 659 (9th Cir. 2011) and opinion vacated, 659 F.3d 761 (9th Cir. 2011)) upholding the constitutionality of requiring a federal pretrial detainee to provide a DNA sample for database purposes as a condition of pretrial release, but the en banc proceeding was subsequently dismissed as moot following entry of the defendant's guilty plea (U.S. v. Pool, 621 F.3d 1213 (9th Cir. 2010), reh'g en banc granted, 646 F.3d 659 (9th Cir. 2011) and opinion vacated, 659 F.3d 761 (9th Cir. 2011)).

In In re Welfare of C.T.L., 722 N.W.2d 484, 486 (Minn. Ct. App. 2006), a Minnesota court held that a state statute requiring collection of a DNA sample from those who have been charged with a crime and have been held to answer following a judicial probable cause determination violates the Fourth Amendment. (*In re Welfare of C.T.L.*, 722 N.W.2d at 491–492.)

In Anderson v. Com., 274 Va. 469, 475, 650 S.E.2d 702 (2007), the Virginia Supreme Court held that the statutorily-authorized seizure of a DNA sample from arrestees is constitutional under the Fourth Amendment as a routine booking procedure analogous to the taking of fingerprints. (*Anderson v. Commonwealth*, 274 Va. at 475–477.)

Finally, in U.S. v. Thomas, 2011 WL 1599641 (W.D. N.Y. 2011), report and recommendation adopted, 2011 WL 1627321 (W.D. N.Y. 2011), the district court adopted a recommendation to find that DNA collection pursuant to federal law, from a federal defendant who has been indicted but not convicted, is constitutional under the Fourth Amendment. (*Id*. at p. *28.) The opinion stated that the defendant's "status as an indicted person does not materially affect the analysis of the privacy right at stake," so

consequently “the government's interest in accurate and rapid identifications outweighs her privacy interest in the collection and analysis of a DNA sample.” (*Ibid*.)

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§ 8:17. Other constitutional considerations

One state court summarized the various constitutional challenges levied upon DNA database laws, and the judiciary's response, as follows: "Challengers to DNA data base statutes have raised issues such as cruel and unusual punishment, equal protection, prohibition against ex post facto laws, free exercise of religion, procedural and substantive due process, right to privacy, the Fifth Amendment right against self-incrimination, separation of powers, and the Fourth Amendment right against unreasonable search and seizure. [Citation.] These cases demonstrate challengers often raise several of these issues on appeal, and generally, these arguments have been unsuccessful." (State v. Norman, 2003 ND 66, 660 N.W.2d 549, 553 (N.D. 2003).)

1) Equal Protection

California's DNA Data Bank Program does not violate the state or federal equal protection rights of those offenders whose samples are collected pursuant to statute. (People v. Travis, 139 Cal. App. 4th 1271, 1290–1293, 44 Cal. Rptr. 3d 177 (1st Dist. 2006).) Under California law, all persons convicted of a felony are treated the same, and the law does not treat two similarly situated groups in an unequal manner. (*People v. Travis*, 139 Cal. App. 4th at 1291–1292.) The Travis court noted that convicted felons are not similarly situated to convicted misdemeanants, because " ' "[a] felon is uniquely burdened by a diverse collection of statutorily imposed disabilities long after his release from prison." [Citations.] On the other hand, when misdemeanants conclude their sentences there is no further obligation nor loss of civil rights. [Citation.] Further, the state has a compelling interest to protect its law-abiding citizens by discouraging the criminal element from repeatedly violating its laws.'" (*People v. Travis*, 139 Cal. App. 4th at 1292, quoting People v. Hibbard, 231 Cal. App. 3d 145, 149, 282 Cal. Rptr. 351 (4th Dist. 1991), fn. omitted; see also Johnson v. Quander, 370 F. Supp. 2d 79, 94–95 (D.D.C. 2005), aff'd, 440 F.3d 489 (D.C. Cir. 2006) [District of Columbia DNA database law does not violate equal protection].)

2) Due Process

California's DNA Data Bank Program does not violate due process protections. (People v. Travis, 139 Cal. App. 4th 1271, 1293, 44 Cal. Rptr. 3d 177 (1st Dist. 2006).) The law "is minimally intrusive, does not infringe upon privacy rights that are recognized as reasonable, and serves a compelling state interest." (*Ibid*.) Accordingly, "[t]he extraction and collection of DNA samples in accordance with medically accepted procedures for inclusion within a state DNA database program 'does not implicate the Due Process Clause.'" (*Ibid*., quoting Rise v. State of Or., 59 F.3d 1556, 1562–1563 (9th Cir. 1995); see also Boling v. Romer, 101 F.3d 1336, 1340–1341 (10th Cir. 1996); Miller v. U.S. Parole Com'n, 259 F. Supp. 2d 1166, 1169 (D. Kan. 2003) (rejected by, U.S. v. Kincade, 345 F.3d 1095 (9th Cir. 2003)); Vanderlinden v. State of Kan., 874 F. Supp. 1210, 1216 (D. Kan. 1995), judgment aff'd, 103 F.3d 940 (10th Cir. 1996); Gaines v. State, 116 Nev. 359, 998 P.2d 166, 174 (2000).)

3) Ex Post Facto Considerations

California's DNA Data Bank Program does not violate constitutional ex post facto prohibitions, even where an offender's conviction predated the effective date of the DNA collection statute. (People v. Travis, 139 Cal. App. 4th 1271, 1294–1295, 44

Cal. Rptr. 3d 177 (1st Dist. 2006); People v. Espana, 137 Cal. App. 4th 549, 554, 40 Cal. Rptr. 3d 258 (4th Dist. 2006).) "The imposition of a DNA testing requirement under Penal Code section 296.1 for felony convictions may constitute a disadvantage or burden, but the statute was neither intended to nor does inflict punishment for commission of the crime." (*People v. Travis*, 139 Cal.App.4th at 1295; see also Johnson v. Quander, 440 F.3d 489, 503 (D.C. Cir. 2006) [neither the federal DNA database law or the District of Columbia's implementation of it are punitive in purpose or effect]; Shaffer v. Saffle, 148 F.3d 1180, 1182 (10th Cir. 1998); Gilbert v. Peters, 55 F.3d 237, 238–239 (7th Cir. 1995); Jones v. Murray, 962 F.2d 302, 309 (4th Cir. 1992), as amended, (Apr. 27, 1992); Kruger v. Erickson, 875 F. Supp. 583, 589 (D. Minn. 1995), aff'd, 77 F.3d 1071 (8th Cir. 1996); Vanderlinden v. State of Kan., 874 F. Supp. 1210, 1216 (D. Kan. 1995), judgment aff'd, 103 F.3d 940 (10th Cir. 1996); Miller v. U.S. Parole Com'n, 259 F. Supp. 2d 1166, 1170–1172 (D. Kan. 2003) (rejected by, U.S. v. Kincade, 345 F.3d 1095 (9th Cir. 2003)).)

4) Fifth Amendment Right Against Self Incrimination

Compelled DNA samples collected pursuant to statutory mandates do not violate the subject's Fifth Amendment right against self incrimination "because DNA samples are not testimonial in nature." (Boling v. Romer, 101 F.3d 1336, 1340 (10th Cir. 1996); see also Shaffer v. Saffle, 148 F.3d 1180, 1181 (10th Cir. 1998); Schmerber v. California, 384 U.S. 757, 764–765, 86 S. Ct. 1826, 16 L. Ed. 2d 908 (1966) [blood test evidence and chemical analysis not testimonial or otherwise communicative].)

5) Free Exercise of Religion

While it has not arisen to any significant extent under the current practice of collecting buccal (inner cheek) swab DNA samples for database purposes, several challenges to DNA blood sample collection have been raised on First Amendment freedom of religion grounds. Reviewing courts have held that DNA database statutes are neutral, generally applicable laws within the meaning of Employment Div., Dept. of Human Resources of Oregon v. Smith, 494 U.S. 872, 110 S. Ct. 1595, 108 L. Ed. 2d 876 (1990), and as such do not infringe upon the constitutional right to free exercise of religion. (Ryncarz v. Eikenberry, 824 F. Supp. 1493, 1502–1503 (E.D. Wash. 1993); see also Shaffer v. Saffle, 148 F.3d 1180, 1181–1182 (10th Cir. 1998).)

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§ 8:18. Familial searching

In April 2008, the California Department of Justice adopted a protocol for conducting "familial searching" using its DNA database. This function can be employed when no offender profile that directly matches a questioned crime scene profile exists in the database, and instead relies upon the principles of inheritance to conduct a search with the objective of identifying close relative(s) of an unknown perpetrator as an alternative investigative lead for law enforcement to pursue.

When a search of a DNA database reveals that no offender profile matches that of the unknown perpetrator, it is possible to modify the search conditions to identify potential relatives of the perpetrator based on the number of shared genetic markers (i.e., alleles) and the rarity of those shared alleles in human populations. Unlike a search for a direct match, a familial search will potentially allow for non-matching sets of alleles at any given genetic marker ("locus") used as a basis for comparison. Because alleles in humans are inherited in a one-for-one relationship from the father and mother, close relatives of a targeted perpetrator can be expected to share more alleles, especially rare alleles, than would unrelated individuals. A familial search relies upon mathematical modeling specific to the DNA database being utilized that determines whether an observed similarity between two DNA profiles is more likely the result of kinship, or mere chance. The CODIS software was not designed to facilitate familial searching, and California created familial search protocols using independently validated methods and programming.

California's familial search procedure revolves around a committee composed of Department of Justice scientists, attorneys, and law enforcement. The committee considers requests for familial searches on a case-by-case basis. Among the criteria considered are whether the case is a serious one with public safety implications, whether all other investigative leads, including upload of the perpetrator's DNA profile into the state DNA database, have been exhausted, whether a sufficiently rare single-source DNA profile attributable to the perpetrator exists, and whether a sufficient amount of DNA from the crime scene remains to conduct additional testing.

Once a familial search is authorized, the State's Richmond DNA laboratory searches the target profile against the convicted offender profiles maintained in the state database. Arrestee profiles are not used for comparison. A top tier of potential relatives is generated based on a kinship index that considers the rarity of shared alleles. Candidate relatives who meet a predetermined statistical threshold are then tested to determine their Y-chromosome forensic profile (or "haplotype"), which is compared to the perpetrator's Y-chromosome haplotype. Any offender who does not have a Y-STR profile concordant with the perpetrator is eliminated from consideration as someone who cannot share a paternal lineage. If one or more offenders from the list of potential relatives do share a Y-STR profile with the perpetrator, the committee reviews the results and decides whether to conduct further inquiry. If so, the further inquiry involves Department of Justice investigators, who review background and demographic data for the offender in question in order to generate information tending to confirm or dispel the hypothesis that the offender is close relative of the perpetrator. Materials reviewed may include birth records, property records, and DMV records. Once this stage of the investigation is complete, the familial search committee will meet again to determine whether the sum of genetic and non-genetic information possessed warrants release of the offender's name to the investigating law enforcement agency as a familial lead.

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§ 8:19. Missing persons DNA database program

In addition to its criminal identification DNA database program, the State of California maintains a DNA database designed to identify missing persons. Known as the Missing Persons DNA Program (MPDP), it is administered by the California Department of Justice and uses DNA analyses and computerized data matching to identify missing and unidentified persons. The program's authorization, functions, and limitations are set forth at Penal Code section 14250.

1) Operation of Program

Local law enforcement agencies collect DNA samples from family members of "high-risk" missing persons. These samples may be from a personal item attributable to the missing person himself or herself, or from a material relative. (Pen. Code, §§ 14250, subd. (a)(3), 14251, subd. (c).) The former may include a hair from a hairbrush, a blood stain, a tooth, a personal item likely to contain cellular material, or something similar. Any reference sample(s) must be voluntarily provided by the missing person's family, and the sample(s) and associated profile will be removed from the DNA database and destroyed at the family's request. (Pen. Code, § 14250, subds. (c)(2), (c)(3), (d).)

A "high-risk" missing person is one "missing as a result of a stranger abduction, a person missing under suspicious circumstances, a person missing under unknown circumstances, or where there is reason to assume that the person is in danger, or deceased, and that person has been missing more than 30 days, or less than 30 days in the discretion of the investigating agency." (Pen. Code, § 14250, subd. (a)(4).)

For comparison purposes, local coroners and medical examiners collect DNA from the remains of unidentified deceased persons. (See Gov. Code, § 27521 [requiring coroners to take DNA samples from unidentified deceased persons for DNA testing].)

Both the missing person and unidentified person DNA samples are sent to the DOJ Bureau of Forensic Services Jan Bashinski DNA Laboratory for DNA analyses, profiling, and comparison. By law, only DNA markers useful for identification purposes are processed for DNA type and, except for a genetic indicator of gender, no markers that code for known biological traits are analyzed. (Pen. Code, § 14250, subd. (a)(2).) At its discretion, the Department of Justice may outsource the processing of DNA samples submitted to the MPDP to outside laboratories. (Pen. Code, § 14251, subd. (c).) The Department of Justice may prioritize cases involving children and homicide victims. (Pen. Code, § 14251, subd. (d)(1).)

The MPDP stores DNA profiles in two primary files: 1) DNA from relatives of reported missing persons or, if available, a sample from the missing person himself or herself. Oftentimes, mitochondrial DNA analysis will be used to attempt to associate a maternal relative of a missing person with unidentified remains; and 2) DNA collected from unidentified human remains. The MPDP also uploads all DNA profiles into the national Combined DNA Index System (CODIS). (Pen. Code, § 14250, subd. (a)(2).) In CODIS, however, missing persons DNA profiles are kept separate from profiles uploaded for criminal identification purposes, and are used only to identify missing persons. (Pen. Code, § 14250, subd. (a)(2).)

If the DNA profile in the unidentified person file "matches" a DNA profile in the missing person file, the appropriate coroner or medical examiner is notified that an identification was made. The coroner or medical examiner then notifies the family of the missing person as well as the investigating law enforcement agency.

As of early 2011, California DOJ has reports on file of over 3,100 "high-risk" missing persons and over 2,900 unidentified persons.

2) Use and Disclosure Limitations

By law, reference samples and corresponding DNA profiles provided by a missing person's family are used "solely for the purpose of identification of the deceased's remains." (Pen. Code, § 14250, subd. (c)(6).) Once unidentified human remains are identified, moreover, all samples provided by living people used to identify those remains must be destroyed by the Department of Justice. (*Ibid*.) The only exception to this mandate is where law enforcement has determined or suspects that the missing person's death was the result of criminal activity. (*Ibid*.)

DNA samples and profiles possessed by the MPDP are confidential, as are the "computer software and database structures" used by the Department of Justice to operate the program. (Pen. Code, § 14250, subds. (d), (i).) Disclosure is permitted only to the following entities: "[P]ersonnel of the Department of Justice, law enforcement officers, coroners, medical examiners, district attorneys, and persons who need access to a DNA sample for purposes of the prosecution or defense of a criminal case … ." (*Ibid*.) A law enforcement officer or agency may, however, disclose the fact that previously unidentified human remains have been positively identified through a DNA match, but only following notification of the deceased person's family. (*Ibid*.)

All DNA profiles and other identification information possessed by the Department of Justice pursuant to the MPDP are exempt from any laws requiring disclosure of government information to the public, such as the California Public Records Act (Gov. Code, §§ 6250 et seq.). (Pen. Code, § 14250, subd. (e)).

Criminal sanctions, monetary fines, and civil liability may be imposed upon those who violate the disclosure restrictions set forth in the MPDP's governing legislation. (Pen. Code, § 14250, subds. (f), (g).)

3) Program Funding

The Missing Persons Database Program is funded by a two dollar fee attached to issuance of all death certificates in California. (Pen. Code, § 14251, subd. (a).) All revenue collected under this provision is routed to the "Missing Persons DNA Data Base Fund," and may be used by the Department of Justice for "establishing and maintaining laboratory infrastructure, DNA sample storage, DNA analysis, and labor costs for cases of missing persons and unidentified remains." (§ 14251, subd. (b).) The Department of Justice may provide funds from this account to counties "for the purposes of pathology and exhumation consistent with this title," and to facilitate training and outreach efforts. (*Ibid*.)

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§ 8:20. Local DNA database programs

State law does not prohibit the development and maintenance of DNA databases, unaffiliated with CODIS, by county and municipal law enforcement agencies. In fact, state law expressly contemplates the existence of such local labs: "Nothing in this section precludes local law enforcement DNA laboratories from maintaining local forensic databases and databanks or performing forensic identification analyses, including DNA profiling, independently from the Department of Justice DNA laboratories and Forensic Identification Data Base and Databank Program." (Pen. Code, § 297, subd. (e).) A local laboratory that is not an SDIS/NDIS participating laboratory is not subject to the state and federal legal authority governing those programs. To maintain such independence, however, a local laboratory cannot receive biological samples from the state DNA Database Program (§ 299.6, subd. (c)), or the direct transfer of any NDIS records. (See NDIS Privacy Act Notice, 61 Fed. Reg. no. 139 (July 18, 1996).)

Additional statutory controls exist that limit the contents and functionality of non-CODIS local DNA databases. Penal Code section 679.12 addresses use of known DNA samples collected from victims of crime as well as samples collected for exclusion purposes. The latter might include a consensual sexual partner of a rape victim, or residents of a home that was burglarized. Section 679.12 precludes law enforcement from using such samples in any investigation other than the one in which they were collected, or uploading such samples into a database that would subject them to comparison to unknown crime scene DNA samples. (Pen. Code, § 679.12, subd. (a)(1) to (3).) The statute identifies one exception to the prohibition on upload of victim and elimination sample profiles into searchable databases: A "limited comparison of samples" in a quality control/quality assurance database is permitted, but only for comparison against samples "that were analyzed concurrently in order to evaluate the DNA typing results for potential contamination, determine the source of contamination when detected, and to ensure that the contaminating profiles were not misidentified as DNA profiles from putative perpetrators." (§ 679.12, subd. (a)(10).)

Penal Code section 679.12 also allow a public DNA laboratory to collect, retain, and compare DNA profiles from laboratory staff and others—such as first responders and crime scene investigators, and equipment manufacturers—who may have inadvertently transferred their own DNA to items of evidence. (Pen. Code, § 679.12, subd. (a)(8).) These quality control "elimination samples" must be provided with the written consent of their donors. (§ 679.12, subd. (a)(8)(i), (ii).)

Local DNA databases have received little mention in California case authority. One exception is Thompson v. Spitzer, 90 Cal. App. 5th 436, 307 Cal. Rptr. 3d 183 (4th Dist. 2023), as modified on denial of reh'g, (May 5, 2023). That case involved a taxpayer lawsuit challenging the constitutionality of an Orange County non-CODIS local DNA database (OCDNA) containing DNA profiles derived from samples collected from people charged with misdemeanors in the county. (90 Cal.App.5th at p. 445.) "In contrast with the statewide program that mandates DNA collection for certain offenses, the OCDNA program obtains DNA samples through a purportedly voluntary exchange process. Specifically, [Orange County District Attorney] prosecutors offer to drop charges or to reduce charges or punishments in exchange for the alleged misdemeanant's DNA sample." (*Id.* at p. 447.) The Court of Appeal in *Thompson* held that a demurrer should not have been granted with respect to plaintiffs' claim that "the waivers obtained from alleged misdemeanants to participate in the OCDNA program are not made knowingly or voluntarily." (*Ibid.*) Specifically, the *Thompson* court agreed with plaintiffs that the waiver form used by the District Attorney to collect the misdemeanant DNA samples did not fully inform the subjects "as to how their DNA will be maintained and used,"

and was thus insufficient as a waiver of privacy rights. (*Id.* at pp. 456.) Of significance to the appellate court was that the waiver did not inform those providing DNA (1) that the samples would be sent to a private testing laboratory in Virginia; (2) how their DNA information would be stored; (3) how long their DNA information would be retained; (4) for what purposes the private laboratory could use their DNA information; or (5) whether any third parties could access their DNA. (*Id.* at pp. 457–458.) Given the potential of a person's DNA to reveal extensive personal information, both at present and in view of future advances in technology, "alleged misdemeanants were not given sufficient information as to how their DNA would be maintained and used." (*Id.* at p. 458.)

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Chapter 9. Statutes of Limitation, "Doe" Warrants, and Preaccusation Delay in Crimes Involving DNA Evidence

§ 9:1. Overview

In light of the ability of DNA database programs to provide investigative leads in sex crime cases that for many years went unsolved, California's Legislature has modified the statute of limitations for felony sex offenses where DNA evidence of the perpetrator's identity has been developed, and has eliminated the limitations period altogether for the most serious sex crimes. In circumstances where extended statutes of limitation are not available but where DNA evidence exists, issuance of a "Doe" arrest warrant and "Doe" complaint based on the perpetrator's DNA profile may operate to commence the prosecution.

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Chapter 9. Statutes of Limitation, "Doe" Warrants, and Preaccusation Delay in Crimes Involving DNA Evidence

§ 9:2. Statutes of limitation in general

A statute of limitations is the legislative determination that prosecution of a crime must be commenced within the specified time period, at the risk of being permanently time-barred. The United States Supreme Court described a statute of limitations as a conclusive presumption that "after a certain time, no quantum of evidence is sufficient to convict. [Citation.] And that judgment typically rests, in large part, upon evidentiary concerns—for example, concern that the passage of time has eroded memories or made witnesses or other evidence unavailable." (Stogner v. California, 539 U.S. 607, 615, 123 S. Ct. 2446, 156 L. Ed. 2d 544 (2003).)

In California, a broad spectrum of crimes is governed by the following statutes of limitation:

- Most misdemeanor offenses must be prosecuted within one year of the crime. (Pen. Code, § 802, subd. (a).) Some narrow exceptions exist. (Pen. Code, § 802, subds. (b), (c), (d).)
- Any crime punishable by death, or life in prison (with or without the possibility of parole) has no limitations period, and may be commenced at any time. (Pen. Code, § 799.)
- Crimes punishable by eight or more years in state prison must be commenced within six years of the crime. (Pen. Code, § 800.)
- Any felony offense other than those falling within other, "specialized" statutes of limitation such as those noted above, must be commenced within three years of the crime. (Pen. Code, § 801.)

Other specialized statutes of limitation exist for use of a minor in the production of pornography (Pen. Code, § 801.2), for false or fraudulent insurance claims (Pen. Code, § 801.5), and for elder abuse or neglect (Pen. Code, § 801.6). In addition, the statute of limitations for many theft-related crimes and other white-collar offenses will not begin to run until the offense is discovered. (Pen. Code, § 803, subds. (c), (e).) For several of the most serious sex crimes, if committed when the victim was less than 18 years old charges may be filed any time before the victim's 40th birthday. (Pen. Code, § 801.1, subd. (a).)

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§ 9:3. Statutes of limitation for felony sex offenses—Regardless of existence of DNA evidence

Effective January 1, 2017, the Legislature eliminated any limitations period for a set of the most serious sex crimes committed after January 1, 2017, where the otherwise applicable 10-year statute of limitations has not expired. (Pen. Code, § 799, subd. (b); Stats. 2016, ch. 777, § 1.) The following sex crimes that meet statutory criteria now may be prosecuted at any time, regardless of the availability of DNA evidence:

Pen. Code, § 261, subd. (a)(1): Sex with person incapable of consenting

Pen. Code, § 261, subd. (a)(2): Rape by force, violence, menace, duress, fear of injury

Pen. Code, § 261, subd. (a)(3): Rape of intoxicated or drugged person incapable of resisting

Pen. Code, § 261, subd. (a)(4): Rape of unconscious person

Pen. Code, § 261, subd. (a)(6): Rape accomplished by threat of future retaliation against victim or other

Pen. Code, § 261, subd. (a)(7): Rape by public official threatening use of authority

Pen. Code, § 262, subd. (a)(1): Spousal rape by force, violence, menace, duress, fear of injury

Pen. Code, § 262, subd. (a)(2): Spousal rape of intoxicated or drugged person incapable of resisting

Pen. Code, § 262, subd. (a)(3): Spousal rape of unconscious person

Pen. Code, § 262, subd. (a)(4): Spousal rape accomplished by threat of future retaliation against victim or other

Pen. Code, § 262, subd. (a)(5): Spousal rape by public official threatening use of authority

Pen. Code, § 264.1: Sex crime committed by acting in concert with another and using force or violence

Pen. Code, § 286, subd. (c)(2): Sodomy by force, violence, menace, duress, fear of injury

Pen. Code, § 286, subd. (c)(3): Sodomy accomplished by threat of future retaliation against victim or other

Pen. Code, § 286, subd. (d): Sodomy acting in concert, and using force or fear or threat of retaliation

Pen. Code, § 286, subd. (g): Sodomy of person incapable of consenting

Pen. Code, § 286, subd. (i): Sodomy of intoxicated or drugged person incapable of resisting

Pen. Code, § 286, subd. (k): Sodomy by public official threatening use of authority

Pen. Code, § 288, subd. (a): Child molest (under age 14) involving substantial sexual conduct. [Note: "Substantial sexual contact" means "penetration of the vagina or rectum of either the victim or the offender by the penis of the other or by any foreign object, oral copulation, or masturbation of either the victim or the offender." (Pen. Code, § 1203.066, subd. (b).)]

Pen. Code, § 288.5: Continuous sexual abuse of a child

Pen. Code, § 288a, subd. (c)(2): Oral copulation by force, violence, menace, duress, fear of injury

Pen. Code, § 288a, subd. (c)(3): Oral copulation accomplished by threat of future retaliation against victim or other

Pen. Code, § 288a, subd. (d): Oral copulation acting in concert, and using force or fear or threat of retaliation

Pen. Code, § 288a, subd. (f): Oral copulation of unconscious person

Pen. Code, § 288a, subd. (g): Oral copulation of person incapable of consenting

Pen. Code, § 288a, subd. (i): Oral copulation of intoxicated or drugged person incapable of resisting

Pen. Code, § 288a, subd. (k): Oral copulation by public official threatening use of authority

Pen. Code, § 289, subd. (a): Foreign object penetration by force, violence, menace, duress, fear of injury, or accomplished by threat of future retaliation against victim or other

Pen. Code, § 289, subd. (b): Foreign object penetration of person incapable of consenting

Pen. Code, § 289, subd. (d): Foreign object penetration of unconscious person

Pen. Code, § 289, subd. (e): Foreign object penetration of intoxicated or drugged person incapable of resisting

Pen. Code, § 289, subd. (g): Foreign object penetration by public official threatening use of authority

For felony sex crimes described in Penal Code section 290, subdivision (c), but that are not included on this list, the most widely applicable statute of limitations is "ten years after commission of the offense." (Pen. Code, § 801.1, subd. (b).) When the victim of a serious sex offense is under 18 years of age, under certain conditions the prosecution may be commenced one year from the date she reports the crime to law enforcement, regardless of when that report takes place. (Pen. Code, § 803, subd. (f).)

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§ 9:4. Statutes of limitation for felony sex offenses—DNA evidence available

In recognition that biological evidence of sex offenses may be suitable for upload into the state's DNA Database, and may not result in a match within the ten-year period set forth in section 801.1, subdivision (b), a special statute of limitations applies to sex offenses listed in Penal Code section 290, subdivision (c), when DNA-based evidence of the perpetrator's identity exists. This provision remains on the books despite the 2016 elimination of a statute of limitations for many of the most serious sex crimes, as discussed *ante*. But, pursuant to Penal Code section 803.6, "[i]f more than one time period described in this chapter applies, the time for commencing an action shall be governed by that period that expires the latest in time." (Pen. Code, § 803.6, subd. (a).)

Codified as Penal Code section 803, subdivision (g), the provision states that if biological evidence is collected and a DNA profile attributable to the perpetrator is generated within two years of the crime, then the statute of limitations only begins to run when "the identity of the suspect is conclusively established by DNA testing." (Pen. Code, § 803, subd. (g)(1).) At that point, the complaint must be filed within one year. (*Ibid*.) This delay in the triggering of the statute of limitations will occur for crimes committed on or after January 1, 2001, or for crimes before that date whose statute of limitations had not expired as of January 1, 2001. (§ 803, subd. (g)(1)(B); see generally Stogner v. California, 539 U.S. 607, 615–616, 123 S. Ct. 2446, 156 L. Ed. 2d 544 (2003) [lapsed statute of limitations cannot be revived without violating ex post facto clause].) For pre-2001 crimes, the DNA evidence must have been collected and analyzed before January 1, 2004. (Pen. Code, § 803, subd. (g)(1)(B).) Sex crimes committed before that date will be subject to the special statute of limitations only if the DNA evidence was analyzed by January 1, 2004. (*Ibid*.)

The question of what constitutes "conclusively" establishing the perpetrator's identity, for purposes of initiating the one-year clock, is unresolved by California courts. Possible answers include: (1) the date the Department of Justice sends its "hit notification letter" to the local DNA laboratory that uploaded the crime scene DNA profile; (2) the date the local DNA laboratory completes its scientific verification of the cold hit and issues a supplemental report to the investigating law enforcement agency; or (3) following the seizure of a new known reference sample from the suspect and its analysis and comparison to the questioned crime scene DNA profile.

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§ 9:5. Federal statute of limitations in DNA cases

Federal law similarly recognizes the need for more flexible limitation periods in cases that may be solved by DNA profile matches occurring after ordinarily applicable limitation periods expire. Accordingly, Congress enacted 18 U.S.C.A. section 3297. It states: "In a case in which DNA testing implicates an identified person in the commission of a felony, no statute of limitations that would otherwise preclude prosecution of the offense shall preclude such prosecution until a period of time following the implication of the person by DNA testing has elapsed that is equal to the otherwise applicable limitation period." (18 U.S.C.A. § 3297, enacted as part of the *Justice For All Act*, Pub.L. 108-405, Title II, § 204(a) (Oct. 30, 2004).) Unlike California's version, the federal statute of limitations for DNA cases applies to any felony offense rather than just sex offenses, and integrates the limitations period applicable to any given crime in the absence of DNA evidence.

The policy rationale for enactment of the federal statute of limitations in DNA cases was reflected in the following statement by the Honorable Sarah V. Hart, Director, National Institute of Justice, to the House of Representative's Committee on the Judiciary, Subcommittee on Crime, Terrorism, and Homeland Security, during its consideration of the *Justice for All Act*:

> A statute of limitations usually reflects a legislative judgment that the burden of prosecuting an old crime may outweigh its benefits. It balances the need to prosecute serious crimes with concerns that a delayed prosecution may be unreliable given the passage of time and faded memories. A statute of limitations may also encourage law enforcement officials to investigate promptly suspected criminal activity.
>
> Where, however, a prosecution is supported by DNA evidence, imposing a statute of limitations does not serve these public interests. The dependability of DNA evidence does not diminish over time and it produces reliable verdicts years after the crime was committed. Likewise, the mechanical application of a fixed statute of limitations can bar a trial even where law enforcement officials have promptly investigated the crime and sought to use DNA evidence. For these reasons, we have recommended that the provisions governing the time period for commencing prosecution in Federal cases be amended so as to toll the limitation period for prosecution in felony cases in which the perpetrator is identified through DNA testing. This reform is necessary to realize the full value of the DNA technology in solving crimes and protecting the public from rapists, killers, and other serious offenders … .
>
> [W]e have recommended remedial legislation to provide that, in felony cases in which the defendant is implicated through DNA testing, the statute of limitations does not begin to run until the DNA identification occurs. Even where crime scene DNA evidence is available, unavoidable delay may occur before the offender can be identified through DNA matching, if he is not convicted until years

later for some other offense which results in a DNA sample being taken and entry of his DNA profile into CODIS. The proposed tolling provision will help to ensure that prosecution will not be barred.

(Http://judiciary.house.gov/legacy/hart071703.pdf at pp. 15–17.)

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§ 9:6. “John Doe” arrest warrants: *People v. Robinson*

With the advent of DNA testing as a means for highly accurate identification of a perpetrator came the possibility of using a DNA profile as the primary (or only) identifier in an arrest warrant issued to commence a prosecution.

California law provides that a felony prosecution is “commenced” for statute of limitations purposes if “[a]n arrest warrant or bench warrant is issued, provided the warrant names or describes the defendant with the same degree of particularity required for an indictment, information, or complaint.” (Pen. Code, § 804, subd. (d).) More broadly, the particularity with which a warrant must describe the person to be arrested is mandated by constitutional and statutory authority governing searches and seizures by warrant. (U.S. Const., 4th Amend.; Cal. Const., art. I, § 13; Pen. Code, § 1525.) “The manifest purpose of this particularity requirement was to prevent general searches. By limiting the authorization to search to the specific areas and things for which there is probable cause to search, the requirement ensures that the search will be carefully tailored to its justifications, and will not take on the character of the wide-ranging exploratory searches the Framers intended to prohibit.” (Maryland v. Garrison, 480 U.S. 79, 84, 107 S. Ct. 1013, 94 L. Ed. 2d 72 (1987).)

In 2010 the California Supreme Court held that a sufficiently discriminating DNA profile, even if the donor of the DNA is unknown, will satisfy the “particularity” requirement underlying issuance of an arrest warrant to commence a prosecution. (People v. Robinson, 47 Cal. 4th 1104, 104 Cal. Rptr. 3d 727, 224 P.3d 55 (2010), cert. denied, 131 S. Ct. 72, 178 L. Ed. 2d 49 (2010).) The defendant in Robinson had sexually assaulted the victim on August 25, 2004, but was not identified as a suspect at the time. DNA analysis of rape kit swabs revealed the perpetrator's profile, with attendant rarity statistics ranging from a one in 650 quadrillion to a one in 33 sextillion chance of a coincidental match to a random person. (*People v. Robinson*, 47 Cal. 4th at 1114–1115.)

The crime was governed by a six-year statute of limitations then applicable to felony sex offenses. In August of 2000, days before the limitations period would have expired, Sacramento County prosecutors and law enforcement issued a “John Doe” complaint and a “John Doe” arrest warrant describing the perpetrator by his 13-locus DNA profile.[1] In September 2000, the perpetrator's DNA profile was uploaded into the State's DNA Database. A match to defendant Robinson resulted. (47 Cal. 4th at 1115.) Following Robinson's arrest, a new known sample of his blood was processed for DNA type and confirmed to match the crime scene profile. (*Ibid.*)

In reviewing the legal sufficiency of the Doe warrant, the court first noted that “[u]nder both federal and state law, an accusatory pleading or arrest warrant may issue with a fictitious name provided it names or describes the person being charged with reasonable certainty.” (47 Cal. 4th at 1131.) The court agreed with a Wisconsin holding that, “‘for purposes of identifying “a particular person” as the defendant, a DNA profile is arguably the most discrete, exclusive means of personal identification possible.’” (47 Cal. 4th at 1134, quoting State v. Dabney, 264 Wis. 2d 843, 2003 WI App 108, 663 N.W.2d 366, 372 (Ct. App. 2003).) In fact, noted the court, a DNA profile is a better descriptor than a name or physical description as is typically set forth in an arrest warrant. (*Ibid.*) The Robinson court concluded that, “[f]or purposes of the Fourth Amendment, … the arrest warrant in question, which described the defendant by his 13-loci DNA profile and included an explanation that the profile had a random match probability such that there was essentially no chance of its being duplicated in the human population except

in the case of genetically identical sibling, complied with the mandate of our federal Constitution that the person seized be described with particularity.” (*Ibid*.)

The court's description of a sufficiently rare DNA profile as having “essentially no chance of … being duplicated in the human population” was not discussed in more depth, or characterized by any particular threshold of statistical rarity. But, with a reference to a discussion in People v. Nelson, 43 Cal. 4th 1242, 1262, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008), the Robinson court implied that a DNA profile used in a valid Doe warrant must exhibit a “reasonable scientific certainty” of attribution to the perpetrator only. (47 Cal.4th at 1134.)

Constitutional standards of particularity of a valid arrest warrant are “clearly” incorporated into California's statutory standard for the particularity with which a warrant must describe a subject to commence a prosecution for purposes of the statute of limitations. (*Robinson*, 47 Cal. 4th at 1135, citing Pen. Code, §§ 804, subd. (d) [particularity requirement for arrest warrant], 950 et seq. [particularity requirements for accusatory pleadings].) Again, a sufficiently rare DNA profile satisfies statutory standards: “[T]he use of a fictitious name and the description of defendant's unique DNA profile adequately described defendant with the particularity required for an indictment, information, or complaint under section 950 et seq.” (*Robinson*, 47 Cal. 4th at 1136.)

The Robinson court observed that it is of no regard that the subject of a DNA Doe warrant has no immediate notice that the warrant has issued (or charged filed by Doe complaint). “The subject receives notice when a warrant is executed, or an accusatory pleading is served, and no other notice is necessarily required.” (47 Cal. 4th at 1135.) The fact that extrinsic information, such as a DNA database match, is required in order to execute a Doe warrant upon its subject does not mitigate the particularity of the suspect's DNA profile as the primary identifier. (47 Cal. 4th at 1142 [“given the reliability of a DNA profile, the requirement of particularity is satisfied although extrinsic information is needed to enable law enforcement officers to execute an arrest warrant based on a fictitious name and DNA profile”]; see also State v. Dabney, 264 Wis. 2d 843, 2003 WI App 108, 663 N.W.2d 366, 372 (Ct. App. 2003) [“No matter how well a warrant describes the individual, extrinsic information is commonly needed to execute it.”].) Nor does commencing a prosecution with a DNA Doe warrant prejudice the defendant or impede his ability to defend against the charges. (47 Cal. 4th at 1136, citing People v. Goscinsky, 52 Cal. App. 62, 64, 198 P. 40 (1st Dist. 1921).)

Footnotes

1 Although the court's opinion refers to the 13-locus profile as “unique” (47 Cal. 4th at 1113), it remains standard practice among forensic DNA analysts to describe the significance of a DNA profile match by the statistical rarity of the profile in question. The court did note that, “[b]y using the descriptive term “unique,” we refer to an individual DNA profile, such as the 13-loci DNA profile of defendant, that has essentially no chance of being duplicated in the human population except in the case of a genetically identical sibling.” (47 Cal. 4th at 1113.)

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§ 9:7. Other case law

While few cases in the United States have addressed DNA-based Doe warrants, some case authority does exist.

In Com. v. Dixon, 458 Mass. 446, 938 N.E.2d 878 (2010), an unknown rapist assaulted two women in 1991. Days before the 15-year statute of limitations would have expired in 2006, a grand jury indicted the still-unknown perpetrator based on a physical description and DNA profile only. In 2008, a DNA database cold hit identified Jerry Dixon as the source of the crime scene DNA, and the indictment was amended to name him as the defendant. The Massachusetts Supreme Court upheld the legal sufficiency of the DNA-based John Doe indictment, stating that, "Where a general John Doe indictment, bereft of any particularity, must fail as generally anonymous, the converse is true of a DNA indictment: it prevails as precisely eponymous." (938 N.E.2d at 884.) In touting the power of DNA to identify a perpetrator, the court observed that "[a] DNA profile is not merely a word 'of description,' [citation] it is, metaphorically, an indelible 'bar code' that labels an individual's identity with nearly irrefutable precision." (938 N.E.2d at 885.)

In State v. Belt, 285 Kan. 949, 179 P.3d 443 (2008), the Kansas Supreme Court agreed "in the abstract" that a DNA-based Doe warrant can satisfy constitutional and statutory particularity requirements. (*State v. Belt*. 179 P.3d at 450.) In Belt, however, the three Doe warrants at issue did not reference the necessary genetic information: "The McPherson County warrants mentioned only DNA loci common to all humans; the Saline County warrants did likewise; the Reno County warrant referred only to a John Doe, listing no loci." (*State v. Belt*. 179 P.3d at 449.) In other words, in two of the warrants the government had only listed two DNA loci by their generic labels, without specifying the actual alleles attributable to the perpetrator. This was insufficient.

In State v. Dabney, 264 Wis. 2d 843, 2003 WI App 108, 663 N.W.2d 366 (Ct. App. 2003), prosecutors in 2000 filed a Doe complaint charging the perpetrator of a 1994 sexual assault based on his DNA profile. Several months later, a DNA database match identified Dabney as the source of the DNA, and the complaint was amended to name him as the defendant. The appellate court affirmed the use of the Doe complaint to commence the prosecution. It stated that, "for purposes of identifying 'a particular person' as the defendant, a DNA profile is arguably the most discrete, exclusive means of personal identification possible." (*State v Dabney*, 663 N.W.2d at 372.) "Thus," concluded the court, "we agree with the State's arguments that the DNA profile satisfies the 'reasonable certainty' requirements for an arrest warrant and answers the 'who is charged' question for a complaint." (*Ibid*.) The court went on to note, however, that the physical description of the perpetrator would have "further enhanced" the Doe complaint and warrant.

Finally, in State v. Davis, 281 Wis. 2d 118, 2005 WI App 98, 698 N.W.2d 823 (Ct. App. 2005), prosecutors issued a Doe complaint identifying the perpetrator of a sexual assault six years earlier by his DNA profile. The profile was developed using RFLP (Restriction Fragment Length Polymorphism) technology. Subsequently, but before the perpetrator was identified as defendant Davis, the crime scene DNA was retested using PCR/STR (Polymerase Chain Reaction/Short Tandem Repeat) technology, and the Doe complaint amended to reflect the new profile. Davis complained that the new DNA profile did not relate back to the expiration of the statute of limitations, because it was not the original identifier used in the complaint. The court rejected this argument, holding that, "The fact that the type of DNA analysis technology changed does not somehow alter the accuracy of the identification. The person with the DNA in the original complaint was the same person with the DNA in the

amended complaint-Davis….. [Davis's] DNA did not change, but remained the same. Thus, it satisfied the reasonable certainty requirements for an arrest warrant and answered the 'who is charged' question required for a sufficient complaint." (698 N.W.2d at 831–832.)

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§ 9:8. Elements of DNA Doe warrants

A Doe arrest warrant premised on the suspect's DNA profile should include several elements, in addition to the more routine components of a warrant that describe the crime and the chronology of the investigation, as well as the probable cause for suspecting the subject of the warrant as the perpetrator.

1) The actual DNA alleles possessed by the perpetrator should be listed on the face of the warrant on a locus-by-locus basis.

2) The rarity of the perpetrator's DNA profile should be expressed statistically on the face of the warrant, as well as in the warrant affidavit, to establish the particularity of the identification and assure the magistrate that there will be no discretion on the part of law enforcement in the execution of the warrant.

3) The "triggering event" of the cold hit should be acknowledged and described in the affidavit, along with a description of the DNA Database and its operation.

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§ 9:9. Preaccusation delay

1) *PEOPLE V. NELSON*

Assuming that the filing of charges is not time barred, it is not uncommon for cases involving DNA evidence to be prosecuted many years after the crime was committed, in view of the relatively recent development of DNA typing technology for use in criminal investigations. In People v. Nelson, 43 Cal. 4th 1242, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008), the California Supreme Court addressed the standards applicable to claims that preaccusation delay—e.g., while DNA technology was evolving to the point at which the crime could be solved—violates due process rights to a fair trial. Preaccusation delay may also be referred to as prefiling or precharging delay.

In February 1976, a 19-year-old Sacramento college student was kidnapped, raped, and murdered. Although Nelson was a suspect in the initial investigation, police were unable to develop enough evidence at the time to make an arrest. The case lay dormant for 25 years. Then, in 2001, Sacramento investigators submitted biological evidence from the crime (vaginal swab, semen stains on the victim's sweater) for DNA analysis and upload into the State's DNA Database. By that time, Nelson's DNA reference sample was also in the Database by virtue of an unrelated conviction. A routine search resulted in a cold hit, linking Nelson to the rape/murder. The Sacramento County District Attorney's Office filed charges against Nelson in 2002, 26 years after the crime. A jury convicted him of first degree murder. (43 Cal. 4th at 1247–1249.)

On appeal, Nelson argued that charging him with the 1976 crimes violated his state and federal due process rights because the long delay "was unjustified and prejudiced his defense."[1] The prejudice typically asserted by a defendant in this situation is that his ability to defend has been unfairly impaired by fading memories, unavailable witnesses, and lost or destroyed physical evidence. The California Supreme Court previously acknowledged that such prejudice may represent a denial of state and federal due process rights, but that any prejudice had to be balanced against the government's justification for the delay in order to make that constitutional finding. (People v. Catlin, 26 Cal. 4th 81, 107, 26 Cal. 4th 1060c, 109 Cal. Rptr. 2d 31, 26 P.3d 357 (2001), as modified, (Sept. 26, 2001).) Questions unanswered until Nelson, however, included whether prejudice to a defendant would be presumed in light of a long preaccusation delay, and whether evidence of a purposeful, tactical delay by law enforcement is a prerequisite to a finding of state due process violations.

The Nelson court answered the first question by holding that prejudice to a defendant will never be presumed, at least in a murder case, regardless of how much time has elapsed between the crime and the arrest/filing of charges. (43 Cal. 4th at 1250.) In a murder case, prejudice must be demonstrated as a matter of fact, because in declining to adopt a statute of limitations for murder the Legislature made a policy decision not to preclude murder prosecutions as a matter of law. (*Ibid.*) While Nelson did not extend this reasoning expressly to crimes other than murder, California's statute of limitations for felony sex crimes in which DNA evidence exists and is promptly analyzed is similarly, but conditionally, unlimited. (Pen. Code, § 803, subd. (g) [providing that prosecution may be commenced one year from the date that the suspect is conclusively identified by a DNA match, e.g., a database cold hit, if other criteria are met].) Thus, the Supreme Court's rejection of presumed prejudice likely has equal applicability to felony sex crime prosecutions solved years later by means of the DNA database.

Nelson went on to define the state constitutional standard governing justification for delay that is weighed against the showing of prejudice. As a point of reference, federal constitutional due process violations premised on preaccusation delay require a finding of deliberate delay by the government in order to gain a tactical advantage over the defendant. (*People v. Catlin*, 26 Cal. 4th at 107 ["A claim based on the federal Constitution also requires a showing that the delay was undertaken to gain a tactical advantage over the defendant"].) It should be noted, however, that actual prejudice to the defendant is still a necessary element. (*Ibid*.)

According to Nelson, the California Constitution does not create quite so rigid a threshold when evaluating the justification for delay and its import. Before Nelson, a series of California appellate opinions had addressed the issue of government delay to varying, and sometimes inconsistent, degrees: People v. Archerd, 3 Cal. 3d 615, 640, 91 Cal. Rptr. 397, 477 P.2d 421 (1970) (abrogated by, People v. Nelson, 43 Cal. 4th 1242, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008)) [state due process violated if prejudice and no legitimate reason for delay, i.e., delay "purposeful", "oppressive", and "deliberate"]; Penney v. Superior Court, 28 Cal. App. 3d 941, 953, 105 Cal. Rptr. 162 (5th Dist. 1972) [holding that a "no legitimate reason" for delay can encompass more than government bad faith, and can include negligence or incompetency]; People v. Hannon, 19 Cal. 3d 588, 610–611, 138 Cal. Rptr. 885, 564 P.2d 1203 (1977) [refusing to resolve the conflicting authorities]; Scherling v. Superior Court, 22 Cal. 3d 493, 506, 149 Cal. Rptr. 597, 585 P.2d 219 (1978) [suggesting in dictum that both negligent and deliberate delay could theoretically result in a denial of due process]. Nelson settled any residual dispute by stating that "under California law, negligent, as well as purposeful, delay in bringing charges may, when accompanied by a showing of prejudice, violate due process." (43 Cal. 4th at 1255.)

The Nelson court pointed out that because the reason for delay is balanced against the showing or prejudice, the more malicious the delay, the less prejudice is required to prove a state due process violation. If the government purposefully delayed in order to gain a tactical advantage, only a "weak" showing of prejudice would be necessary. Conversely, due process is more tolerant of "merely negligent" delay, in which case "a greater showing" of prejudice would be required of the successful defendant. (43 Cal. 4th at 1256.)

Applying these considerations to the Nelson facts, the court held that the decision not to charge Nelson in 1976 given the lack of proof beyond a reasonable doubt was an appropriate ethical and legal judgment that fully comported with "standards of fair play and decency." (43 Cal. 4th at 1256.) Moreover, the police agency's decision to pursue DNA testing after modern DNA techniques were validated and readily available was simply a resource allocation issue and not indicative of negligence or bad faith. (43 Cal. 4th at 1256–1257.)

2) OTHER CASE LAW

The California Supreme Court addressed a preaccusation delay claim in People v. Bracamontes, 12 Cal. 5th 977, 292 Cal. Rptr. 3d 281, 507 P.3d 939 (Cal. 2022), cert. denied, 143 S. Ct. 739, 214 L. Ed. 2d 387 (2023), a capital case. The defendant had murdered a young girl in 1991, but was not charged until 2003. He argued that the delay caused evidence to be lost that he could have presented in the penalty phase, thus violating due process protections. (*Id*. at p. 986.) The prosecution argued that the delay was justified given the state of the evidence in 1991, and in view of developments in forensic science since then. Of significance to the court was the fact that there had been no indications of sexual assault when the autopsy was performed, and while various swabs of the victim's body were collected none bore evidence of sperm. (*Id*. at pp. 983, 988.) The medical examiner thus concluded that no sexual assault took place which, "while reasonable, may have set back the investigation." (*Id*. at p. 988.) "[T]he inability to detect sperm on the victim's body not only deprived investigators of DNA evidence but also a motive for Laura's murder," noted the court. (*Ibid*.) Expert testimony later explained that the method of extracting DNA from a swab, and transferring it to a slide, used in 1991 had later been abandoned because it was "often ineffective" and could produce false negative results. (*Id*. at p. 987.) Reexamination of the physical evidence as part of a 2003 cold case review utilized updated methods, and revealed the presence of sperm cells on the swabs—which were then associated with the defendant. In any event, the RFLP (restriction fragment length polymorphism) DNA typing technology available in 1991 required more cellular material than had been present on the oral swabs. (*Ibid*.)

Accordingly, held the *Bracamontes* court, the delay of over 20 years was "'investigative delay, nothing else.'" (12 Cal.5th at p. 989.) It was not engineered by the government to create a tactical advantage. (*Ibid*.) Further, the impact of the prefiling delay on the defendant's ability to fully and fairly litigate the guilt or penalty phases of the trial appeared to be "minimal," and the claimed prejudice was speculative. (*Ibid*.) The court consequently denied the defendant's claim.

In People v. Cordova, 62 Cal. 4th 104, 194 Cal. Rptr. 3d 40, 358 P.3d 518 (2015), the California Supreme Court considered a preaccusation delay claim in a capital case solved with a DNA database "cold hit." The defendant committed his crime in 1979, when he brutally raped and murdered a young girl. His name never came up in the initial investigation, and he moved to Canada shortly afterwards. The defendant avoided detection for the next 23 years. In 2002, the Contra Costa Sheriff's crime laboratory developed a DNA profile for the killer from vaginal swabs collected during the 1979 autopsy. The profile was uploaded into SDIS and NDIS databases, and immediately hit the defendant. He had been in CODIS since 2001, after being convicted of child molestation offenses in Colorado. Cordova was arrested and charged with murder. A jury convicted him in late 2006, and voted for death in early 2007. At trial, a defense motion to dismiss on grounds of preaccusation delay was denied, and the California Supreme Court affirmed. (62 Cal.4th at p. 120.)

Drawing heavily upon *Nelson*, the Court found that Cordova's assertion of prejudice based on delay was, at best, speculative. (62 Cal.4th at p. 120.) Although potential defense witnesses had died in the intervening years, "[n]o reason exists to believe any of these witnesses would have supplied exonerating, rather than incriminating, evidence, or any evidence at all." Moreover, the court noted that the defendant "was able to, and did, present evidence in his defense." More significantly, the court found that the 23-year delay in bringing charges was justified because the police did not identify Cordova before the 2002 cold hit, and investigators were not negligent in their efforts. "Sometimes," the court wrote, "a crime simply is not solved immediately but must await some break in the case …." The court recognized that the 2002 cold hit was that break. (*Id*. at p. 120.)

In People v. Smothers (2021) 66 Cal.App.5th 829, the Court of Appeal affirmed the trial court's denial of defense motions to dismiss on grounds of pretrial delay, which had emphasized the 33-year gap between the crime and the defendant's prosecution for its commission. (66 Cal.App.5th at pp. 855-860.) In the eyes of the court, justification for delay was strong:

> [L]aw enforcement agencies believed there was insufficient evidence to charge Smothers in 1983, and at that time DNA analysis did not exist. DNA analysis for law enforcement purposes was not available until the mid-1990s but those analyses yielded results with less specificity and greater uncertainty than later DNA protocols. In addition, the Crime Lab needed to validate the new technology before implementing it into casework, so it was not until 2001 that the Lab approved the use of the more advanced DNA analysis that was ultimately used to match Smothers's DNA with the evidence at the crime scene.

(*People v. Smothers*, 66 Cal.App.5th at 857.) The court also pointed to evidence of the police department's and crime lab's limited resources as factors in the delay, while noting that the investigation and prosecution proceeded promptly once new leads were developed. (*People v. Smothers*, 66 Cal.App.5th at 858.) Also contributing to the court's conclusion was the serious nature of the offense (murder), the fact that "nothing in the record indicat[ed] the prosecution caused the delay or allowed the case to languish to take advantage of Smothers," and the absence of evidence of prosecutorial negligence. (*People v. Smothers*, 66 Cal.App.5th at 859.) "On balance," therefore, "the People's strong justification for delay outweighed the various prejudices we assume Smothers suffered." (*People v. Smothers*, 66 Cal.App.5th at 858.)

Footnotes

1 Note that an allegation of preaccusation delay, or precharging delay, differs from constitutional speedy trial rights, which apply only after a defendant is arrested or charged. (People v. Martinez, 22 Cal. 4th 750, 754–755, 94 Cal. Rptr. 2d 381, 996 P.2d 32 (2000).)

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Forensic DNA Evidence: Science and the Law Ch. 10 Introduction

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Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 10. Discovery in DNA Cases

Introduction

Cases in which DNA testing has taken place present the need to understand what material has been generated in the laboratory that is available to the opposing party pursuant to discovery rules and other disclosure obligations. This chapter provides a summary of the law of discovery in California criminal cases, describes items commonly provided by the prosecution related to DNA testing, and, finally, discusses more unusual discovery-related circumstances that may arise. Of course, the scope of appropriate discovery in any case hinges upon the facts of that particular case. Thus, the discussion presented herein is a comprehensive but not all-encompassing survey of DNA discovery issues. A defendant's own retained or appointed expert, for example, may identify additional items of interest to seek as discovery from the prosecution.

In addition, this chapter addresses how the prospects of consuming a crime scene DNA sample through testing and retesting raise legal issues regarding disclosure of results.

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Forensic DNA Evidence: Science and the Law § 10:1

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Chapter 10. Discovery in DNA Cases

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§ 10:1. California discovery law

In California criminal cases, the exchange of information between parties before trial is governed by both state statutory authority and federal constitutional mandates. Penal Code sections 1054 to 1054.10 control most aspects of discovery in criminal cases, while the rights to due process of law and a fair trial set forth in the Fifth and Fourteenth Amendments to the United States Constitution require the prosecution to disclose material, exculpatory information in its possession notwithstanding statutory procedures. Both sources of discovery law are discussed below.

1) Exclusivity of Statutory Scheme

California's discovery statutes provide the exclusive source of procedural and substantive authority for the reciprocal exchange of pretrial information, as informed by overlapping constitutional mandates discussed below. Specifically, Chapter 10 of Title 6 of the Penal Code, found at sections 1054 to 1054.10, "shall be the only means by which the defendant may compel the disclosure or production of information from … agencies which the prosecuting attorney or investigating agency may have employed to assist them in performing their duties." (Cal. Pen. Code, § 1054.5, subd. (a).) So too does section 1054.5, subdivision (a), instruct trial courts that "[n]o order requiring discovery shall be made in criminal cases except as provided in this chapter." Section 1054 describes the purpose of the criminal discovery statutes as, in part, "to provide that no discovery shall occur in criminal cases except as provided in this chapter, other express statutory provisions, or as mandated by the Constitution of the United States." (§ 1054, subd. (e).)

2) Informal Discovery of Scientific Evidence; Motion to Compel

Most, if not all, information provided by parties to a criminal action should be exchanged informally, without the participation of the trial court. (Pen. Code, § 1054.5, subd. (b).) With respect to scientific evidence in particular, the prosecution in every criminal case must provide the defense with the following:

> Relevant written or recorded statements of witnesses or reports of the statements of witnesses whom the prosecutor intends to call at the trial, including any reports or statements of experts made in conjunction with the case, including the results of physical or mental examinations, scientific tests, experiments, or comparisons which the prosecutor intends to offer in evidence at the trial.

(Pen. Code, § 1054.1, subd. (f).) A potential limitation on the prosecution's duty under this provision is the qualification that the material described must be disclosed "if it is in the possession of the prosecuting attorney or if the prosecuting attorney knows it to be in the possession of the investigating agencies." (§ 1054.1.)

But, the law also imposes upon the prosecution a general duty to make inquiries of its investigating agencies—including crime laboratories—and disclose material that is reasonably accessible even if not actually known to the prosecutor beforehand. (See In re Littlefield, 5 Cal. 4th 122, 133–135, 19 Cal. Rptr. 2d 248, 851 P.2d 42 (1993); People v. Little, 59 Cal. App.

4th 426, 433, 68 Cal. Rptr. 2d 907 (3d Dist. 1997).) As noted, it is well-established that government criminalists and crime laboratories participating in a case investigation are considered part of the prosecution team. (In re Brown (1998) 17 Cal.4th 873, 877 [Orange County Sheriff-Coroner, Department of Forensic Science Services]; People v. Whalen (2013) 56 Cal.4th 1, 64 [California Department of Justice criminalist].) So too are private-sector crime laboratories that perform work for the prosecution (Bracamontes v. Superior Court (2019) 42 Cal.App.5th 102, 116, 119) and those who participate in a SART (Sexual Assault Response Team) examination (People v. Uribe (2008) 162 Cal.App.4th 1457, 1479, 1481).

If a criminal defendant is unsatisfied with the discovery provided by the prosecution following an "informal" request, he may formally ask the trial court to compel discovery of the item(s) sought. (Pen. Code, § 1054.5, subd. (b).)

3) Subpoena Duces Tecum

A subpoena duces tecum (SDT) is a court order for disclosure of documents, issued on behalf of the court by an attorney. An SDT requires that a custodian of records certify that the documents are accurate and reliable package them in such a way as to preclude tampering, and submit them directly to the court. (Evid. Code, §§ 1560, subd. (c), 1561.) An SDT that indicates that the records described should be submitted directly to the defendant's lawyer is improper and invalid. By law, the court must review all records submitted by SDT before ordering their release in whole or in part to the litigants. (Evid. Code, § 1560, subds. (b), (c)(3) ["the records shall be … directed … to the officer, body, or tribunal conducting the hearing …"]; Carlson v. Superior Court, 58 Cal. App. 3d 13, 21, 129 Cal. Rptr. 650 (4th Dist. 1976) ["The issuance and service of a subpoena duces tecum … is not legal process in the sense it entitles the person on whose behalf it was issued to obtain access to the records described in it until there has been a judicial determination that person is legally entitled to view or receive them"].)

An SDT is not authorized as a means of case discovery from an investigating agency. The statutory discovery procedures outlined above, i.e., informal discovery and motions to compel discovery where disputes arise, are by law "the only means by which the defendant may compel the disclosure or production of information from … law enforcement agencies which investigated or prepared the case against the defendant … ." (Pen. Code, § 1054.5, subd. (a); see also § 1054, subd. (e) ["no discovery shall occur in criminal cases except as provided by this chapter, other express statutory provisions, or as mandated by the Constitution of the United States"]; People v. Superior Court (Barrett), 80 Cal. App. 4th 1305, 1312–13, 96 Cal. Rptr. 2d 264 (4th Dist. 2000).) Crime laboratories that do forensic work for the prosecution are considered part of the investigative team, thus bringing them within the ambit of the statutory discovery rules. (People v. Superior Court (Barrett), 80 Cal. App. 4th 1305, 1313, 96 Cal. Rptr. 2d 264 (4th Dist. 2000); In re Brown, 17 Cal. 4th 873, 880, 72 Cal. Rptr. 2d 698, 952 P.2d 715 (1998).) Accordingly, an SDT issued to a crime lab demanding case-specific information is invalid.

A defendant in a criminal case may, however, issue a valid SDT to a crime lab—even one that did analysis in that case—if the SDT seeks non-case-specific information possessed by the lab in its general capacity as a third-party government agency. (See *Barrett*, 80 Cal. App. 4th at 1315–17.) The key determination is whether the SDT seeks material from the lab as an investigating agency or as a third party. For example, laboratory protocols and quality control manuals may be sought via SDT because they are general materials possessed by the agency for general operational purpose and were not generated in connection with a particular case. (See *Barrett*, 80 Cal. App. 4th at 1317 ["To the extent Barrett is seeking records that CDC maintains in the regular course of running Calipatria State Prison, Barrett is trying to obtain material from a third party. [Citation.] The reciprocal discovery statutory scheme [in Section 1054 et seq.] has no application to discovery sought from third parties"].)

4) Discovery of Material from a Laboratory's Private-Sector Vendor

The concept of investigating agencies informs, as noted, the scope of informal discovery owed by the prosecution in criminal cases. In addition to the discussion provided by *People v. Superior Court (Barrett)*, *supra*, 80 Cal.App.4th 1305, a 2018 decision from the Court of Appeal shed additional light on the subject. What gave rise to the case was the ubiquitous use of laboratory technology, instrumentation, and software developed and sold by private-sector vendors. It addressed whether those companies, at least potentially, are "investigating agencies" for purposes of Penal Code section 1054.1.

In October 2018, the California Court of Appeal decided People v. Superior Court (Dominguez), 28 Cal. App. 5th 223, 239 Cal. Rptr. 3d 71 (4th Dist. 2018). It was a murder case, in which the San Diego Police Department (SDPD) conducted DNA testing on a pair of bloody gloves found near the crime scene. There was a DNA mixture present on the interior of the gloves. The SDPD lab used its STRmix probabilistic genotype software to interpret the results. Before trial, the defense made an informal discovery request for the STRmix user manual, software program, and source code, as well as ESR's internal validation studies. (28 Cal.App.5th at p. 228.) "ESR" refers to New Zealand's Environmental Science and Research Limited, a government research institute that developed STRmix.

The prosecutor declined to provide those items, because the user manual was copyrighted, the software would not work without a license from ESR, SDPD lacked the knowledge or capacity to extract and provide the source code from the software, and SDPD did not possess ESR's general internal validation records. (*Dominguez*, *supra*, 28 Cal.App.5th at p. 228.) Not wanting to obtain the items directly from ESR subject to ESR's nondisclosure agreement, the defendant asked the trial court to compel discovery through the prosecution, arguing that ESR was a member of the prosecution team because it provided the SDPD with the software, as well as training and support. (*Id*. at p. 229; see also People v. Davis, 75 Cal. App. 5th 694, 721–722, 290 Cal. Rptr. 3d 661 (3d Dist. 2022), review denied, (June 1, 2022) ["a defendant in a criminal matter may obtain access to the STRmix source code under a nondisclosure agreement"].) "Defense counsel primarily argued that he had a right to look inside the proverbial "black box" that is STRmix." (*Dominguez*, *supra*, 28 Cal.App.5th at p. 230.) The trial judge granted the defendant's motion to compel, and ordered the prosecution to provide the ESR materials. (*Id*. at pp. 230–231.) The prosecution turned to the Court of Appeal, seeking a writ directing the trial court to reverse course and deny the discovery motion. (*Id*. at p. 231.)

The Court of Appeal sided with the prosecution and did just that. (*Dominguez*, *supra*, 28 Cal.App.5th at p. 232.) The appellate court's reasoning turned in part on its determination that the SDPD was not actually in possession of the source code and ESR validation records. (*Id*. at p. 233.) But, was ESR a member of the broader "prosecution team," such that the District Attorney would have to provide those items? Penal Code section 1054.1, which sets forth the material and information to be provided by the prosecution, qualifies that disclosure of an item need occur only "if it is in the possession of the prosecuting attorney or if the prosecuting attorney knows it to be in the possession of the investigating agencies." (§ 1054.1.) This means that the material must reasonably accessible by the prosecution. (See In re Littlefield (1993) 5 Cal.4th 122, 135–136.) In the aggregate, this refers to the "prosecution team," a concept borrowed from constitutional *Brady* obligations. (*Dominguez*, *supra*, 28 Cal.App.5th at p. 234.)

The court framed the question as "whether ESR's provision of a software program, related support, and relevant updates, as well as the prosecution's use of that software in this case, is enough to make it a member of the prosecution team within the meaning of our criminal discovery statutes and *Brady*." (*Dominguez*, *supra*, 28 Cal.App.5th at pp. 235–236.) It concluded that ESR was not part of "the prosecution team" for discovery purposes, despite having provided the SDPD lab with STRmix software, training, support, and updates.

Notably, ESR did not play any actual role in the investigation of the crime, or even have knowledge of the underlying events. (*Dominguez*, *supra*, 28 Cal.App.5th at p. 236.) And, just creating the software did not imply ESR's active participation in the investigation; the law enforcement laboratory running the software played that role by determining the number of DNA contributors, differentiating DNA peaks from artifacts, evaluating the STRmix data in light of the parameters programmed by that lab, ensuring that the STRmix run was valid based on review of the program's diagnostics, and performing comparisons to databases or persons of interest. (*Id*. at p. 237.) Nor did the availability of training, technical support, and software updates from ESR render ESR a member of the prosecution team. (*Id*. at pp 237–238.) Those services were rarely provided, played no role in the case at hand, and were available at the discretion of the SDPD lab. (*Id*. at pp 237–238.) Further, the SDPD lab's internal validation of the software took place independent of ESR. (*Id*. at p. 238.)

Thus, whether a third party is a member of the prosecution team for discovery purposes depends upon that entity's degree of involvement with the specific investigation at issue. There may be slight involvement imputed by that third party's creation of the technology employed, but not significant enough to presume that material possessed by the third party is under control

of the District Attorney or investigating agencies. It bears noting, however, that the Court of Appeal expressed some concern over "the ever-growing level of technical automation in our criminal justice system." (*Dominguez*, *supra*, 28 Cal.App.5th at p. 240.) Yet, the court also noted that "STRmix is used by both prosecution and defense teams; it is not marketed as solely a prosecutorial device. And we hesitate to assign an entity membership in a prosecutorial team simply based on one possible use of its product." (*Ibid*.)

As for STRmix, the court also held that there was nothing inherently exculpatory about the software itself, and no indication that it had not performed reliably in this case. (*Dominguez*, *supra*, 28 Cal.App.5th at pp. 240–241.) The prosecution therefore had no obligation to provide a copy of STRmix to the defense. (*Id*. at p. 241.) Finally, the court took no position on discovery of ESR's user manuals, because ESR had not had an opportunity to appear and explain the basis for its assertion of a trade secret privilege over those materials, argue its position on the nondisclosure agreement attached to its user manuals, and discuss whether discovery of the manuals would run afoul of federal copyright law. (*Id*. at pp. 241–243.)

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Forensic DNA Evidence: Science and the Law § 10:2

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Chapter 10. Discovery in DNA Cases

§ 10:2. Informal discovery in DNA cases: routine disclosures

As noted, Penal Code section 1054.1, subdivision (f), requires the prosecution to provide the defense with "any reports or statements of experts made in conjunction with the case, including the results of physical or mental examinations, scientific tests, experiments, or comparisons which the prosecutor intends to offer in evidence at the trial." As a general guideline, the information provided pursuant to this provision should include everything an independent expert would require to make a fair and thorough assessment of whether the reported DNA test results are accurate and reliable.

When a laboratory has performed DNA casework as part of an investigation, discovery typically includes, but may not be limited to, the following materials:

1) Laboratory Reports, Including Any Amended or Supplemental Reports

The laboratory report is the core record of results provided to the agency requesting DNA testing, and consequently a crucial item of discovery. Most commonly the laboratory's client agency is the investigating law enforcement agency, with the case detective as the primary contact for the crime laboratory. Sometimes, however, the laboratory's client contact will be the case prosecutor or even another laboratory. Reports generally include a record of all evidence and reference items and their dates received, which tests or examinations were conducted, the genetic markers or the name of the commercially prepared kit used for testing, the results of the tests, the conclusions reached by the analyst, any associations made between an evidence profile and a reference profile, the statistical significance of the association, the name and signature of the analyst who performed the testing, the date of the technical and administrative review, and the initials of the reviewers. The report may also include a table of results for each item tested.

2) Chain of Custody Information

This documentation typically includes handwritten documents or printouts from electronic tracking systems. At a minimum, this documentation should include names, dates, and storage locations for all transfers of an evidence item. Multiple chain of custody forms may be used for a single piece or subset of evidence. This may occur when a portion of an evidence item is sent to another laboratory or outside facility for testing. Laboratories may also use multiple types of evidence tracking. For example, one chain of custody form may be used to record transfers of an item to and from a laboratory (external chain), and another may be used to track that same item as it moves from location to location within the laboratory (internal chain).

3) Documentation of the Technical and Administrative Review Processes

A review of all case data is required before a laboratory reports a test result or uploads a DNA profile to CODIS. There are two internal review processes commonly conducted. First, a "technical review" is a review of all laboratory work done in a case. This is a check that all laboratory procedures have been appropriately followed, any deviations from protocol have been documented and approved, and that all conclusions documented in the case file are supported by the data, laboratory policy,

the reviewer, and are accurately represented in the report. These reviews are commonly documented on a checklist, or set of checklists that record all items reviewed within the case file. The review may also be documented on each page of the case file. The name of the reviewer, the pages reviewed, and the review completion date should all be recorded on the review form.

Second, the "administrative review" may be completed by the same analysts who performed the technical review or by a different analyst or administrator. Administrative review is the process of evaluating case notes and the report for correctness and adherence to laboratory policies. An administrative reviewer checks a final report for correct spelling and grammar, as well as to confirm that the data and conclusions in the case file are accurately represented. Examination and analysis notes in the case file are evaluated as to their completeness.

4) Bench Notes

"Bench notes" are all contemporaneous notes generated during the course of DNA analysis, and is the technical record of testing done for an evidence or reference item. One court characterized bench notes as "step-by-step written documentation of the tests conducted by the laboratory and the results of those tests … ." (J.H.H. v. State, 897 So. 2d 419, 424 (Ala. Crim. App. 2004).) Bench notes may include handwritten or typed examination notes, photographs, diagrams, charts, procedural check sheets, and instrument printouts. This documentation should include dates for tests performed and initials of each analyst performing the documented activities. It should detail the samples tested and what controls were used. Paperwork should follow the laboratory's approved technical procedures, with any deviations noted. The documentation should be complete and clear such that a second party can conceptually recreate the testing using the information contained in the case file.

5) Electropherograms for All Samples and Controls

Electropherograms are printouts of the data generated by the genetic analyzer instrument. These printouts represent the genetic profile as detected by the genetic analyzer. They should show a series of peaks at each of the tested loci. (See Roberts v. U.S., 916 A.2d 922, 927 (D.C. 2007) [an electropherogram is a "graph that displays a series of different-colored peaks of different heights," and "[i]f a peak represents an allele, the type of allele—the number of short-tandem-repeat (STR) patterns in that allele—is indicated by the peak's location on the horizontal axis of the electropherogram within each locus"].) Each peak should be labeled with its allele designation, or an alternative characterization as determined by the analyst (e.g. artifact, pull-up). The size of the peak, the peak area, the scan number at which the peak was detected by the genetic analyzer, or other relevant information may also be included either on the peak label or in the results table associated with each sample. Frequently, laboratories will perform multiple runs of a sample to ensure reproducible results. Even when multiple injections of a sample are collected, it is common practice to include only one injection per sample in the case file for single source good quality samples. However, for mixed samples or incomplete profiles, it is common for more than one run of a sample to be included in the case file.

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§ 10:3. Informal discovery in DNA cases: additional materials

In addition to the standard discovery materials listed above relating to DNA casework, defense counsel may request additional information from prosecution testing laboratories if relevant to case facts and strategies. Such requests are, of course, made through the case prosecutor pursuant to controlling discovery statutes. The following materials are often among the additional items requested:

1) Electronic STR Typing Data

An electronic record of the STR typing process typically can be downloaded onto a compact disc and provided as discovery. This includes the analyzed data represented by the electropherograms, as well as any duplicate analyzed data not included in the case file. The electronic data include a record of all analysis parameters used for the analysis of the sample files. This also includes the "raw" or unanalyzed electronic files. These files are the electronic data recorded by the genetic analyzer. A compact disc containing raw data and other information does not, however, necessarily include the software necessary to view the data contained therein.

2) Laboratory Technical Procedures

These are the technical protocols for the testing that has been performed in a case. Technical procedures contain all parameters for each test that a laboratory has validated for use. Typically, any check sheets contained in the bench notes are a condensed version of the technical procedures. Materials used, steps in the testing process, analysis parameters, documentation and interpretation guidelines, and validation references are all commonly included within these documents. A laboratory should also have technical procedures for any quality control testing of reagents or for software programs used for analysis. These procedures are typically available in either paper or electronic form.

3) Operations and/or Policy Manuals

These documents are operations guides for an entire laboratory or a laboratory unit (e.g. drug analysis, DNA casework, ballistics). General policies and work practices that are not included in the technical procedures may be found here. These may be provided in paper form or electronically.

4) Allele Frequency Data Tables

Allele frequency data tables are the published allele frequency data sets relied upon in generating profile rarity statistics. These may be provided as literature references. Note, however, that although Evidence Code section 721, subdivision (a), provides the opportunity to cross-examine an expert about the materials on which the expert relied in forming an opinion, it does not provide a corresponding right to obtain those materials as pretrial discovery. (Evid. Code, § 721, subd. (a).)

5) Unintended Transfer / Contamination Records

DNA laboratories keep a record of all instances of contamination that occur during testing. These records reflect contamination of one DNA sample with DNA from an external source (e.g., the analyst inadvertently "shedding" cellular material), contamination with DNA from another evidence or reference sample in the same testing set (e.g. cross-contamination), or contamination with highly concentrated amplified PCR product from another evidence or reference sample (systemic contamination). Copies of physical contamination records are not generally provided in a discovery packet. Because contamination events beyond a particular window of time have little or no bearing on the DNA test results recorded in any given case, discovery on the issue is appropriately limited by date. For example, contamination incidents for a particular date range may be reported in the package (e.g., "No instances of contamination were reported for the dates five days before the beginning of testing to five days after the conclusion of testing.").

It is important to note that any instances of contamination that occur within a case during testing will be detailed in the case report and any troubleshooting and root cause analysis documented in detail in the bench notes. This includes the instance of contamination report that will be included in the laboratory's contamination records. Therefore, any request for laboratory contamination records outside of the case file documentation may involve details from analysts and testing results not involved with the case at hand.

The California Supreme Court discussed discovery of lab contamination records in People v. Cordova, 62 Cal. 4th 104, 194 Cal. Rptr. 3d 40, 358 P.3d 518 (2015). There, the defense at trial sought discovery of laboratory contamination records from a private sector laboratory that had performed DNA testing for the prosecution. While there was no contamination involved in Cordova's casework, the defense was nonetheless interested in unintended transfer which had taken place in other, unrelated, casework over the laboratory's 20-year history. (*Id*. at pp. 121–123.) The trial court denied the request, and the California Supreme Court agreed with that ruling. It held that the contamination records did not fall under Brady v. Maryland, 373 U.S. 83, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963), which requires the prosecution in every case to give the defense all information that is both favorable to the accused (i.e., could help the defense or hurt the prosecution) and material to the outcome of the case (there is a reasonable probability it would make a difference). (*Id*. at p. 124.) The court cited several practical, common-sense reasons for its conclusion. (*Id*. at pp. 124–125.)

First, the lab tested the evidence samples, and reported the results, more than a year before it tested Cordova's reference blood sample. Contamination in this case was thus impossible, regardless of what happened at other times in other cases. Second, "defendant had available a far more probative means to challenge [the lab's] results if, in fact, those results were unreliable. He could simply have retested the evidence himself." The court's point here was that what makes lab records *Brady* material is their potential to cast doubt on the reliability of the test results. When the requested records would have dubious value in that regard, the fact that new testing could take place can push the records entirely out of the realm of evidence "favorable to the accused." In *Cordova*, not only did the defense conduct its own DNA testing, but the results were consistent with the outcome of prosecution testing. Third, significant non-forensic evidence in the case corroborated the DNA-based identification of the defendant as the perpetrator. This meant that "[i]t would have been a remarkable coincidence if a cold hit had falsely implicated defendant." (*Id*. at p. 125.) In sum, "[i]t is not reasonably probable that discovery of what may have occurred in other cases would have caused the jury to doubt in this case that defendant was the source of the sperm in the victim's body, or would otherwise have affected the verdict." (*Ibid*.)

6) Corrective Action Records

These records reflect laboratory actions taken to correct deviations from laboratory protocol or quality standards (e.g., the use of an expired reagent or using an incorrect instrument setting for the analysis of samples). These records, like contamination information, are typically available for a specific date range only, beyond which they have little relevance to the accuracy and reliability of the test result at issue in the case.

7) Internal Validation Studies for Particular Techniques and Instruments

Validation documentation is the record of experiments conducted to approve a new method for use in a laboratory. At a minimum, each testing method used on case samples must have been internally validated at the laboratory. These are often voluminous documents, and thus are commonly made available for inspection instead of photocopied. (See Schaffer v. Superior Court, 185 Cal. App. 4th 1235, 1242–1244, 111 Cal. Rptr. 3d 245 (2d Dist. 2010), review denied, (Oct. 13, 2010) [statutory discovery obligation satisfied by making files open to inspection in lieu of duplication].) The purpose and content of validation studies is discussed in further detail below.

8) Proficiency Test Results

DNA analysts must periodically take "proficiency tests" in order to satisfy laboratory accreditation standards as well as internal lab requirements. The tests are periodic performance-based evaluations using externally-prepared test materials. The results for analysts involved in the testing are commonly provided as discovery. Proficiency test results are also commonly provided for the reviewers of a case.

9) Evidence of the Laboratory's Accreditation Status

This may include a photocopy of the accreditation certificate or the final audit report for the most recent audit cycle.

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§ 10:4. Physical sample splits for defense testing

Requests for defense DNA testing or re-testing of crime scene evidence may or may not be granted by the trial court, depending upon the amount of evidence available. Several cases illustrate the spectrum of possible outcomes.

Where an evidence item has not been subjected to DNA testing at all, and defense testing would consume the evidence, there is no defense right to conduct such testing unilaterally and the trial court is within its discretion to deny such a request. (People v. Cooper, 53 Cal. 3d 771, 815–816, 281 Cal. Rptr. 90, 809 P.2d 865 (1991).) Under those circumstances, however, the prosecution may agree to send the evidence to a laboratory chosen by stipulation, under the condition that the results be released to both parties. (*People v. Cooper*, 53 Cal.3d at 816.) Alternatively, it would be good practice for the prosecution to permit the defense to have an expert present as an observer when the prosecution's DNA testing occurs. (People v. Varghese, 162 Cal. App. 4th 1084, 1094, 76 Cal. Rptr. 3d 449 (4th Dist. 2008).) Should the defense challenge the test results, however, the prosecutor may call the defense expert as a percipient witness to corroborate its own expert's opinions. (People v. Bolden, 29 Cal. 4th 515, 552, 127 Cal. Rptr. 2d 802, 58 P.3d 931 (2002).)

Another scenario is where the prosecution has already conducted DNA testing on an item of evidence, and some testable evidence remains, but any subsequent testing would likely result in consumption of the remainder of the sample. Under these circumstances the trial court is justified in denying a defense request to take possession of the remainder of the sample, conduct testing, and keep the results confidential. (*People v. Varghese*, 162 Cal. App. 4th at 1095.) A trial court acts within its discretion, however, to order that the defense be allowed to take possession of the remainder of the sample on the condition that the results of testing are disclosed to both parties. (*Ibid*.) In that event the prosecution is entitled to the defense test results as corroboration should the defense challenge the prosecution's test results. (*Ibid*.)

Finally, when sufficient sample remains for both the defense and prosecution to conduct testing or re-testing independently, an order denying the defense the opportunity to do so will violate his Sixth Amendment right to effective assistance of counsel. (Prince v. Superior Court, 8 Cal. App. 4th 1176, 1180, 10 Cal. Rptr. 2d 855 (4th Dist. 1992) [equally divided swab was sufficient for five tests by each party].) The defense test results need not be disclosed to the prosecution unless they are going to be presented as evidence at trial. (*Ibid*.) As the Prince court stated, "allowing the defense to conduct an independent test of the DNA will not unfairly prejudice the People or result in injustice. If the test matches Prince with the crime, defense counsel will not call the expert and the case will proceed on evidence already possessed by the People as if the defense test had not been made." (*Ibid*.)

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§ 10:5. DNA Data Bank Program discovery

Given the high volume of "cold hits" reported by the Department of Justice's DNA Data Bank Program, it is appropriate to describe additional documentation generated by that program which may be available as discovery in resulting criminal prosecutions. State law, moreover, expressly authorizes discovery of DNA Data Bank Program materials in cold hit cases: "A defendant's DNA and other forensic identification information developed pursuant to this chapter shall be available to his or her defense counsel upon court order made pursuant to … Section 1054 … ." (Pen. Code, § 299.5, subd. (g); see also Pen. Code, § 299.5, subd. (j) ["It is not a violation of this chapter to furnish DNA or other forensic identification information of the defendant to his or her defense counsel for criminal defense purposes in compliance with discovery"].) The following information is contained within the "hit file" generated by the Department of Justice's DNA Data Bank Program in cold hit cases, and is routinely provided as discovery to the defense upon request:

1) The Hit Notification Letter

This is the official notification issued by the state database administrator to the DNA casework laboratory that uploaded the crime scene evidence profile(s). This notification includes the name and state identification number of the offender to whom the evidence profile matched.

2) The Specimen Match Detail Report

This report is the record of the match generated by a CODIS search. It shows the profile and specimen number that was searched, next to the database specimen profile and specimen number to which it hit. The report will specify how many loci the profiles have in common and at which stringency. Stringency is rated as high, moderate, or low. For a locus from a single source or from a locus in a mixture where a foreign contributor's genotype was determined, the match will be at a high stringency (e.g., the offender and the evidence profile both have a 12,15 at D3S1358). For a locus where a single genotype cannot be determined, the match may be at medium stringency (e.g., the foreign contributor's possible genotypes determined at D3S1358 are 12,12 or 12,15 or 15,15, and the offender has a 12,15). An offender's name is not listed on this report. The specimen number must be checked against the submission database by an administrator to determine the offender's name and state identification number.

3) Photocopy of the Offender's Sample Submission Card

This is the information card submitted with the offender's buccal sample. It is completed by the personnel at the jail or prison or other facility conducting the collection, and includes notation of the offense that has triggered the collection obligation, as well as a thumbprint of the subject for later verification in the event of a database match.

4) Chain of Custody Information, Including the Chronology of the Testing Process

5) Electropherograms for Both the Original Analysis and the Confirmation Analysis

For each database match that is generated, a confirmation analysis is performed before information about the hit is released to the casework laboratory. This involves re-testing the reference submission to confirm that samples were not switched during the original analysis.

6) Procedural Check Sheets

7) Documentation of the Technical and Administrative Review Process

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§ 10:6. DNA Data Bank Program disclosure limitations

1) State Law Limitations

State law limits disclosure of other DNA profiles and other forensic identification information maintained by the DNA Data Bank Program, other than the information described above pertaining to a criminal defendant's own DNA profile and related information. Specifically, no DNA profile, and no data bank or database information, is available to a criminal defendant by way of subpoena or other discovery mechanism. (Pen. Code, § 299.5, subd. (h).) Penal Code section 299.5, subdivision (h), provides:

> Except as provided in subdivision (g)[1] and in order to protect the confidentiality and privacy of database and data bank information, the Department of Justice and local public DNA laboratories shall not otherwise be compelled in a criminal or civil proceeding to provide any DNA profile or forensic identification database or data bank information or its computer database program software or structures to any person or party seeking such records or information whether by subpoena or discovery, or other procedural device or inquiry.

(See also Pen. Code § 299.5, subd. (a) [codifying confidentiality of contents of DNA Database and exempting same from laws governing public disclosure of state government materials]; Pen. Code, § 299.5, subd. (f) [limiting disclosure of DNA Database information to enumerated law enforcement agencies]; cf. State v. Dykes, 252 Kan. 556, 847 P.2d 1214 (1993) [affirming denial of defense discovery of state DNA database profiles to conduct statistical research]; People v. Days, 31 Misc. 3d 586, 915 N.Y.S.2d 852 (County Ct. 2011) [affirming denial of defense discovery of "partial matches in New York state DNA database].) Criminal and civil sanctions for unauthorized use or disclosure of DNA Database information are set forth in Penal Code section 299.5, subdivision (i).

2) Federal Limitations

Because California uploads the contents of its offender DNA database into the National DNA Index System (NDIS), the State is subject to federal disclosure restrictions as well. Federal law provides as follows:

> The [National DNA Index System] shall include only information on DNA identification records and DNA analyses that are …
>
> (3) maintained by Federal, State, and local criminal justice agencies … pursuant to rules that allow disclosure of stored DNA samples and DNA analyses only
>
> (A) to criminal justice agencies for law enforcement identification purposes;
>
> (B) in judicial proceedings, if otherwise admissible pursuant to applicable statutes or rules;

(C) for criminal defense purposes, to a defendant, who shall have access to samples and analyses performed in connection with the case in which such defendant is charged; or

(D) if personally identifiable information is removed, for a population statistics database, for identification research and protocol development purposes, or for quality control purposes.

(42 U.S.C.A. § 14132, subd. (b)(3).) Subdivision (3)(C) states that the only database records that may be provided to a criminal defendant "for criminal defense purposes" are those relating to the DNA analysis done in conjunction with that particular case. Sanctions for violating federal nondisclosure restrictions may include terminating a state's participation in the national DNA database: "Access to the index established by this section is subject to cancellation if the quality control and privacy requirements described in subsection (b) of Section 14132 are not met." (42 U.S.C.A. § 14132, subd. (c).)

Footnotes

1 Subdivision (g), in turn, refers to a criminal defendant's ability to receive DNA Database information concerning his or her specific case.

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§ 10:7. Other laboratory material that may be of interest as discovery

While a comprehensive collection of all laboratory operational and background materials would be outside the scope of practical or permissible discovery in any given case, case facts may dictate that particular attention be focused on certain aspects of those operations. For example, a pretrial hearing on the admissibility of a new scientific technique employed to test case evidence may justify discovery of internal validation studies of that technique conducted by the laboratory. Or, indications that instrumentation malfunctioned may require discovery of instrument calibration and repair records. Accordingly, several sources of potential additional discovery are addressed here.

1) Quality Control Data

Prior to the use of any critical chemical reagent, test kit, or instrument for DNA analysis, quality control testing must be conducted to ensure its functionality. It is a laboratory's responsibility to establish procedures for ensuring that all reagents and instruments are preforming as expected within established parameters before initiating testing. Chemical reagents may be purchased prepared from outside vendors or may be prepared in-house. Each laboratory is responsible for designating which reagents are critical reagents. These may include extraction reagents and test kits. These reagents must be tested for performance and the absence of contaminants prior to use for DNA testing. Regents that are used after PCR amplification are generally not considered critical, and may be evaluated and monitored with continued use on case samples.

2) Instrument Repair and Calibration Records

Instrument such as genetic analyzers, quantitation platforms, robotics, and thermalcyclers, as well as laboratory implements such as pipettes, balances, and pH meters, must be evaluated, maintained, and/or calibrated on a periodic basis. This is commonly done on an annual or bi-annual schedule. If maintenance or repairs are performed on a piece of equipment, a performance evaluation may be required to clear it for continued use.

Laboratories must develop quality control procedures, and maintain records of all testing. Maintenance and repair records for all instruments and lab equipment should also be maintained. These records include manufacturer information, lot numbers, testing dates and results.

3) Validation Studies

Any testing method that is used in a forensic setting must provide reliability and reproducibility. In research settings, scientific tests are repeated hundreds, and sometimes thousands, of times, to prove reproducibility and increase confidence in the reliability of results. In a forensic setting, any single piece of evidence has the expectation of being tested once and perhaps twice. Therefore, the test that is performed must have a proven record of reproducibility. Validation studies are a set of tests performed to show that a testing method is acceptable for use in a forensic laboratory. In 2004 the Scientific Working Group on DNA Testing Methods (SWGDAM) released Revised Validation Guidelines. These guidelines were developed to address new and

developing technologies and to encompass the Quality Assurance Standards for Forensic DNA Testing Laboratories. They detail the steps that should be included in the validation of new testing methods used in the forensic laboratory. A validation study should establish that a procedure can produce reliable results under a specific set of conditions. It also must show the limits of the procedure and its parameters.

Two types of validations are required to introduce a new testing method or instrument platform into a forensic laboratory. First, a developmental validation is a set of experiments conducted by a manufacturer, laboratory, academic, research, or other institution, to demonstrate the accuracy, precision, and reproducibility of a novel testing method. This includes publication of the procedure or underlying principles in peer-reviewed journals. Second, an internal validation is a set of experiments conducted by a laboratory prior to the use of a new method in that laboratory. This is a test of the in-house performance of the new method. For laboratory systems, each individual lab in the system must conduct a separate internal validation prior to use of the method for testing. Internal validations are used to establish parameters for testing, and develop protocols, quality assurance procedures, and interpretation guidelines. Each new testing platform requires a new validation study.

Specific experiments included in a developmental (or external) validation include:

• Characterization of genetic markers: This includes determination of the marker's chromosomal location, mode of inheritance, the technology used for detection, and the type of marker.

• Species specificity: Genetic markers used for human identification must show no cross reactivity with other animal species. Species test encompass common domestic animals (e.g. dog, cat, rat, skunk) as well as species with close genetic ties to humans (e.g. gorilla, chimpanzee, orangutan).

• Sensitivity studies: This test determines the quantity of DNA needed to produce reliable results.

• Stability studies: These tests examine the methods ability to produce DNA typing results from a variety of substrates under varying environmental conditions (e.g. blood on wood left outside in hot dry conditions for two months).

• Reproducibility studies: The measurement of a technique's ability to produce consistent, reproducible results across multiple test replicates, multiple analysts within the same laboratory, and between separate laboratories.

• Case-type samples: This measures if the new technique is able to produce acceptable results on the type of samples commonly used in the testing laboratory (e.g. offender reference buccal samples).

• Population studies: An examination of the distribution of the genetic marker across several populations.

• Mixture studies: A measure of how well the genetic marker preforms in mixed samples.

• Precision and accuracy: This test measures results from multiple runs of one sample. Measurements are evaluated to determine the mean and standard deviation for the sizing of each marker.

• PCR-related procedures: An evaluation of the effects of amplification of specific markers must be conducted. This includes an examination of how the marker performs in a multiplex (i.e. several markers amplified in the same reaction at the same time), determination of optimal reaction conditions (e.g. thermalcycler parameters), detection parameters, and validation of positive and negative controls.

Depending on the technology being developed, some of these experiments may be omitted if not applicable.

Internal validations are not as extensive as developmental validations. They must include at a minimum:

• Known and non-probative evidence samples: These samples are previously typed samples from cases with either no probative value;

• Reproducibility and precision;

• Sensitivity and stochastic effects;

• Mixture studies;

• Contamination;

• Qualifying test: the final test required to demonstrate the method's readiness for use on case samples.

For any modification of a testing procedure, a performance evaluation must be conducted to determine whether the modification is able to produce reliable results within the laboratory. Performance checks are used to check up on the continued performance of a procedure, or to evaluate the continued consistent performance of an instrument. Any time instrument maintenance procedures alter the operating efficiency of an instrument, a performance check must be conducted. In addition, if an instrument is moved from one location to another within a laboratory (e.g., new room, or new position with in the same room), or to a new laboratory location (e.g., new building), a performance check must be performed. New software versions also require, at a minimum, a performance check.

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§ 10:8. *Brady v. Maryland*

1) Legal Principles

In every criminal case, the prosecution has an affirmative duty to disclose to the defense all material exculpatory or impeaching information possessed by an investigating agency, which includes crime labs that performed testing in the case. This is known as the "*Brady*" obligation, in reference to Brady v. Maryland, 373 U.S. 83, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963). The Supreme Court in Brady held that "the suppression by the prosecution of evidence favorable to an accused upon request violates due process where the evidence is material either to guilt or to punishment, irrespective of the good faith or bad faith of the prosecution." (Brady v. Maryland, 373 U.S. 83, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963).) "Material" evidence, in turn, is defined as follows: "The evidence is material only if there is a reasonable probability that, had the evidence been disclosed to the defense, the result of the proceeding would have been different. A 'reasonable probability' is a probability sufficient to undermine confidence in the outcome." (U.S. v. Bagley, 473 U.S. 667, 682, 105 S. Ct. 3375, 87 L. Ed. 2d 481 (1985).)

If information possessed by the prosecution is either exculpatory or impeaches a prosecution witness, the prosecutor is under an ongoing mandate to provide it to the defense whether in response to a defense request or not. (U.S. v. Agurs, 427 U.S. 97, 107, 96 S. Ct. 2392, 49 L. Ed. 2d 342 (1976) (holding modified by, U.S. v. Bagley, 473 U.S. 667, 105 S. Ct. 3375, 87 L. Ed. 2d 481 (1985)); see also In re Sassounian, 9 Cal. 4th 535, 544, 37 Cal. Rptr. 2d 446, 887 P.2d 527 (1995) [evidence is "favorable" if it "either helps the defendant or hurts the prosecution"].) Brady information may directly oppose guilt and lead to an acquittal, but in need not rise to this level. It could also be evidence that would mitigate punishment, evidence that would support defense testimony or a defense theory, evidence that impeaches a prosecution witness's credibility, or evidence that supports a defense pretrial motion. Prosecutors should err on the side of caution in providing potential Brady material to the defense: "To the extent the prosecutor is uncertain about the materiality of a piece of evidence, 'the prudent prosecutor will resolve doubtful questions in favor of disclosure.'" (U.S. v. Alvarez, 86 F.3d 901, 905 (9th Cir. 1996).)

The Brady obligation exists even if the prosecution is actually unaware of material favorable to the defense in the possession of one of its investigating agencies, such as the crime laboratory. As the Brady court put it, "[t]he suppression by the prosecution of evidence favorable to an accused … violates due process … irrespective of the good faith or bad faith of the prosecution." (Brady v. Maryland, 373 U.S. 83, 87, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963).) The crime laboratory is a member of the prosecution team, and information it possesses is thus also considered in the possession of the case prosecutor, at least on a constructive basis. (In re Brown, 17 Cal. 4th 873, 879–880, 72 Cal. Rptr. 2d 698, 952 P.2d 715 (1998); Martinez v. Wainwright, 621 F.2d 184, 188 (5th Cir. 1980) [prosecutor deemed to be in possession of RAP sheet in medical examiner's files]; U.S. ex rel. Smith v. Fairman, 769 F.2d 386, 391 (7th Cir. 1985) [Brady violation where exculpatory information about the operability of a firearm existed in the laboratory's file following a ballistics examination, even though never provided to the prosecutor].)

The United States Supreme Court has determined that Brady is not the proper framework for assessing postconviction claims of due process violations. (District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 2320, 174 L. Ed. 2d 38 (2009) ["[A defendant's] right to due process is not parallel to a trial right, but rather must be analyzed in light of the fact that he has already been found guilty at a fair trial, and has only a limited interest in postconviction relief. *Brady*

is the wrong framework"].) And, no violation of due process takes place if the defense does not receive *Brady* material before entering into a plea bargain. (U.S. v. Ruiz, 536 U.S. 622, 633, 122 S. Ct. 2450, 153 L. Ed. 2d 586 (2002).)

2) Case Law Examples Involving Forensic Science

In In re Brown, 17 Cal. 4th 873, 72 Cal. Rptr. 2d 698, 952 P.2d 715 (1998), the defendant was convicted of murder with special circumstances and sentenced to death. He had shot and killed a police officer and wounded four other people in a shooting spree. The defense at trial was one of diminished capacity, with the defendant claiming that he had been under the influence of methamphetamine when the shooting occurred. The prosecution provided rebuttal evidence that gas chromatography mass spectrometry toxicology testing showed no drugs in his blood at the time. (*In re Brown*, 17 Cal. 4th at 876.) The defense never received, however, a radioactive immunoassay screening test performed by the laboratory on the defendant's blood sample indicating the presence of phencyclidine (PCP). (*In re Brown*, 17 Cal. 4th at 877.) The court held that the nondisclosure violated Brady's principles. "The positive RIA test would have been more than simply the linchpin of this defense," stated the court. "As independent scientific evidence of PCP in petitioner's blood at the time of the crimes, it would have enhanced the credibility of the other evidence of PCP intoxication it tended to corroborate." (*In re Brown*, 17 Cal. 4th at 889.) This conclusion was not affected by the fact that the RIA test was most likely a false positive result. (*In re Brown*, 17 Cal. 4th at 902.)

In People v. Garcia, 17 Cal. App. 4th 1169, 22 Cal. Rptr. 2d 545 (4th Dist. 1993), as modified on denial of reh'g, (Aug. 31, 1993), the prosecution became aware during appellate proceedings that a Highway Patrol accident reconstruction expert who had testified at trial had been used erroneous methods in calculating automobile speeds as a basis for courtroom opinions in this and other cases. (*People v. Garcia*, 17 Cal. App. 4th at 1176, 1180.) This information, according to the court, clearly fell within the scope of Brady and should have been disclosed to the defense when it was discovered. (*People v. Garcia*, 17 Cal. App. 4th at 1180–1181; see also People v. Johnson, 142 Cal. App. 4th 776, 786, 48 Cal. Rptr. 3d 439 (5th Dist. 2006) [Brady material should be disclosed by prosecutor even if obtained while case is on appeal].) Specifically, the Garcia court held that "[t]he District Attorney's … review … revealed a significant number of errors by [the expert] with respect to speed calculations. This information alone clearly constituted evidence related to [the expert's] credibility as the prosecution's chief expert witness … . [T]his information alone constituted exculpatory evidence the District Attorney was obligated to turn over … ." (*People v. Garcia,* 17 Cal. App. 4th at 1180.)

In People v. Salazar, 35 Cal. 4th 1031, 29 Cal. Rptr. 3d 16, 112 P.3d 14 (2005), a forensic pathologist testified about the cause and timing of death in an infant homicide case. Information existed, but was not disclosed, that in another case the expert pathologist had changed his opinion based on, allegedly, nonmedical information and in order to fit the prosecution's new theory of the case. (*People v. Salazar*, 35 Cal. 4th at 1043, 1047–1048.) The court held that no Brady error occurred. Although it agreed that the information about the pathologist's inconsistencies in the earlier case would have been favorable impeachment evidence for the defense (*People v. Salazar*, 35 Cal. 4th at 1048), the court also concluded that the information was not material such that a reasonable probability existed of a better outcome for the defense had the information been known at trial. (*People v. Salazar*, 35 Cal. 4th at 1051.) "The evidence does not strongly support—if at all—petitioner's claim that [the expert] was a mere puppet of the prosecution and thus should have been disbelieved in this case. Moreover, even if petitioner could have succeeded in impeaching [the expert], equivalent testimony was supplied by other witnesses and could have been supplied by still others. In light of that testimony, as well as other circumstantial evidence of petitioner's guilt, it is not reasonably probable the result would have been different had the defense sought to use" the impeaching information. (*People v. Salazar*, 35 Cal. 4th at 1052.)

3) Examples of Potential *Brady* Evidence

Prosecutors and laboratory personnel should be vigilant for the existence of potential Brady material. The following list provides examples of such information. It is not exclusive, and offered for illustration purposes only. In addition, of course, whether anything constitutes favorable material information within the meaning of Brady depends upon the facts of a given case and significance of the information in that context.

- Any scientific observation, instrument output, result, or conclusion that could be viewed by the defense as favorable on the issue of guilt or punishment;
- Any laboratory event in a particular case that could be used by the defense in that case to challenge or otherwise attack results favoring the prosecution (e.g., contamination, false positive or false negative screening result, instrument malfunction, disagreement regarding interpretation of pattern match evidence);
- An analyst's false or misleading testimony in past case(s);
- An analyst's previous error(s) or discrepancies of such number or significance as to demonstrate incompetence to conduct the testing at issue in particular case;
- A witness's tampering with evidence, stealing evidence, or otherwise acting in a manner that impeaches his or her honesty or credibility.

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§ 10:9. Observation of testing by defense expert

Occasionally the defense in a criminal case seeks access to the government crime laboratory in order to permit its DNA expert to observe the prosecution's DNA testing. Laboratories may agree to this request, or may resist, citing the heightened risk of contamination carried by additional persons in close proximity to microscopic DNA evidence, as well as laboratory security concerns and the burden on laboratory staff to accompany and monitor defense representatives during testing.

A request that representatives of an opposing party view DNA testing as it occurs should be weighed against the ability of an outside expert to assess the validity of testing after it takes place based on laboratory records. Most laboratories' protocols and technical procedures are designed to permit outside experts to independently and critically review the testing process and the reliability of its conclusions through a review of bench notes, electronic data, checklists, and other materials. "[S]cientific evidence can usually be double-checked by other scientists for error or contributing factors … ." (Imwinkelried & Faigman, *Evidence Code Section 802: The Neglected Key to Rationalizing the California Law of Expert Testimony*, (2009) 42 Loy.L.A. L.Rev. 427, 446.)

Further, earning accreditation by the American Society of Crime Laboratory Directors/Laboratory Accreditation Board (ASCLD/LAB), requires a laboratory to document its test results "such that in the absence of the analyst, another competent analyst or supervisor could evaluate what was done and interpret the data." (ASCLD/LAB Int'l, *Supplemental Requirements for the Accreditation of Forensic Science Testing Laboratories*© (2006) 10 [ASCLD/LAB-International standard 4.13.2.5].) This principle was key to the Tenth Circuit's conclusion that independent expert opinion evidence based in part upon DNA testing performed by another analyst did not violate the Confrontation Clause: "[DNA] analysts are trained to record their data and processes in a manner that allows other analysts to review the information in order to draw an independent judgment about the DNA analysis and to testify to that independent judgment drawn from others' reports." (U.S. v. Pablo, 625 F.3d 1285, 1294, 83 Fed. R. Evid. Serv. 1298 (10th Cir. 2010), petition for cert. filed (U.S. Mar. 31, 2011).)

In People v. Cooper, 53 Cal. 3d 771, 816, 281 Cal. Rptr. 90, 809 P.2d 865 (1991), the California Supreme Court suggested that defense participation in prosecution DNA testing was not a right, but depended upon the discretion of the prosecution and the court: "The prosecution and court allowed the defense to participate in the testing on condition that the prosecution learn the results. The defense could choose to accept the condition or not participate in the testing. Forcing such a choice does not violate the Constitution or any other provision of law."

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§ 10:10. Preservation of biological evidence for later testing

The question may arise whether government DNA laboratories have a legal obligation to preserve biological samples, or portions thereof, for hypothetical subsequent testing. A related concern is how long such samples should or must be saved. For many years, laboratories referred to retained and preserved evidentiary samples as "*Nation* samples," in reference to the California Supreme Court's 1980 decision People v. Nation, 26 Cal. 3d 169, 161 Cal. Rptr. 299, 604 P.2d 1051 (1980). *Nation* has been eclipsed as controlling authority on this topic, however, by more recent decisional authority of the United States Supreme Court: California v. Trombetta, 467 U.S. 479, 104 S. Ct. 2528, 81 L. Ed. 2d 413 (1984) and Arizona v. Youngblood, 488 U.S. 51, 109 S. Ct. 333, 102 L. Ed. 2d 281 (1988).

1) Nation and Hitch

In People v. Nation, 26 Cal. 3d 169, 161 Cal. Rptr. 299, 604 P.2d 1051 (1980), the California Supreme Court held that a defendant's due process right to a fair trial requires the government to "take reasonable measures" to both retain and "adequately preserve" biological evidence in a case "if there is a reasonable possibility that [additional testing] would be favorable to the defendant on the issue of guilt or innocence." (*Id*. at pp. 176, 177.) The *Nation* requirement of retention and preservation did not hinge upon a request from a charged defendant, because often the evidence would be in the possession of law enforcement well before a suspect is charged with the crime.

Notably, *Nation* was concerned only with making biological evidence available to the defense before trial, so that the judge or jury would be able to access all evidence material to the charge, enhancing the reliability of the outcome to the degree possible. (26 Cal.3d at p. 177.) *Nation* did not specify any particular time period that evidence should be retained and preserved.

The holding in *Nation* was premised on its predecessor case People v. Hitch, 12 Cal. 3d 641, 117 Cal. Rptr. 9, 527 P.2d 361 (1974). There, the California Supreme Court considered the implications of a government policy to discard the "test ampoule," the "bubbler tube," and a "reference ampoule" from breath alcohol tests. *Hitch* concluded that, "if, given the availability of the test ampoule and its contents, and the reference ampoule, there is a reasonable possibility that they would constitute favorable evidence on the issue of guilt or innocence, then such evidence must be disclosed." (*Id*. at p. 649.) Retention and preservation are, of course, prerequisites of disclosure.

But, following *Hitch* and *Nation*, the United States Supreme Court in a pair of decisions reformulated the standard of evidence preservation required by federal due process. That standard superseded *Hitch* and *Nation*.

2) Trombetta and Youngblood

The first of the more recent cases, California v. Trombetta, 467 U.S. 479, 104 S. Ct. 2528, 81 L. Ed. 2d 413 (1984), held that law enforcement agencies have a duty, under the due process clause of the Fourteenth Amendment, to preserve evidence "that might be expected to play a significant role in the suspect's defense." (*Id*. at p. 488.) But, continued the Supreme Court, that duty is triggered *only* where the evidence possesses *apparent exculpatory value and is of "such a nature that the defendant would*

be unable to obtain comparable evidence by other reasonably available means." (*Id*. at p. 489, emphasis added.) The second case, Arizona v. Youngblood, 488 U.S. 51, 109 S. Ct. 333, 102 L. Ed. 2d 281 (1988), further limited the obligation to preserve evidence by holding that the "failure to preserve potentially useful evidence" is not a due process violation "unless a criminal defendant can show bad faith on the part of the police …." (*Id*. at pp. 57, 58.) California Courts have long recognized these standards as controlling. (See, e.g., People v. Beeler, 9 Cal. 4th 953, 976, 39 Cal. Rptr. 2d 607, 891 P.2d 153 (1995); People v. Roybal, 19 Cal. 4th 481, 509–510, 19 Cal. 4th 1231a, 79 Cal. Rptr. 2d 487, 966 P.2d 521 (1998), as modified, (Jan. 13, 1999).)

Thus, there exists a constitutional obligation to preserve evidence that has apparent exculpatory value and is uniquely useful, and even then a constitutional violation only occurs if the evidence is destroyed in bad faith.

3) Penal Code Section 1417.9

Penal Code section 1417.9 (see also § 12:10, *infra*) is a statutory evidence preservation rule. It became effective on January 1, 2001, and mandates the retention of "any object or material that contains or includes biological material that is secured in connection with a [felony] criminal case," as long as the convicted person remains incarcerated in connection with the case, in order to preserve the possibility of a motion for DNA testing brought under Section 1405. (Pen. Code, § 1417.9, subd. (a).) Misdemeanor convictions do not fall within the evidence retention mandate. (88 Ops.Cal.Atty.Gen. 77 (2005).)

This mandate was interpreted by a statewide task force as requiring preservation of all items that have a "reasonable likelihood" of containing biological evidence. (Postconviction Testing/Evidence Retention Task Force, *Postconviction DNA Testing: Recommendations for Retention, Storage, and Disposal of Biological Evidence* (2002), at p. 1 http://ag.ca.gov/publications/finalproof.pdf.) The Task Force advised further that, "if there is any reasonable question, the item should be retained." (*Ibid*.) Agencies possessing physical evidence should not be required, however, "to retain material without apparent evidentiary value, or material that is clearly collateral to any question of identity." (*Id*. at p. 6.)

Biological evidence may be disposed of when all defendants incarcerated in connection with the case are released from incarceration. The investigating agency, crime laboratory, or other governmental entity that possesses biological evidence may destroy the evidence before that time, however, under the following conditions and as long as no other provision of law requires its retention:

1) The entity possessing the evidence provides written notification of its intentions to the person or persons remaining incarcerated in the case, all counsel of record, the county Public Defender, the county District Attorney, and the Attorney General. (§ 1417.9, subd. (b)(1).)

2) No motion for postconviction testing, or notification that such a motion will be filed, is received within 90 days following the notification. (§ 1417.9, subd. (b)(2)(A), (B).)

3) No sworn declaration of innocence that has been filed with a court is received within 90 days following the notification. (§ 1417.9, subd. (b)(2)(C).)

In any event, before an agency in possession of biological evidence proceeds with destruction of the items pursuant to the procedures set forth above, it is advisable that the investigating officers of the case be contacted and advised, so that any concerns or objections they have can be considered.

4) Postconviction Discovery and Preservation Orders

The only postconviction discovery authorized by statute other than Penal Code section 1405 in this state is limited to cases resulting in conviction for a serious or violent felony, with a sentence of 15 years or more imposed. (Pen. Code, § 1054.9, subd. (a).) Note that, prior to 2020, this provision was even more restrictive, finding application only in death penalty and life

imprisonment cases. (See Stats. 2019, ch. 483, § 1, eff. Jan. 1, 2020.) Penal Code section 1054.9 may be utilized in the context of a petition for writ of habeas corpus or a motion to vacate a judgment. (§ 1054.9, subd. (a); see People v. Superior Court (Pearson) (2010) 48 Cal.4th 564, 571-573.) Discovery potentially available under section 1054.9 is limited to "materials in the possession of the prosecution and law enforcement authorities to which the same defendant would have been entitled at time of trial." (§ 1054.9, subd. (c); see In re Steele (2004) 32 Cal.4th 682, 695.) Significantly, section 1054.9 does not overlap with Penal Code section 1405, and cannot be used to obtain postconviction DNA testing. (§ 1054.9, subd. (d) ["The procedures for obtaining access to physical evidence for purposes of postconviction DNA testing are provided in Section 1405, and this section does not provide an alternative means of access to physical evidence for those purposes"]; see Satele v. Superior Court (2019) 7 Cal.5th 852, 858, fn. 3.)

It should be noted that, independent of the operation of Penal Code section 1417.9, trial courts in capital cases may issue postconviction orders for preservation of evidence that may be subject to future discovery in the context of a habeas proceeding. (People v. Superior Court (Morales) (2017) 2 Cal.5th 523, 533; Bracamontes v. Superior Court (2019) 42 Cal.App.5th 102, 110.) This is to ensure that any time lapse before appointment of habeas counsel does not result in destruction of evidence. With the expansion of postconviction discovery rights to a broader range of convicted felons following amendments to Penal Code section 1054.9 (effective January 1, 2020), there may also be an analogous basis for issuance of evidence preservation orders in those noncapital cases falling within the revised scope of section 1054.9. Of course, noncapital cases do not present the same procedural or chronological concerns, which may impact this analysis. Nonetheless, "because the superior court has jurisdiction under Penal Code section 1054.9 to grant postconviction discovery to the extent consistent with the statute, the court has the inherent power under Code of Civil Procedure section 187 to order preservation of evidence that would potentially be subject to such discovery." (*Morales, supra*, 2 Cal.5th at p. 534.)

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Chapter 11. Admissibility of DNA Evidence at Trial

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§ 11:1. *People v. Kelly* and *Sargon Enterprises, Inc.*

1) Overview

In California, the admissibility of scientific evidence at trial is governed by People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976) (Kelly). By screening new or novel scientific evidence through consideration of its fundamental reliability, the trial court applying Kelly ideally will protect the jury from influence by unreliable science, or by science whose reliability has been insufficiently demonstrated.

Patterned after Frye v. U.S., 293 F. 1013, 34 A.L.R. 145 (App. D.C. 1923), the Kelly admissibility test was retained as controlling authority in California after the United States Supreme Court in Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469, 37 Fed. R. Evid. Serv. 1 (1993) (Daubert) overruled Frye and set forth a new set of judicial considerations for proposed scientific evidence. (People v. Leahy, 8 Cal. 4th 587, 604, 34 Cal. Rptr. 2d 663, 882 P.2d 321 (1994).)

2) Purpose

Kelly's admissibility filter is intended to relieve layperson jurors of the burden of evaluating the appropriate weight to be given technical subject matter. As the Kelly court observed, jurors may "give considerable weight to 'scientific' evidence when presented by 'experts' with impressive credentials," and there may be a "'misleading aura of certainty'" surrounding a new scientific process. (*Kelly*, 17 Cal. 3d at 31–32.) Less technical and esoteric scientific disciplines, which jurors can evaluate using "their own common sense and good judgment," do not present this risk and thus are not subject to Kelly admissibility hearings. (People v. Venegas, 18 Cal. 4th 47, 80, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998); see also People v. Clark, 5 Cal. 4th 950, 1017–1018, 22 Cal. Rptr. 2d 689, 857 P.2d 1099 (1993) (disapproved of by, People v. Doolin, 45 Cal. 4th 390, 87 Cal. Rptr. 3d 209, 198 P.3d 11 (2009)) [Kelly not applicable to blood spatter testimony because analytical methods used produce no "'aura of scientific infallibility'"]; People v. DePriest, 42 Cal. 4th 1, 39–40, 63 Cal. Rptr. 3d 896, 163 P.3d 896 (2007), as modified, (Oct. 24, 2007) [shoe print evidence does not implicate concerns underlying Kelly because jurors are able to see patterns themselves and can readily evaluate the reliability of comparison methodology and related opinion testimony]; People v. Lucas, 60 Cal. 4th 153, 223–225, 177 Cal. Rptr. 3d 378, 333 P.3d 587 (2014) [summarizing *Kelly* standard and holding that handwriting comparison evidence, "based on everyday processes of observation and analysis," was not "'scientific'" enough to necessitate a *Kelly* admissibility hearing].)

The California Supreme Court summarized the two principal themes animating the Kelly standard as follows:

> Because the inventions and discoveries which could be considered "scientific" have become virtually limitless in the years since *Frye* was decided, application of its principle has often been determined by reference to its narrow "common sense" purpose, i.e., to protect the jury from techniques which, though "new," novel, or "'experimental,'" convey a "'misleading aura of certainty.'" [Citations.] [¶] This approach has produced two discernable themes. First, *Kelly*/*Frye* only applies to that limited class of expert testimony which is based, in whole or part, on a technique, process, or theory which is new to science and, even more so, the law. The courts are willing to

> forego admission of such techniques completely until reasonably certain that the pertinent scientific community no longer views them as experimental or of dubious validity… . [¶] The second theme in cases applying *Kelly*/*Frye* is that the unproven technique or procedure appears in both name and description to provide some definitive truth which the expert need only accurately recognize and relay to the jury. The most obvious examples are machines or procedures which analyze physical data. Lay minds might easily, but erroneously, assume that such procedures are objective and infallible. [Citations.]

(People v. Stoll, 49 Cal. 3d 1136, 1155–1156, 265 Cal. Rptr. 111, 783 P.2d 698 (1989).)

Nor are expert opinions based on "observable scientific data" independently subject to *Kelly* scrutiny. (People v. Jones, 57 Cal. 4th 899, 939, 161 Cal. Rptr. 3d 295, 306 P.3d 1136 (2013), as modified on denial of reh'g, (Oct. 2, 2013) and petition for cert. filed (U.S. Feb. 14, 2014); see also People v. Stoll, 49 Cal. 3d 1136, 1157, 265 Cal. Rptr. 111, 783 P.2d 698 (1989) ["absent some special feature which effectively blindsides the jury, expert opinion testimony is not subject to *Kelly* …"]).)

3) Kelly's Three-Prong Test

Accordingly, the California Supreme Court in Kelly established a three-prong test to be applied by a trial court to assess the fundamental reliability of a new scientific technique. Specifically, the proponent of scientific evidence must demonstrate that,

1) the technique or method is sufficiently established to have gained general acceptance in its field;

2) testimony with respect to the technique and its application is offered by a properly qualified expert; and

3) correct scientific procedures have been used in the particular case.
(People v. Wash, 6 Cal. 4th 215, 242, 24 Cal. Rptr. 2d 421, 861 P.2d 1107 (1993), citing *Kelly*, 17 Cal. 3d at 30; see also People v. Cook, 40 Cal. 4th 1334, 1344, 58 Cal. Rptr. 3d 340, 157 P.3d 950 (2007) [summarizing Kelly's three-prong test]; People v. Doolin, 45 Cal. 4th 390, 445, 87 Cal. Rptr. 3d 209, 198 P.3d 11 (2009).) The core of the Kelly evaluation is whether a new scientific technique has been generally accepted by the relevant scientific community, which in turn demonstrates its fundamental reliability. (*Kelly*, 17 Cal. 3d at 30.) As such, Kelly calls for the proponent of scientific evidence to provide evidence more akin to a survey of scientists and laboratories than a "nuts and bolts" showing of how and why the technique works. (See People v. Shirley, 31 Cal. 3d 18, 55, 181 Cal. Rptr. 243, 723 P.2d 1354 (1982) ["[I]n reviewing the scientific acceptance of the modified ceiling approach de novo under *Kelly*, we are not required to decide whether such methodology is 'reliable as a matter of "scientific fact," but simply whether it is generally accepted as reliable by the relevant scientific community'"].)

It is important to note that scientific evidence admitted following a Kelly hearing is not immune from subsequent challenge at trial by the opponent. The reliability and validity of the technique or methodology can be explored and challenged on both cross-examination and with presentation of rebuttal expert witness testimony. (People v. Stoll, 49 Cal. 3d 1136, 1159, 265 Cal. Rptr. 111, 783 P.2d 698 (1989); Evid. Code, § 721, subd. (a).) The prosecution also may call, in rebuttal, another expert of comparable background to challenge defense expert methods.

This chapter will discuss California case law that has developed around application of the Kelly test, as well as other key considerations and legal authorities bearing upon the admissibility of scientific evidence in California. Daubert and its progeny will be addressed as well. The application of these principles of admissibility to DNA evidence in California courts will be described. Finally, this chapter will describe the still-evolving case law concerning a defendant's Sixth Amendment confrontation clause right to challenge forensic science evidence.

4) *Sargon Enterprises, Inc.*

In 2012, the California Supreme Court discussed and clarified principles relating to admissibility of scientific evidence and other expert witness opinion testimony in Sargon Enterprises, Inc. v. University of Southern Cal., 55 Cal. 4th 747, 149 Cal. Rptr. 3d 614, 288 P.3d 1237, 286 Ed. Law Rep. 1191 (2012). *Sargon Enterprises* involved a breach of contract civil lawsuit, in which Sargon, the plaintiff company, sought to prove future earnings losses as a result of the defendant's failure to provide reports about the results of a clinical study conducted using dental implant technology patented by Sargon. The trial court excluded, as unduly speculative, Sargon's proffered expert testimony about how the breach of contract likely would impact Sargon's future growth, earnings, and market share. (*Id*. at pp. 761–767.) Although the Court of Appeal had reversed, the California Supreme Court disagreed and affirmed the trial court's ruling.

In so doing, the Supreme Court discussed the rules of evidence, and principles underlying, admission of expert testimony. Specifically *Sargon Enterprises* explained the scope of Evidence Code section 801, which permits trial courts to assess whether expert opinions will be based on the type of matters experts may reasonably rely upon. (55 Cal.4th at pp. 769–770 [discussing Evidence Code section 801, subdivision (b)].) If this test is not met, expert opinions may be excluded as speculative or irrelevant. (55 Cal.4th at p. 770.) Under Evidence Code section 802, moreover, a trial court may further "inquire into, not only the type of material on which an expert relies, but also whether that material actually supports the expert's reasoning. 'A court may conclude that there is simply too great an analytical gap between the data and the opinion proffered.' [Citations.]" (*Id*. at p. 771.) In sum, "under Evidence Code sections 801, subdivision (b), and 802, the trial court acts as a gatekeeper to exclude expert opinion testimony that is (1) based on matter of a type on which an expert may not reasonably rely, (2) based on reasons unsupported by the material on which the expert relies, or (3) speculative." (*Id*. at pp. 771–772.)

That being said, *Sargon Enterprises* also cautioned trial courts not to use their gatekeeper function to assign weight to, or evaluate the relative persuasiveness of, competing expert opinions. (55 Cal.4th at p. 772.) Instead, the trial court "must simply determine whether the matter relied on can provide a reasonable basis for the opinion or whether that opinion is based on a leap of logic or conjecture. The court does not resolve scientific controversies." (*Ibid*.) Thus, the trial court

> conducts a "circumscribed inquiry" to "determine whether, as a matter of logic, the studies and other information cited by experts adequately support the conclusion that the expert's general theory or technique is valid." [Citation.] The goal of trial court gatekeeping is simply to exclude "clearly invalid and unreliable" expert opinion. [Citation.] In short, the gatekeeper's role "is to make certain that an expert, whether basing testimony upon professional studies or personal experience, employs in the courtroom the same level of intellectual rigor that characterizes the practice of an expert in the relevant field." [Citation.]

(*Ibid*.)

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§ 11:2. *People v. Kelly*: Procedure

1) Evidence Code Section 405

A pretrial hearing concerning the admissibility of scientific evidence is governed by Evidence Code sections 402 and 405. One commentator summarizes the procedural posture of a Kelly hearing as follows:

> Since *Kelly* is designed to withhold expert testimony that is too unreliable to be evaluated properly, the question whether the underlying scientific principle or technique has been generally accepted by the relevant scientific community should be governed by section 405 of the California Evidence Code. Under section 405, the judge should exclude the expert testimony unless the proponent convinces the judge by a preponderance of the evidence that the principle or technique in question meets the *Kelly* standards of acceptance. If after the hearing it is unclear to the judge whether the required scientific consensus has developed, the judge should exclude the expert evidence.

(Mendez, *Expert Testimony and the Opinion Rule: Conforming the Evidence Code to the Federal Rules*, (2003) 37 U.S.F.L.Rev. 411, 426 (footnotes omitted).) Section 405 of the Evidence Code provides that,

> When the existence of a preliminary fact is disputed, the court shall indicate which party has the burden of producing evidence and the burden of proof on the issue as implied by the rule of law under which the question arises. The court shall determine the existence or nonexistence of the preliminary fact and shall admit or exclude the proffered evidence as required by the rule of law under which the question arises.

(Evid. Code, § 405, subd. (a).) In other words, under section 405, the trial court has exclusive authority to determine the existence of a preliminary fact, which in the context of scientific evidence is whether the proponent has demonstrated that the technique meets the standards set forth in Kelly. (See People v. Ashmus, 54 Cal. 3d 932, 971–972, 2 Cal. Rptr. 2d 112, 820 P.2d 214 (1991) [applying principles of section 405 to review of Kelly ruling].) This procedure is distinguished from that specified in Evidence Code section 403, authorizing the court to make only a preliminary determination regarding sufficiency. (See People v. Herrera, 83 Cal. App. 4th 46, 63, 98 Cal. Rptr. 2d 911 (5th Dist. 2000).)

2) Applicable Burden

The proponent of scientific evidence must show by a preponderance of the evidence that Kelly's standards are satisfied. (See Evid. Code, § 114.)

The California Court of Appeal discussed the *Kelly* doctrine in In re O.D., 221 Cal. App. 4th 1001, 1006–1007, 164 Cal. Rptr. 3d 578 (1st Dist. 2013), review filed, (Jan. 7, 2014). The case involved a juvenile accused of burglary and identification evidence of a palm print match. The juvenile sought exclusion of the expert testimony concerning the match under *Kelly*, claiming that the "ACE-V" fingerprint comparison technique[1] was no longer generally accepted by the relevant scientific community. The trial court denied the motion and received the palm print evidence. The Court of Appeal held that, as a matter of law, *Kelly* did not pertain to the fingerprint (or palm print) comparison technique. (221 Cal.App.4th at p. 1006.) Although *Kelly* does apply in juvenile proceedings (*id*. at p. 2006 [citing Welf. & Inst. Code, § 701]), "fingerprint comparison is not the type of scientific technique *Kelly* governs since it can easily be understood by nonexperts and is unlikely to convey a misleading aura of certainty." (221 Cal.App.4th at p. 1007.) In so finding, the court expressly distinguished DNA testing technology, noting that its nature requires that it remain subject to *Kelly* requirements. (*Ibid.*) Additionally and interestingly, the court also implied that qualitative components of an expert's testimony may actually lessen or increase the need for *Kelly*-based scrutiny; here, the expert's testimony "was particularly unlikely to convey a misleading aura of certainty because [she] openly acknowledged that fingerprint comparisons are inherently subjective and that no study establishes their infallibility." (*Ibid*.)

3) Appellate Review

Appellate review of a trial court's finding, pursuant to Kelly, that the fundamental validity of a new scientific methodology such as DNA testing has been "sufficiently established to have gained general acceptance in the particular field in which it belongs" is a "mixed question of law and fact subject to limited de novo review." (People v. Reilly, 196 Cal. App. 3d 1127, 1134, 242 Cal. Rptr. 496 (1st Dist. 1987); People v. Venegas, 18 Cal. 4th 47, 85, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998).) Review is "limited" because the trial court's determination of "any and all supportable findings of 'historical' fact or credibility" are given deference, and only then, given those "assumptions," will the reviewing court decide whether there has been general acceptance as a matter of law. (*Reilly*, 196 Cal. App. 3d at 1135.)

In conducting its review, the appellate court may consult relevant decisions from other jurisdictions as well as the scientific literature to the extent these can provide the Court with useful information "on the question of [the] consensus … of scientists" with respect to the scientific technique at issue. (*Reilly*, 196 Cal. App. 3d at 1134–35; People v. Brown, 40 Cal. 3d 512, 533–35, 230 Cal. Rptr. 834, 726 P.2d 516 (1985), judgment rev'd, 479 U.S. 538, 107 S. Ct. 837, 93 L. Ed. 2d 934 (1987) and (rejected by, People v. Cain, 171 Ill. App. 3d 468, 121 Ill. Dec. 887, 525 N.E.2d 1194 (4th Dist. 1988)); People v. Soto, 21 Cal. 4th 512, 541, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999) [approving appellate court reliance on "the very latest scientific opinions, including those published during the appellate phase of the case"]; see also People v. Allen, 72 Cal. App. 4th 1093, 1099, 85 Cal. Rptr. 2d 655 (2d Dist. 1999).)

Ruling on prongs two and three are reviewed for an abuse of discretion. (*Kelly*, 17 Cal. 3d at 39; People v. Reilly, 196 Cal.App.3d 1127, 1154–1155.)

Footnotes

1 ACE-V: Analysis, Comparison, Evaluation, Verification.

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§ 11:3. *People v. Kelly*: "New" scientific techniques

1) New Techniques

"*Kelly/Frye* only applies to that limited class of expert testimony which is based, in whole or part, on a technique, process, or theory which is new to science and, even more so, the law." (People v. Stoll, 49 Cal. 3d 1136, 1156, 265 Cal. Rptr. 111, 783 P.2d 698 (1989); see also People v. Webb, 6 Cal. 4th 494, 524, 24 Cal. Rptr. 2d 779, 862 P.2d 779 (1993).) A scientific technique is unlikely to be perceived by courts as "new" if it has been subjected to "repeated use, study, testing and confirmation by scientists or trained technicians." (People v. Leahy, 8 Cal. 4th 587, 605, 34 Cal. Rptr. 2d 663, 882 P.2d 321 (1994).)

Once a particular scientific technology—such as PCR/STR DNA testing—is held in a published appellate decision to be generally accepted, new or varied applications of that fundamentally unchanged technology generally do not raise a prong one Kelly question requiring further prong one hearings. (People v. Jones, 57 Cal. 4th 899, 937, 161 Cal. Rptr. 3d 295, 306 P.3d 1136 (2013), as modified on denial of reh'g, (Oct. 2, 2013) and petition for cert. filed (U.S. Feb. 14, 2014); see also People v. Hill, 89 Cal. App. 4th 48, 58, 107 Cal. Rptr. 2d 110 (2d Dist. 2001) [new and varied PCR/STR testing kits do not require new prong one hearing; citing cases]; People v. Venegas, 18 Cal. 4th 47, 79, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998) [rejecting notion that there was a legally significant prong one distinction between RFLP testing conducted by different laboratories using different genetic markers]; People v. Cooper, 53 Cal. 3d 771, 812–814, 281 Cal. Rptr. 90, 809 P.2d 865 (1991) [rejecting contention that electrophoresis had to undergo new prong one analysis when used to test new enzymes and serum proteins such as transferrin]; People v. Reilly, 196 Cal. App. 3d 1127, 1136–1137, 242 Cal. Rptr. 496 (1st Dist. 1987) [protocol variations "in the buffer solution, the amount of electric current, the length of time allowed for separation and migration, the type and thickness of the gel (medium), and the catalytic agent used for staining" were not considered separately as implicating general acceptance of the electrophoresis technique for five genetic marker systems]; People v. Smith, 107 Cal. App. 4th 646, 665, 132 Cal. Rptr. 2d 230 (2d Dist. 2003) ["the use of polymerase chain reaction and short tandem repeats technology to analyze a mixed-source forensic sample is neither a new or novel technique or methodology"]; People v. Fierro, 1 Cal. 4th 173, 214, 3 Cal. Rptr. 2d 426, 821 P.2d 1302 (1991) [rejecting argument that the new multisystem method of electrophoresis represented a new technology for Kelly purposes]; People v. Smith, 215 Cal. App. 3d 19, 27–28, 263 Cal. Rptr. 678 (1st Dist. 1989) [rejecting defense argument that appellate courts must separately decide the admissibility of different electrophoretic methods—particularly the multisystem method]; People v. Bury, 41 Cal. App. 4th 1194, 1202, 49 Cal. Rptr. 2d 107 (2d Dist. 1996) [prong one hearing not required for latest incarnation of breath testing device]; People v. Wash, 6 Cal. 4th 215, 242–243, 24 Cal. Rptr. 2d 421, 861 P.2d 1107 (1993) [rejecting distinction between electrophoretic testing of semen and blood given the fundamental validity of electrophoresis].)

Thus, variations in procedure and application of a generally accepted technology may not create a "new" technology such that admissibility must be evaluated under Kelly's precepts.

In People v. Cooper, 53 Cal. 3d 771, 281 Cal. Rptr. 90, 809 P.2d 865 (1991), for example, the California Supreme Court rejected a defense challenge to the novel use of electrophoresis technology to identify the serum protein transferrin. (*People v. Cooper*, 53 Cal. 3d at 812.) Even though electrophoresis had "only recently been used to test for transferrin," the court held that application to be reliable as a matter of law because the technique as a whole had been generally accepted. (*Ibid.*) In support of its finding the court cited People v. Smith, 215 Cal. App. 3d 19, 27, 263 Cal. Rptr. 678 (1st Dist. 1989), for the proposition

that "once electrophoresis is admissible, criticism of any specific methodology goes to the weight of the evidence, not its admissibility." (*People v. Cooper*, 53 Cal. 3d at 813.) Only the core technology, not its evolving uses and new applications, was germane to the question of Kelly general acceptance.

In People v. Jackson, 163 Cal. App. 4th 313, 77 Cal. Rptr. 3d 474 (3d Dist. 2008), as modified, (June 5, 2008), the court considered the trial court's ruling that admissibility of test results obtained using the Identifiler DNA test kit, which employs PCR (Polymerase Chain Reaction)/STR (Short Tandem Repeat) technology, need not be subjected to a prong one Kelly hearing to determine its fundamental validity. The defendant had argued at trial that such a hearing was necessary given the differences between the Identifiler kit and predecessor PCR/STR kits known as Profiler and Cofiler Plus, including the addition of several new loci for analysis. (163 Cal. App. 4th at 324.)

The Jackson court affirmed the trial court's ruling. (163 Cal. App. 4th at 325.) It held that, "[a]lthough defendant has identified seven changes in the Identifiler kit from the previous test kits, defendant has not shown that these differences change the *methodology* of the testing of the DNA. The changes … appear to increase the accuracy and efficiency of the same methodology of PCR/STR testing." (*Ibid*.) "[I]t appears," concluded the court, that "Identifiler is a new and improved version of the same scientific procedure already generally accepted by the scientific community." (*Ibid*.)

In People v. Henderson, 107 Cal. App. 4th 769, 132 Cal. Rptr. 2d 255 (4th Dist. 2003), the defendant argued that use of capillary electrophoresis to test mixed source DNA samples was not generally accepted in the scientific community. (107 Cal. App. 4th at 785.) This argument was rejected in the trial and appellate courts, as follows: "*Kelly* first prong analysis only applies to a new technique or procedure. Although capillary electrophoresis is a new technique for which first prong analysis is appropriate, capillary electrophoresis on a particular type of DNA sample does not constitute a different scientific technique. Rather, it involves a technique, which has gained general acceptance, as applied to a particular set of circumstances." (107 Cal. App. 4th at 786, fn. omitted.)

2) Scientific Techniques

Further, trial courts must assess whether a disputed technique or method is actually scientific in nature, thus bringing it under the auspices of a Kelly evaluation. In People v. Nelson, 43 Cal. 4th 1242, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008), the California Supreme Court addressed this issue with respect to DNA statistics.

The case involved the prosecution of a defendant who had been identified as the perpetrator of a murder through a DNA database search. Under such circumstances at least two[1] statistical expressions of the meaning of a DNA profile match can be provided: (1) the rarity of the profile shared by the defendant and the perpetrator, and (2) the chance of a random match to that profile when searching through a database of a given size. The latter statistic is sometimes referred to as the "database probability" statistic. Thus the issue arose of whether the admissibility of one or both of these statistics at trial required a prong one Kelly hearing assessing whether the relevant scientific community generally accepts a particular statistical approach as a fundamentally valid scientific technique in a cold hit case. (*People v. Nelson*, 43 Cal.4th at 1258–1260.)

Nelson held that the choice of statistics in a cold hit DNA case is a question of legal relevancy and probative value for trial court judges to resolve, not a question of science for scientists to resolve. (*People v. Nelson*, 43 Cal.4th at 1265.) Thus, it does not implicate Kelly's foundational requirement of general acceptance. Adopting language used by an out-of-state appellate court, Nelson observed that any debate emphasized by appellant "'is a disagreement over the competing questions to be asked, not the methodologies used to answer those questions… . These competing schools of thought do not question or challenge the validity of the computations and mathematics … .'" (*People v. Nelson*, 43 Cal.4th at 1264, quoting U.S. v. Jenkins, 887 A.2d 1013, 1022–1023 (D.C. 2005).) In other words, scientists can debate the best statistic for the jury to hear—the rarity of the DNA profile itself, or the database probability, or both, or neither—but it is not a scientific debate about the math underlying any of the competing approaches. Every scientist will agree which numbers to key on the calculator to answer each question. Instead, it is merely scientists debating legal relevancy issues. (*People v. Nelson*, 43 Cal.4th at 1264.) While scientists can debate points

such as relevance and probative value, it does not transform those subjects into scientific issues implicating Kelly. Accordingly, general acceptance under Kelly's first prong, in this context at least, was held to be a non-issue.

Footnotes

1 Although other, more esoteric, statistical approaches were also discussed in *Nelson*, the two described herein are the most important given the holding of the case.

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§ 11:4. *People v. Kelly*: Prong one / general acceptance

1) Definition

Under Kelly's first prong the proponent must establish the reliability of a scientific technique. (See, e.g., People v. Cook, 40 Cal. 4th 1334, 1345, 58 Cal. Rptr. 3d 340, 157 P.3d 950 (2007).) "Reliability," for Kelly admissibility purposes, means that a particular scientific technique "'must be *sufficiently established to have gained general acceptance in the particular field in which it belongs*'" in order to be admissible. (People v. Reilly, 196 Cal. App. 3d 1127, 1135, 242 Cal. Rptr. 496 (1st Dist. 1987), quoting People v. Kelly, 17 Cal. 3d 24, 30, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976), and Frye v. U.S., 293 F. 1013, 1014, 34 A.L.R. 145 (App. D.C. 1923), emphasis in original; People v. Venegas, 18 Cal. 4th 47, 76, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998).) Kelly's first prong tests the "fundamental validity of a new scientific technology." (People v. Cooper, 53 Cal. 3d 771, 812–814, 281 Cal. Rptr. 90, 809 P.2d 865 (1991); see also People v. Farmer, 47 Cal. 3d 888, 913, 254 Cal. Rptr. 508, 765 P.2d 940 (1989) (abrogated by, People v. Waidla, 22 Cal. 4th 690, 94 Cal. Rptr. 2d 396, 996 P.2d 46 (2000)).)

"'General acceptance,' in turn, means a consensus drawn from a typical cross-section of the relevant, qualified scientific community." (People v. Leahy, 8 Cal. 4th 587, 612, 34 Cal. Rptr. 2d 663, 882 P.2d 321 (1994).) The Kelly test does not demand "absolute unanimity of views in the scientific community … . Rather, the test is met if use of the technique is supported by a clear majority of the members of that community." (People v. Guerra, 37 Cal. 3d 385, 418, 208 Cal. Rptr. 162, 690 P.2d 635 (1984).) In determining the question of general acceptance, courts "must consider the quality, as well as quantity, of the evidence supporting or opposing a new scientific technique. Mere numerical majority support or opposition by persons minimally qualified to state an authoritative opinion is of little value … ." (*People v. Leahy*, 8 Cal. 4th at 612.)

General acceptance, however, "does not require unanimity, a consensus of opinion, or even majority support by the scientific community." (*People v. Leahy*, 8 Cal. 4th at 601.) As the California Supreme Court stated, "'Nothing in the *Kelly* test requires that there be one and only one approach to a scientific problem. The question is whether scientists significant in number or expertise publicly oppose a technique as unreliable, not whether some scientists believe there may be an alternative, perhaps even better, technique available.'" (People v. Nelson, 43 Cal. 4th 1242, 1263, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008).) Further, "*Kelly* does not apply to every dispute among experts, even strident, deep-seated ones. Experts frequently clash, even about basic principles and issues. Such disagreement does not trigger application of the Kelly test; instead, what is required is the utilization of a new scientific technique." (People v. Johnson, 139 Cal. App. 4th 1135, 1148, 43 Cal. Rptr. 3d 587 (5th Dist. 2006).)

2) Determining General Acceptance

In evaluating general acceptance, the court "determines from the professional literature and expert testimony whether or not the new scientific technique is accepted as reliable in the relevant scientific community and whether 'scientists significant either in number or expertise publicly oppose [a technique] as unreliable.'" (People v. Soto, 21 Cal. 4th 512, 519, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999), quoting People v. Axell, 235 Cal. App. 3d 836, 854, 1 Cal. Rptr. 2d 411 (2d Dist. 1991); People v. Reilly, 196 Cal. App. 3d 1127, 1134–35, 242 Cal. Rptr. 496 (1st Dist. 1987); see also People v. Shirley, 31 Cal. 3d 18, 55, 181 Cal. Rptr. 243, 723 P.2d 1354 (1982); People v. Leahy, 8 Cal. 4th 587, 611, 34 Cal. Rptr. 2d 663, 882 P.2d 321 (1994) [approving trial

court review of "'published writings in scholarly treatises and journals' in lieu of live testimony" to help resolve the question of "scientific consensus"].)

Significantly, Kelly does not require—nor does it permit—trial judges to determine the "actual reliability" of the new technique. (People v. Barney, 8 Cal. App. 4th 798, 810, 10 Cal. Rptr. 2d 731 (1st Dist. 1992), distinguished on other grounds in *People v. Soto*, 21 Cal. 4th at 538.) "[C]ourts are ill suited to make such determinations." (People v. Bolden, 29 Cal. 4th 515, 546, 127 Cal. Rptr. 2d 802, 58 P.3d 931 (2002).) Reliability as a matter of scientific fact is not for the trial court to decide in the resolution of any Kelly-based admissibility dispute. (People v. Axell, 235 Cal. App. 3d 836, 854, 1 Cal. Rptr. 2d 411 (2d Dist. 1991).) As the California Supreme Court stated in a hypnosis case, "our duty is not to decide whether hypnotically induced recall of witnesses is reliable as a matter of 'scientific fact,' but simply whether it is generally accepted as reliable by the relevant scientific community." (*People v. Shirley*, 31 Cal. 3d at 55, emphasis in original.)

Nor does Kelly require that the validity of the a scientific procedure be re-evaluated each time it reappears in a case: "Once a trial court has admitted evidence based upon a new scientific technique, and the decision is affirmed on appeal by a published appellate decision, the precedent so established may control subsequent trials … ." (*Kelly*, 17 Cal.3d at 32.) This is an "important corollary" to the rule in Kelly. (*People v. Venegas*, 18 Cal. 4th at 53 ["if a published appellate decision in a prior case has already upheld the admission of evidence based on [a prong one] showing, that decision becomes precedent for subsequent trials in the absence of evidence that the prevailing scientific opinion has materially changed."]; see also People v. Doolin, 45 Cal. 4th 390, 447, 87 Cal. Rptr. 3d 209, 198 P.3d 11 (2009); People v. Bolden, 29 Cal. 4th 515, 545, 127 Cal. Rptr. 2d 802, 58 P.3d 931 (2002); People v. Riel, 22 Cal. 4th 1153, 1192, 96 Cal. Rptr. 2d 1, 998 P.2d 969 (2000); People v. Henderson, 107 Cal. App. 4th 769, 776–77, 132 Cal. Rptr. 2d 255 (4th Dist. 2003).)

Thus, "appellate endorsement of a [scientific technique] ends the need for case-by-case adjudication" at the trial court level. (People v. Brown, 40 Cal. 3d 512, 530, 230 Cal. Rptr. 834, 726 P.2d 516 (1985), judgment rev'd, 479 U.S. 538, 107 S. Ct. 837, 93 L. Ed. 2d 934 (1987) and (rejected by, People v. Cain, 171 Ill. App. 3d 468, 121 Ill. Dec. 887, 525 N.E.2d 1194 (4th Dist. 1988)).) In fact, trial courts may look beyond California to cases from other jurisdictions in ascertaining whether a particular scientific technique is generally accepted. (*Id.*; see also People v. Axell, 235 Cal. App. 3d 836, 854, 1 Cal. Rptr. 2d 411 (2d Dist. 1991) ["The court may also consider decisions from other jurisdictions … in deciding whether a technique is generally accepted."]; see also *People v. Reilly*, 196 Cal. App. 3d at 1134–35; *People v. Soto*, 21 Cal. 4th at 541 [approving appellate court reliance on "the very latest scientific opinions, including those published during the appellate phase of the case"]; People v. Allen, 72 Cal. App. 4th 1093, 1099, 85 Cal. Rptr. 2d 655 (2d Dist. 1999).)

This rule of stare decisis contains an important corollary, however. The admissibility of scientific evidence previously addressed by appellate courts can again be called into question when "new evidence is presented reflecting a change in the attitude of the scientific community." (*Kelly*, 17 Cal. 3d at 32.) Kelly general acceptance determinations "are not static; they represent analyses of the state of science, and state of the law, as of the time the cases were decided. 'Science, like time, marches on' (*People v. Yorba*, 209 Cal. App. 3d 1017, 1023, 257 Cal. Rptr. 641 (4th Dist. 1989)), and the cases do not stand for the proposition that certain techniques or procedures are subject to *Kelly*'s foundational requirements whenever they arise, forevermore." (People v. Johnson, 139 Cal. App. 4th 1135, 1149, 43 Cal. Rptr. 3d 587 (5th Dist. 2006).)

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§ 11:5. *People v. Kelly*: Prong two

"*Kelly*'s second prong requires that the testifying expert be properly qualified to testify regarding the reliability of the scientific technique used." (People v. Cook, 40 Cal. 4th 1334, 1346, 58 Cal. Rptr. 3d 340, 157 P.3d 950 (2007); People v. Kelly, 17 Cal. 3d 24, 30, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976).) Further, the testifying expert must "understand the technique and its underlying theory, and be thoroughly familiar with the procedures that were in fact used in the case at bar to implement the technique," in order to address Kelly's third prong concerning the manner in which the scientific technique was applied in a given case. (People v. Venegas, 18 Cal. 4th 47, 81, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998).)

As with all other expert witness qualification questions, the trial court's assessment is governed by Evidence Code sections 720 and 801. Section 720, subdivision (a), provides that "[a] person is qualified to testify as an expert if he has special knowledge, skill, experience, training, or education sufficient to qualify him as an expert on the subject to which his testimony relates … ." Subdivision (b) provides that "[a] witness' special knowledge … may be shown by any otherwise admissible evidence, including his own testimony." Evidence Code section 801, subdivision (b), states that an expert may render an opinion "[b]ased on matter (including his special knowledge, skill, experience, training, and education) perceived by or personally known to the witness or made known to him at or before the hearing, whether or not admissible, that is of a type that reasonably may be relied upon by an expert in forming an opinion upon the subject to which his testimony relates, unless an expert is precluded by law from using such matter as a basis for his opinion."

"The trial court is given considerable latitude in determining the qualifications of an expert and its ruling will not be disturbed on appeal unless a manifest abuse of discretion is shown. [Citations.]" (*Kelly*, 17 Cal. 3d at 39; see also People v. Cooper, 53 Cal. 3d 771, 813, 281 Cal. Rptr. 90, 809 P.2d 865 (1991).)

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§ 11:6. *People v. Kelly*: Prong three

Kelly's third prong requires that the proponent "demonstrate that correct scientific procedures were used in the particular case. [Citations.]" (People v. Kelly, 17 Cal. 3d 24, 30, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976).) In contrast to the general acceptance inquiry, the third-prong inquiry is case-specific. "[I]t inquires into the matter of whether the procedures actually utilized in the case were in compliance with that methodology and technique, as generally accepted by the scientific community." (People v. Venegas, 18 Cal. 4th 47, 78, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998); see also People v. Jones, 57 Cal. 4th 899, 941, 161 Cal. Rptr. 3d 295, 306 P.3d 1136 (2013), as modified on denial of reh'g, (Oct. 2, 2013) and petition for cert. filed (U.S. Feb. 14, 2014); People v. Roybal, 19 Cal. 4th 481, 504, 505, 19 Cal. 4th 1231a, 79 Cal. Rptr. 2d 487, 966 P.2d 521 (1998), as modified, (Jan. 13, 1999).)

The third-prong hearing has been described as a "limited" showing, and assumes that the technique or methodology at issue has met the prong one general acceptance standard. (*People v. Venegas*, 18 Cal. 4th at 78.) "[A]lthough third-prong hearings will survive a showing of general acceptance," one court noted, "they obviously will not approach the level of complexity of a full-blown *Kelly-Frye* hearing in which the question of general acceptance is litigated. All that is necessary in the limited third-prong hearing is a foundational showing that correct scientific procedures were used." (People v. Barney, 8 Cal. App. 4th 798, 825, 10 Cal. Rptr. 2d 731 (1st Dist. 1992).)

Unlike scientific disciplines that are readily comprehensible by the jury, such that results and conclusions can be critically weighed and evaluated by a layperson without predicate judicial factfinding, DNA evidence is subject to judicial scrutiny under Kelly's third prong in any given case. The California Supreme Court described this distinction as follows:

> DNA evidence is different. Unlike fingerprint, shoe track, bite mark, or ballistic comparisons, which jurors essentially can see for themselves, questions concerning whether a laboratory has adopted correct, scientifically accepted procedures for generating autorads or determining a match depend almost entirely on the technical interpretations of experts. [Citation.] Consideration and affirmative resolution of those questions constitutes a prerequisite to admissibility under the third prong of *Kelly*.

(*People v. Venegas*, 18 Cal. 4th at 81.)

Kelly's third-prong inquiry, however, does not "cover all derelictions in following the prescribed scientific procedures" such as "mislabeling, mixing the wrong ingredients, or failing to follow routine precautions against contamination." (*Venegas*, 18 Cal. 4th at 81.) Such missteps "amount only to '[c]areless testing affect[ing] the weight of the evidence and not its admissibility.'" (*Ibid.*; People v. Cooper, 53 Cal. 3d 771, 814, 281 Cal. Rptr. 90, 809 P.2d 865 (1991) [" 'the *Kelly-Frye* rule tests the fundamental validity of a new scientific methodology, not the degree of professionalism with which it is applied. [Citation.] Careless testing affects the weight of the evidence and not its admissibility, and must be attacked on cross-examination or by other expert testimony'"]; see also People v. Farmer, 47 Cal. 3d 888, 913, 254 Cal. Rptr. 508, 765 P.2d 940 (1989) (abrogated by, People v. Waidla, 22 Cal. 4th 690, 94 Cal. Rptr. 2d 396, 996 P.2d 46 (2000)); People v. Cua, 191 Cal. App. 4th 582, 591,

119 Cal. Rptr. 3d 391 (1st Dist. 2011), review denied, (Apr. 20, 2011).) Thus, "[w]here the prosecution shows that the correct procedures were followed, criticisms of the techniques go to the weight of the evidence, not its admissibility." (People v. Brown, 91 Cal. App. 4th 623, 647, 110 Cal. Rptr. 2d 750 (5th Dist. 2001).)

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§ 11:7. Admissibility of DNA Typing Technology, Statistical Methods, and Related Software

1) Polymerase Chain Reaction (PCR) / Short Tandem Repeat (STR) Analysis

The fundamental validity of polymerase chain reaction (PCR), as well as its Short Tandem Repeat (STR) analysis applications, is well-established as reflected by appellate decisions in California, as well as state and federal courts nationwide. Many of those decisions specifically considered and endorsed the PCR/STR-based Profiler Plus® and COfiler® testing kits, whose loci are combined in the 15-locus Identifiler® kit currently employed by many laboratories in California and elsewhere. (See People v. Cordova, 62 Cal. 4th 104, 125–126, 194 Cal. Rptr. 3d 40, 358 P.3d 518 (2015) [holding that the Identifiler® testing kit is not a new scientific technique and does not require a prong one *Kelly* hearing as an admissibility prerequisite]; See People v. Jackson, 163 Cal. App. 4th 313, 323, 77 Cal. Rptr. 3d 474 (3d Dist. 2008), as modified, (June 5, 2008) [Identifiler kit "examines 15 STR locations as opposed to the 13 different STR locations examined under the combination of the prior 'Cofiler' and 'Profiler Plus' kits"].)

For example, in People v. Hill, 89 Cal. App. 4th 48, 107 Cal. Rptr. 2d 110 (2d Dist. 2001), the court considered the admissibility of DNA test results based on a laboratory's analysis of sexual assault evidence swabs using the PCR-based "DQ-Alpha Polymarker" and "Profiler Plus" test kits. The court held that the evidence had been properly admitted, noting that "California courts have recognized that two methodologies are widely used in forensic DNA testing: restriction fragment length polymorphism (RFLP) and PCR. [Citation.] There are three subtypes of PCR testing: DQ-Alpha, which tests a single genetic marker; Polymarker, which tests five genetic markers; and the STR, which tests three or more genetic markers. [Citation.] The RFLP and PCR methodologies, including the PCR subtypes, have acquired general acceptance in the scientific community. [Citations.]" (89 Cal. App. 4th at 57.) In so holding, the Hill court cited, among other cases, People v. Wright, 62 Cal. App. 4th 31, 34, 72 Cal. Rptr. 2d 246 (1st Dist. 1998) [PCR/Polymarker test generally accepted); People v. Morganti, 43 Cal. App. 4th 643, 662–671, 50 Cal. Rptr. 2d 837 (1st Dist. 1996), as modified on denial of reh'g, (Mar. 27, 1996) [PCR/DQ-Alpha test generally accepted]; People v. Allen, 72 Cal. App. 4th 1093, 1099–1101, 85 Cal. Rptr. 2d 655 (2d Dist. 1999) [PCR/STR testing generally accepted].)

Subsequently, in People v. Jones, 57 Cal. 4th 899, 936–937, 161 Cal. Rptr. 3d 295, 306 P.3d 1136 (2013), as modified on denial of reh'g, (Oct. 2, 2013) and petition for cert. filed (U.S. Feb. 14, 2014), the California Supreme Court reviewed with approval decisional authority holding that various forensic science applications of PCR technology are generally accepted for *Kelly* purposes. In particular, *Jones* noted that "PCR analysis of the DQ-Alpha gene is now firmly established as a scientific technique that satisfies the *Kelly* test." (*Id*. at p. 937; see also People v. Doolin, 45 Cal. 4th 390, 446–447, 87 Cal. Rptr. 3d 209, 198 P.3d 11 (2009) [describing DQ-Alpha testing procedure in detail]; People v. Morganti, 43 Cal. App. 4th 643, 662, 50 Cal. Rptr. 2d 837 (1st Dist. 1996), as modified on denial of reh'g, (Mar. 27, 1996) [same].)

Other cases discussing and reiterating the general acceptance of PCR/STR testing technology include People v. Cua, 191 Cal. App. 4th 582, 593–594, 119 Cal. Rptr. 3d 391 (1st Dist. 2011), review denied, (Apr. 20, 2011); People v. Jackson, 163 Cal. App. 4th 313, 324, 77 Cal. Rptr. 3d 474 (3d Dist. 2008), as modified, (June 5, 2008); People v. Smith, 107 Cal. App. 4th 646, 665–666, 132 Cal. Rptr. 2d 230 (2d Dist. 2003); People v. Henderson, 107 Cal. App. 4th 769, 776–779, 132 Cal. Rptr. 2d 255 (4th Dist. 2003); U.S. v. Gipson, 383 F.3d 689, 697 (8th Cir. 2004); U.S. v. Ewell, 252 F. Supp. 2d 104, 108, (D.N.J. 2003), aff'd, 189 Fed. Appx. 120 (3d Cir. 2006); *United States v. Trala*, 162 F. Supp. 2d at 343, 347–348; State v. Jones, 678 N.W.2d 1, 6–7, 24–

25 (Minn. 2004); State v. Keightley, 147 S.W.3d 179, 189 (Mo. Ct. App. S.D. 2004); State v. Whittey, 149 N.H. 463, 821 A.2d 1086, 1095–1096 (2003); State v. Faulkner, 103 S.W.3d 346, 358–59 (Mo. Ct. App. S.D. 2003); People v. Shreck, 22 P.3d 68, 71, 80–82, 90 A.L.R.5th 765 (Colo. 2001), as modified, (May 14, 2001); State v. Keightley, 147 S.W.3d 179, 188–89 (Mo. Ct. App. S.D. 2004). In addition, the United States Supreme Court recently observed that "STR testing is extremely discriminating, can be used on small samples, and is 'rapidly becoming the standard.'" (District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 2315, 174 L. Ed. 2d 38 (2009)].)

2) Mixed DNA Sample Analysis

A number of courts have held that STR analysis of mixed DNA samples is generally accepted in a forensic context. (People v. Stevey, 209 Cal. App. 4th 1400, 1411, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013); see also People v. Smith, 107 Cal. App. 4th 646, 671–672, 132 Cal. Rptr. 2d 230 (2d Dist. 2003) [the trial court's finding "that the mixed sample analysis of deoxyribonucleic acid by means of short tandem repeats is accepted by the scientific community was well reasoned, based upon extensive expert testimony, and exhaustive review of the literature and case law"]; People v. Henderson, 107 Cal. App. 4th 769, 773, 132 Cal. Rptr. 2d 255 (4th Dist. 2003) ["the added complication of analyzing a multiple source DNA sample did not affect the admissibility of the evidence, but, instead, was a consideration for the jury in weighing the evidence and determining the credibility and accuracy of the DNA test results"]; see also U.S. v. Trala, 386 F.3d 536, 541–542, 65 Fed. R. Evid. Serv. 791 (3d Cir. 2004), cert. granted, judgment vacated, 546 U.S. 1086, 126 S. Ct. 1078, 163 L. Ed. 2d 849 (2006).)

Note, however, that courts continue to carefully scrutinize proffered mixture interpretation evidence, and may exclude it in cases where laboratories become overly aggressive and interpret complex mixtures in ways not supported by their own validated protocols. An example of this is found in United States v. Williams (N.D. Cal. 2019) 382 F.Supp.3d 928. *Williams* involved a pretrial defense motion to exclude prosecution evidence that a defendant contributed DNA to a mixed sample. The sample had been interpreted with a probabilistic genotyping program called Bullet. The question presented to the court was "whether Bullet was validated to analyze the mixture at issue here." (*Id.* at p. 929.) The court concluded that it was not, because the mixture in the case may have consisted of more than four contributors, while the Bullet program had been validated by the laboratory only for mixtures of up to four contributors. (*Id.* at pp. 929, 931.) Ultimately, the question was one of reliability under Rule 702 of the Federal Rules of Evidence. (*Id.* at p. 935.) Based on the body of evidence presented, the court found that the DNA analyst "did not reliably conclude that only four individuals contributed DNA to the mixture at issue." (*Id.* at p. 936.) Of significance to the court was evidence that SERI, the laboratory in question, "demonstrated an inability to distinguish five-person mixtures from four-person mixtures. During the GlobalFiler validation study, it did not correctly identify a single five-person mixture. [The analyst] asserted that these errors occurred because 'by coincidence,' the individuals who contributed DNA to the study shared alleles. But a 100% rate of error gives no confidence in SERI's ability to be accurate if faced with the same coincidence in the real world." (*Id.* at p. 937.)

3) Capillary Electrophoresis Instrumentation

Use of capillary electrophoresis instrumentation in conjunction with PCR/STR testing has been determined to be generally accepted. (See, e.g., People v. Smith, 107 Cal. App. 4th 646, 671–672, 132 Cal. Rptr. 2d 230 (2d Dist. 2003); People v. Henderson, 107 Cal. App. 4th 769, 781–785, 132 Cal. Rptr. 2d 255 (4th Dist. 2003); State v. Faulkner, 103 S.W.3d 346, 359 (Mo. Ct. App. S.D. 2003); State v. Butterfield, 2001 UT 59, 27 P.3d 1133, 1143–1145 (Utah 2001).)

4) Statistics: The Product Rule

Calculating the statistical significance of a DNA profile match has been the subject of Kelly scrutiny in California courts for more than 20 years. The first appellate court decision on the topic, People v. Axell, 235 Cal. App. 3d 836, 1 Cal. Rptr. 2d 411 (2d Dist. 1991), involved RFLP[1] testing. The Axell court affirmed the admissibility of the DNA evidence, including population frequency statistics. A year later, however, another California appellate court concluded otherwise, holding that there was no

general acceptance among scientists concerning calculation of DNA statistics. (People v. Barney, 8 Cal. App. 4th 798, 819, 10 Cal. Rptr. 2d 731 (1st Dist. 1992); see also People v. Wallace, 14 Cal. App. 4th 651, 660, 17 Cal. Rptr. 2d 721 (1st Dist. 1993) [same].)

Several years of conflicting opinions from various courts of appeal ensued, along with significant additions to the scientific literature on population frequency statistics based on published data sets collected on an international basis. (See, e.g., *The Evaluation of Forensic DNA Evidence* (1996) National Research Council, Nat'l Academy of Sciences; *VNTR Population Data: A Worldwide Study* (1993) Vols. I–IV, Federal Bureau of Investigation.) Finally, in 1999, the California Supreme Court held that DNA population frequency statistics generated using the unmodified product rule are generally accepted under Kelly's first prong, in view of the published developments in the field. (People v. Soto, 21 Cal. 4th 512, 538–541, 88 Cal. Rptr. 2d 34, 981 P.2d 958 (1999).) The following discussion sets forth the current views of California appellate courts on the admissibility of DNA statistics.

When a match occurs between a suspect's DNA profile and the DNA profile developed from a sample left by the perpetrator at a crime scene, "the DNA profile of the matched samples is compared to the DNA profiles of other available DNA samples in a relevant population database or databases in order to determine the statistical probability of finding the matched DNA profile in a person selected at random from the population or populations to which the perpetrator of the crime might have belonged." (*People v. Soto*, 21 Cal. 4th at 518.) "Experts calculate the odds or percentages—usually stated as one in some number—that a random person from the relevant population would have a similar match." (People v. Wilson, 38 Cal. 4th 1237, 1239, 45 Cal. Rptr. 3d 73, 136 P.3d 864 (2006).)

"Databases have … been developed to determine population frequencies of the various alleles that may be detected using PCR. [Citation.] … Once population frequencies have been determined for each locus, the analyst must calculate the probability that a person at random would have the same combination of matches at all loci." (People v. Reeves, 91 Cal. App. 4th 14, 31, 109 Cal. Rptr. 2d 728 (1st Dist. 2001), as modified on denial of reh'g, (Aug. 28, 2001).) "The most straightforward means of making this calculation is through application of the 'product rule.'" (People v. Venegas, 18 Cal. 4th 47, 65, 74 Cal. Rptr. 2d 262, 954 P.2d 525 (1998).) The "product rule" posits that the probability of several things occurring together is the product of their separate probabilities. (See Kaye, *DNA Evidence: Probability, Population Genetics, and the Courts*, (1993) 7 Harv. J.L. & Tech. 101, 127–128.) "The essence of the product rule is the multiplication of individual band probabilities to arrive at an overall probability statistic expressed as a simple fraction, such as 1 in 100,000." (*Venegas*, 18 Cal. 4th at 66.) "Thus, the product rule is simply the multiplication of the frequencies found at each locus studied. The result is a probability statistic that reflects the overall frequency of the complete DNA profile. It is often quite small." (People v. Reeves, 91 Cal. App. 4th 14, 31, 109 Cal. Rptr. 2d 728 (1st Dist. 2001), as modified on denial of reh'g, (Aug. 28, 2001).)

"[T]he number derived from the product rule 'represents two concepts: (1) the frequency with which a particular DNA profile would be expected to appear in a population of unrelated people, in other words, how rare is this DNA profile ("rarity statistic"), and (2) the probability of finding a match by randomly selecting one profile from a population of unrelated people, the so-called "random match probability."' [Citation.]" (People v. Turner (2020) 10 Cal.5th 786, 801-802; People v. Nelson, 43 Cal. 4th 1242, 1266, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008).) It is "settled that the product rule reliably shows the rarity of the profile in the relevant population." (*People v. Nelson*, 43 Cal. 4th at 1263, citing *People v. Soto*, 21 Cal. 4th 512.) "It is relevant for the jury to know that most persons of at least major portions of the general population could not have left the evidence samples." (*People v. Wilson*, 38 Cal. 4th at 1245.) The "product rule," underlying calculation of random match probability statistics, is now universally accepted in the forensic DNA scientific community for use in evaluating the rarity of a given forensic DNA profile developed using PCR-based technology. (*People v. Reeves*, 91 Cal. App. 4th at 38–42; *People v. Soto*, 21 Cal. 4th at 541; State v. Gore, 143 Wash. 2d 288, 21 P.3d 262, 308–311, (2001), as amended, (Mar. 29, 2001) and as amended, (Apr. 6, 2001) and (overruled by, State v. Hughes, 154 Wash. 2d 118, 110 P.3d 192 (2005)); Smith v. State, 702 N.E.2d 668, 673–674 (Ind. 1998); State v. Jackson, 255 Neb. 68, 582 N.W.2d 317, 325 (1998); People v. Pope, 284 Ill. App. 3d 695, 220 Ill. Dec. 309, 672 N.E.2d 1321, 1327–28 (4th Dist. 1996); Com. v. Rosier, 425 Mass. 807, 685 N.E.2d 739, 743–744 (1997); see also U.S. v. Gaines, 979 F. Supp. 1429, 1441, 48 Fed. R. Evid. Serv. 419 (S.D. Fla. 1997); U.S. v. Shea, 957 F. Supp. 331, 341–

343, 46 Fed. R. Evid. Serv. 1375 (D.N.H. 1997), aff'd, 159 F.3d 37, 50 Fed. R. Evid. Serv. 516 (1st Cir. 1998); U.S. v. Lowe, 954 F. Supp. 401, 418–419, 46 Fed. R. Evid. Serv. 316 (D. Mass. 1996).)

5) Admissibility of "Source Attribution" Statement; DNA Test Results In the Absence of Statistics

Courts in California and elsewhere have accepted that it may be reasonable for an expert to attribute a crime scene DNA profile to a particular person when that person possesses a matching profile that is sufficiently rare. (See, e.g., People v. Cordova, 62 Cal. 4th 104, 131, 194 Cal. Rptr. 3d 40, 358 P.3d 518 (2015); People v. Nelson, 43 Cal. 4th 1242, 1262, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008); People v. Wilson, 38 Cal. 4th 1237, 1248–49, 45 Cal. Rptr. 3d 73, 136 P.3d 864 (2006); People v. Johnson, 139 Cal. App. 4th 1135, 1146, 43 Cal. Rptr. 3d 587 (5th Dist. 2006); U.S. v. Garcia-Ortiz, 528 F.3d 74, 83 (1st Cir. 2008); U.S. v. Ewell, 252 F. Supp. 2d 104, 109 (D.N.J. 2003), aff'd, 189 Fed. Appx. 120 (3d Cir. 2006); Young v. State, 388 Md. 99, 879 A.2d 44, 56–57 (2005).) This is known as a "source attribution" statement. As the Nelson court stated, "when the odds are like those here, it might be appropriate for the expert to testify that, except for identical twins or maybe close relatives, "it can be concluded to a reasonable scientific certainty that the evidence sample and the defendant sample came from the same person." (*People v. Nelson*, 43 Cal. 4th at 1262, internal quotation marks omitted.)

In fact, an authority cited by the California Supreme Court in Nelson for the above proposition, People v. Johnson, 139 Cal. App. 4th 1135, 43 Cal. Rptr. 3d 587 (5th Dist. 2006), itself quoted a Maryland appellate court case in which a source attribution statistic was provided by the prosecution expert without *any* accompanying statistics. The reviewing court, in Young v. State, 879 A.2d 44, found no error. It reasoned as follows:

> When the random match probability is sufficiently minuscule, the DNA profile may be deemed unique. In such circumstances, testimony of a match is admissible without accompanying contextual statistics. In place of the statistics, the expert may inform the jury of the meaning of the match by identifying the person whose profile matched the profile of the DNA evidence as the source of that evidence; i.e. the expert may testify that in the absence of identical twins, it can be concluded to a reasonable scientific certainty that the evidence sample and the defendant sample came from the same person. [Citation.]

(*Young v. State*, 879 A.2d at 56–57.)

Recently, the California Court of Appeal arrived at the same conclusion. In People v. Cua, 191 Cal. App. 4th 582, 119 Cal. Rptr. 3d 391 (1st Dist. 2011), review denied, (Apr. 20, 2011), the prosecution elicited expert testimony of a 15-locus match between a questioned single-source crime scene DNA sample and the defendant's profile. Without providing a random match probability statistic, the witness testified that the crime scene DNA "belonged" to the defendant—known as a "source attribution" statement. (*People v. Cua*, 191 Cal. App. 4th at 596.) The defendant objected that such evidence was scientifically invalid and inadmissible under Kelly's first prong. The court held that admission of the source attribution statement was proper. The court pointed to research establishing that "the average random match probability for unrelated individuals for even 13 STR loci is less than one in a trillion, even in populations with reduced genetic variability," and noted as well that the 1996 NCR II Report (National Research Council, *The Evaluation of Forensic DNA Evidence* (1996)) contemplated source attribution statements as potentially reasonable scientific inferences based on a DNA profile's "'probable uniqueness.'" (*People v. Cua*, 191 Cal. App. 4th at 599.) The court concluded that, "We know of no categorical prohibition, at least in this state, on source attribution—expression by an otherwise qualified expert of an opinion that the quantitative and qualitative correspondence between an evidentiary sample and a known sample from a defendant establishes identity to a reasonable scientific certainty… . While the criminalist was not asked to calculate the rarity statistic of such a match using the product rule, we can readily infer that the odds would also be here, as in Nelson, "astronomical" and "tantamount to saying that defendant left the evidence at the crime scene." (*People v. Cua*, 191 Cal. App. 4th at 600–601, quoting People v. Nelson, 43 Cal. 4th 1242, 1259, 78 Cal. Rptr. 3d 69, 185 P.3d 49 (2008).)

A similar issue arose in People v. Her, 216 Cal. App. 4th 977, 157 Cal. Rptr. 3d 40 (3d Dist. 2013). There, the trial court permitted prosecution evidence that two partial DNA profiles identified at the crime scene were consistent with the defendant as a possible contributor of the DNA in the mixtures, even though no statistics were provided. (*Id*. at p. 980.) The Court of Appeal affirmed. It noted that "DNA testimony need not be accompanied by statistical analysis" to be relevant and admissible. (*Id*. at pp. 980–981.) The court relied on the fact that the prosecution DNA expert had generated a DNA profile, from a third mixture, that matched the defendant's profile with an associated statistical rarity provided of one in 150 quintillion. Therefore "because the partial profile [for which no statistics were generated] was consistent with the profile of the major contributor to the other bloodstains on the pillow, which bore defendant's profile, it was relevant to support the People's theory that defendant killed John Lone Eagle. The court did not abuse its discretion in admitting the evidence." (*Id*. at p. 982.)

6) Y-STR Analysis

DNA testing kits that process identification markers located on the Y-chromosome ordinarily occur when samples are insufficient in volume or quality to permit useful results using standard 13- or 15-locus STR testing kits. The most common application of Y-STR testing is in sexual assault cases featuring a mixture of the victim's and perpetrator's cellular material, where the victim's DNA may otherwise mask lower levels of the perpetrator's DNA. Engaging in Y-STR analysis provides test results exclusively reflecting the DNA type attributable to the male contributor to the mixture. Because Y-STR analysis generally employs the same testing methods and analytical processes applicable to autosomal PCR/STR typing kits, courts considering the validity of Y-STR testing kits have generally favored admissibility of Y-STR results.

In 2012, for the first time, a California appellate court reached this conclusion. In People v. Stevey, 209 Cal. App. 4th 1400, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013), the defendant was convicted of various sex crimes. Y-STR testing with the "Yfiler kit" was performed on pubic hairs collected during the investigation. (209 Cal. App. 4th at 1407–1408.) A prosecution expert testified that the Y-chromosome haplotype matched the defendant's, and a statistical rarity estimate was given. (*Id*. at 1408.) The trial court denied a defense request to hold a hearing under People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976), to determine whether the Y-STR testing was a generally accepted technique in the relevant scientific community. (*Id*. at 1410.) The Court of Appeal affirmed, holding that "Y-STR testing does not embrace new scientific techniques" and thus is not subject to a first prong *Kelly* determination. (*Id*. at 1412.) The *Stevey* court described how the methods and technologies involved in Y-STR analysis are analogous to those used in conventional STR typing, and it cited a number of cases from other jurisdictions affirming the fundamental reliability of the technique. (*Id*. at 1412–1415.) It further held that "use of the counting method and the confidence factor as a conservative adjustment to the statistical probability of a match is also generally accepted within the scientific community." (*Id*. at 1415.) A number of cases from other jurisdictions have reached similar conclusions about Y-STR typing. (See, e.g., State v. Calleia, 414 N.J. Super. 125, 148–149, 997 A.2d 1051 (App. Div. 2010), judgment rev'd, 206 N.J. 274, 20 A.3d 402 (2011); Shabazz v. State, 265 Ga. App. 64, 592 S.E.2d 876, 879 (2004); Curtis v. State, 205 S.W.3d 656, 661 (Tex. App. Fort Worth 2006), petition for discretionary review refused, (Feb. 28, 2007); State v. Russell, 141 Wash. App. 733, 172 P.3d 361, 365 (Div. 2 2007).)

7) Mitochondrial DNA Analysis

The reliability of mitochondrial DNA testing, including evidence of the statistical significance of test results, has been considered by a number of courts that decided to permit its introduction into evidence. (See, e.g., People v. Stevey, 209 Cal. App. 4th 1400, 1414–1415, 148 Cal. Rptr. 3d 1 (3d Dist. 2012), review denied, (Jan. 30, 2013) [holding, in part, that mitochondrial DNA testing and its statistical methods are generally accepted as reliable by the scientific community]; Wagner v. State, 160 Md. App. 531, 864 A.2d 1037, 1046 (2005) [citing cases]; see also U.S. v. Beverly, 369 F.3d 516, 531, 64 Fed. R. Evid. Serv. 357, 2004 FED App. 0136P (6th Cir. 2004); U.S. v. Coleman, 202 F. Supp. 2d 962, 970 (E.D. Mo. 2002); State v. Pappas, 256 Conn. 854, 776 A.2d 1091, 1105 (2001); Magaletti v. State, 847 So. 2d 523, 528 (Fla. Dist. Ct. App. 2d Dist. 2003); Lewis v. State, 889 So. 2d 623, 673 (Ala. Crim. App. 2003).)

8) Probabilistic Genotype Software

In 2016, forensic DNA laboratories began using probabilistic genotype software to assist in the qualitative interpretation of DNA mixtures. The software generates statistical models of observed allele combinations. The results of such modeling are likelihood ratios that compare competing theories in a case.

In June 2015, the Scientific Working Group on DNA Analysis Methods (SWGDAM) issued a document entitled *Guidelines for the Validation of Probabilistic Genotyping Systems*. (Available at www.swgdam.org/publications.) It includes the following general description of the technology at pages two-three:

> A probabilistic genotyping system is comprised of software, or software and hardware, with analytical and statistical functions that entail complex formulae and algorithms. Particularly useful for low-level DNA samples (i.e., those in which the quantity of DNA for individuals is such that stochastic effects may be observed) and complex mixtures (i.e., multi-contributor samples, particularly those exhibiting allele sharing and/or stochastic effects), probabilistic genotyping approaches can reduce subjectivity in the analysis of DNA typing results. Historical methods of mixture interpretation consider all interpreted genotype combinations to be equally probable, whereas probabilistic approaches provide a statistical weighting to the different genotype combinations. Probabilistic genotyping does not utilize a stochastic threshold. Instead, it incorporates a probability of alleles dropping out or in. In making use of more genotyping information when performing statistical calculations and evaluating potential DNA contributors, probabilistic genotyping enhances the ability to distinguish true contributors and non-contributors. A higher LR [likelihood ratio] is typically obtained when evaluating a person of interest (POI) who is a true contributor to the evidence profile, and a lower LR is typically obtained when the POI is not a true contributor. While the absence of an allele or the presence of additional allele(s) relative to a reference sample may support an exclusion, probabilistic genotyping approaches allow inclusion and exclusion hypotheses to be considered by calculating a LR in which allele drop-out and drop-in may be incorporated.

(See Moss, Note, The Admissibility of TrueAllele: A Computerized DNA Interpretation System (2015) 72 Wash. & Lee L. Rev. 1033, 1061 ["TrueAllele relies on a class of algorithms derived from a Bayesian statistical analysis called Monte Carlo-Markov Chain (MCMC) modeling. The MCMC statistical approach has been used in a variety of situations to successfully model many complex data sets"].)
(Footnote omitted.) The two principle software packages utilizing a probabilistic genotype approach are TrueAllele® and STRmix®.

In 2022, People v. Davis, 75 Cal. App. 5th 694, 290 Cal. Rptr. 3d 661 (3d Dist. 2022), review denied, (June 1, 2022) became the first published California decision on the admissibility of probabilistic genotype software. *Davis* involved the murder of an elderly woman in her home during a burglary. The primary contention on appeal was the trial court should have excluded, pursuant to People v. Kelly, 17 Cal. 3d 24, 130 Cal. Rptr. 144, 549 P.2d 1240 (1976), expert witness testimony relying on DNA results generated by STRmix software. The court described STRmix as "a method of DNA analysis that involves the use of probabilistic genotyping computer software to aid in the interpretation and evaluation of forensic evidentiary samples that contain a mixture of DNA from multiple contributors." (*Davis*, *supra*, 75 Cal.App.5th at p. 708.) Probabilistic genotyping, in turn, is "software, or software and hardware, with analytical and statistical functions that entail complex formulae and algorithms that assist in the qualitative interpretation of a DNA mixture. [Citation.] The system uses the power of computing to exclude or include contributors to a DNA mixture. If a contributor is included, the software is used to calculate likelihood ratios that compare propositions including the contributor in question to mutually exclusive propositions that do not include the contributor in question. The resulting likelihood ratios can provide a measure of support for one proposition over the other. [Citations.] The

likelihood ratios are "'generally expressed as follows: a match between the suspect and the evidence is (x number) of times more probable than a coincidental match.'" (*People v. Superior Court (Dominguez)* (2018) 28 Cal.App.5th 223, 228.)"

The court recounted expert testimony presented by the prosecution at trial, explaining how STRmix functioned:

> Eric Halsing, a senior criminalist with the DOJ, analyzed the DNA mixture on the shoelace using the STRmix method. Prior to explaining the results of his analysis, he described the STRmix method of DNA analysis. First, the criminalist evaluates the STR DNA-typing results and determines how many contributors are present in a DNA mixture. This number is then entered into the software program, which "deconvolutes" or interprets the mixture by using mathematical principles to come up with sets of genotypes or DNA profiles for the individuals that could possibly have contributed to the mixture. After the deconvolution process is completed (i.e., the mixture has been interpreted), the next step involves the calculation of likelihood ratios. The software program randomly picks values for a number of different variables, using widely accepted mathematical principles to either accept or reject proposed DNA profiles based on those random values. This step is repeated up to billions of times. The DNA profiles are then ranked as to how well they fit the actual mixture. The software program assigns a statistical match probability to the sets of DNA profiles. The significance of the match is expressed in a likelihood ratio, which compares two conditional probabilities. Essentially, the likelihood ratio answers the question: Under which set of conditions is this DNA mixture better explained? At trial, Halsing emphasized that the STRmix method does not answer the question: How likely is it that a certain person is a contributor to the DNA mixture? Rather, the likelihood ratio is a numerical expression that explains that a DNA mixture is "x" number of times more probable or better explained as a combination of DNA from a certain group of people than as a combination of DNA from another group of people.

(*Davis*, *supra*, 75 Cal.App.5th at p. 709.) In addressing the question of general acceptance of STRmix by the relevant scientific community, as required by *Kelly*, the *Davis* court also provided a detailed description of testimony by John Buckleton, Ph.D., one of the creators of STRmix, presented by the prosecution at the *Kelly* hearing. (*Davis*, *supra*, 75 Cal.App.5th at pp. 713-715.) The Court of Appeal summarized the trial court *Kelly* proceedings thusly: "Testimony at the hearing established that the STRmix method has been subjected to extensive empirical testing and found to be accurate and reliable by the FBI and numerous forensic laboratories. And while no published California appellate decision has specifically addressed the admissibility of STRmix evidence under the first prong of *Kelly*, numerous courts across the country have concluded that the STRmix method has gained general acceptance within the relevant scientific community." (*Id.* at p. 717.)

The Court of Appeal deemed this to be "ample evidence supporting a finding of general acceptance." (*Davis*, *supra*, 75 Cal.App.5th at p. 717.) It concluded that "the trial court did not err in determining that the STRmix method of DNA analysis is generally accepted as reliable by the relevant scientific community, such that expert testimony relying on the method satisfied the first requirement of the *Kelly* test." (75 Cal.App.5th at p. 701.) "[T]he record reflects that STRmix has been used for DNA analysis since 2012 and is widely used by forensic laboratories across the world. At the time of the December 2017 *Kelly* hearing, STRmix was in use by 44 forensic laboratories worldwide, including 30 in the United States. The United States Army began using STRmix in 2014 and it has been used by the FBI since 2015 and the DOJ since 2016. The scientific and mathematical principles behind STRmix are well established and widely accepted in the scientific community, and STRmix has been the subject of numerous peer-reviewed articles published in scientific journals." (*Id.* at p. 717.) The court cited several scientific publications in particular that had been judicially noticed: (1) Buckleton et al., *The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity* (March 2009) vol. 64, No. 2, Journal of Forensic Sciences 393; (2) Coble & Bright, *Probabilistic genotyping software: An overview* (Jan. 2019) vol. 38, Forensic Science International: Genetics 219; and (3) Bright et al., *Internal validation of STRmix™—A multi laboratory response to PCAST* (May 2018) vol. 34, Forensic Science International: Genetics 11. (*Ibid.*) Further, observed the court, "[t]estimony at the hearing established that the STRmix method

has been subjected to extensive empirical testing and found to be accurate and reliable by the FBI and numerous forensic laboratories." (*Ibid*.)

To the contrary, no evidence had been presented by defendant Davis in the trial court "showing that the STRmix method is publicly opposed as unreliable by scientists significant either in number or expertise." (*Davis*, *supra*, 75 Cal.App.5th at p. 717.) In particular, the Court of Appeal considered the impact of a draft report issued by the National Institute of Standards and Technology (NIST), "a nonregulatory scientific research agency within the United States Department of Commerce." (*Ibid*.) That report, titled *DNA Mixture Interpretation: A NIST Scientific Foundation Review* (2021), had opined that "there is currently not enough publicly available data to enable an external and independent assessment of the degree of reliability of DNA mixture interpretation practices, including the use of probabilistic genotyping software systems." (*Id*. at p. 718.) The reason for that dearth of data, the NIST report explained, was that forensic laboratories typically do not publish their internal validation data. (*Ibid*.) The *Davis* court, having scrutinized the NIST report and public comments submitted in response to the draft, concluded that the report did "not show that the STRmix method has failed to gain general acceptance in the relevant scientific community." (*Id*. at pp. 718-719.) Indeed, the report offered no opinion "as to whether STRmix is a reliable method of DNA mixture interpretation." (*Id*. at p. 719.) Nothing about the draft NIST report altered the Court of Appeal's conclusion that STRmix had been generally accepted by the relevant scientific community. (*Id*. at p. 719.)

Other case law, and academic commentary, had also emerged on the admissibility of probabilistic genotype software. One 2017 journal article, based on the author's research into the issue, asserted that "[c]ourts have nearly universally admitted the results of these programs over objection in *Frye/Daubert* litigation, [fn] and in at least one case, a defendant used results to convince prosecutors to support vacating his conviction [fn]." (Roth, Machine Testimony (2017) 126 Yale L.J. 1972, 2019 & fn. 247; see *United States v. Gissantaner* (6th Cir. 2021) __ F.3d __ [2021 U.S.App. Lexis 6465, *17-*18 [STRmix "has garnered wide use in forensic laboratories across the country. More than 45 laboratories use it, including the FBI and many state law enforcement agencies. At this point, STRmix is the 'market leader in probabilistic genotyping software.' [Citation.] [¶] Consistent with this reality, numerous courts have admitted STRmix over challenges to its general acceptance in the relevant scientific community"] United States v. Tucker (E.D.N.Y. 2020, 18 CR 0119) 2020 U.S. Dist. Lexis 3055, *8-*13 [discussing STRmix® admissibility and reviewing related decisions across jurisdictions]; United States v. Lewis (D.Minn. 2020, 18-cr-194) 2020 U.S. Dist. Lexis 38705 [extensive discussion of probabilistic genotyping software and related admissibility issues]; State v. Simmer (Neb. 2019) 935 N.W.2d 167 [same]; United States v. Gissantaner (W.D. Mich. 2019) 417 F.Supp.3d 857 [STRmix® results not admissible under Daubert analysis]; People v. Bullard-Daniel, 54 Misc. 3d 177, 42 N.Y.S.3d 714 (County Ct. 2016) [STRmix software admissible under *Frye* test]; Note: The Admissibility of TrueAllele: A Computerized DNA Interpretation System (2015) 72 Wash. & Lee L. Rev. 1033; State v. Wakefield, 47 Misc. 3d 850, 9 N.Y.S.3d 540 (Sup 2015) [TrueAllele software admissible under *Frye* test].)

Courts and commentators have also devoted attention to questions of discovery related to this kind of interpretive software; in particular, whether the manufacturer's "source code" and other programming details must be provided to the opponent of the evidence in order to provide a sufficient basis on which to understand and potentially challenge the reliability of results. (See Imwinkelried, Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques (2016) 66 DePaul L. Rev. 97; see People v. Davis, 75 Cal. App. 5th 694, 721–722, 290 Cal. Rptr. 3d 661 (3d Dist. 2022), review denied, (June 1, 2022) ["a defendant in a criminal matter may obtain access to the STRmix source code under a nondisclosure agreement"].) For a discussion of California case authority addressing the prosecution's discovery obligations related to commercial mixture interpretation software, see Chapter 10:1, subsection 4, ante.

Note, however, that courts continue to carefully scrutinize proffered mixture interpretation evidence, and may exclude it in cases where laboratories become overly aggressive and interpret complex mixtures in ways not supported by their own validated protocols. An example of this is found in United States v. Williams (N.D. Cal. 2019) 382 F.Supp.3d 928. Williams involved a pretrial defense motion to exclude prosecution evidence that a defendant contributed DNA to a mixed sample. The sample had been interpreted with a probabilistic genotyping program called Bullet. The question presented to the court was "whether Bullet was validated to analyze the mixture at issue here." (*Id.* at p. 929.) The court concluded that it was not, because the mixture in

the case may have consisted of more than four contributors, while the Bullet program had been validated by the laboratory only for mixtures of up to four contributors. (*Id.* at pp. 929, 931.) Ultimately, the question was one of reliability under Rule 702 of the Federal Rules of Evidence. (*Id.* at p. 935.) Based on the body of evidence presented, the court found that the DNA analyst "did not reliably conclude that only four individuals contributed DNA to the mixture at issue." (*Id.* at p. 936.) Of significance to the court was evidence that SERI, the laboratory in question, "demonstrated an inability to distinguish five-person mixtures from four-person mixtures. During the GlobalFiler validation study, it did not correctly identify a single five-person mixture. [The analyst] asserted that these errors occurred because 'by coincidence,' the individuals who contributed DNA to the study shared alleles. But a 100% rate of error gives no confidence in SERI's ability to be accurate if faced with the same coincidence in the real world." (*Id.* at p. 937.)

Footnotes

1 Restriction Fragment Length Polymorphism.

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§ 11:8. *Daubert v. Merrell Dow Pharmaceuticals, Inc.*

In its 1993 decision, Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469, 37 Fed. R. Evid. Serv. 1 (1993), the United States Supreme Court overruled Frye and changed the manner in which the admissibility of scientific evidence is determined in federal courts. In Daubert, plaintiffs filed a civil lawsuit in federal court against the manufacturer (Merrell Dow) of an anti-nausea drug, claiming that the drug's use caused birth defects. Merrell Dow moved for summary judgment, supported by a declaration from an expert epidemiologist who asserted that no relevant published studies concluded that the drug could cause complications in fetal development. The plaintiffs submitted opposing expert declarations disagreeing with that interpretation of the literature. The declarations cited unpublished studies indicating a causal link between Merrell Dow's drug and fetal malformations.

The district court granted Merrell Dow's motion for summary judgment, finding that plaintiffs' proffered scientific evidence did not satisfy Frye's "general acceptance" standard. The Ninth Circuit Court of Appeals affirmed (see Daubert v. Merrell Dow Pharmaceuticals, Inc., 951 F.2d 1128, 34 Fed. R. Evid. Serv. 1145 (9th Cir. 1991), judgment vacated, 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469, 37 Fed. R. Evid. Serv. 1 (1993)), but the Supreme Court reversed.

The Supreme Court held that the Frye test was superseded by enactment of the Federal Rules of Evidence in 1975. (See 28 U.S.C.A.) Addressing expert witness testimony, rule 702 of the Federal Rules of Evidence states that, "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise." Nothing in this rule, observed the Supreme Court,

> establishes "general acceptance" as an absolute prerequisite to admissibility. Nor does [Merrell Dow] present any clear indication that Rule 702 or the Rules as a whole were intended to incorporate a "general acceptance" standard. The drafting history makes no mention of *Frye*, and a rigid "general acceptance" requirement would be at odds with the "liberal thrust" of the Federal Rules and their "general approach of relaxing the traditional barriers to 'opinion' testimony." [Citations.] … Given the Rules' permissive backdrop and their inclusion of a specific rule on expert testimony that does not mention "general acceptance," the assertion that the Rules somehow assimilated *Frye* is unconvincing.

(*Daubert*, 509 U.S. at 588–589.) The Daubert Court concluded that Frye's "austere standard" was "absent from and incompatible with the Federal Rules of Evidence, [and] should not be applied in federal trials." (*Daubert*, 509 U.S. at 589, fn. omitted.)

In place of Frye's general acceptance standard, the Daubert Court set forth a series of factors that federal trial courts may consider —but which do not represent a definitive checklist—when screening scientific evidence for both relevance and evidentiary trustworthiness within the meaning of rule 702 of the Federal Rules of Evidence.[1] These factors are aimed at permitting the trial court to determine whether the proposed scientific evidence "supported by appropriate validation—i.e., 'good grounds,' based on what is known." (*Daubert*, 509 U.S. at 590.) No one factor's presence or absence is necessarily dispositive of the question. The factors are:

1) Whether the scientific theory or technique can be or has been tested;

2) Whether the theory or technique has been subjected to peer review and publication;

3) The known or potential rate of error, and whether standards exist for the technique's use;

4) General acceptance in the relevant scientific community.
(*Daubert*, 509 U.S. at 593–594; see also Kumho Tire Co., Ltd. v. Carmichael, 526 U.S. 137, 119 S. Ct. 1167, 143 L. Ed. 2d 238, 50 Fed. R. Evid. Serv. 1373 (1999) [applying Daubert standard to technical, as opposed to scientific, expert evidence].) The Daubert Court emphasized that a rule 702 inquiry in this regard is "a flexible one. Its overarching subject is the scientific validity —and thus the evidentiary relevance and reliability—of the principles that underlie a proposed submission. The focus, of course, must be solely on principles and methodology, not on the conclusions that they generate." (*Daubert*, 509 U.S. at 594–595.)

Footnotes

1 "We are confident that federal judges possess the capacity to undertake this review. Many factors will bear on the inquiry, and we do not presume to set out a definitive checklist or test." (509 U.S. at 593.)

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§ 11:9. Chain of custody considerations

When physical evidence has been subjected to scientific analysis, the proponent of the evidence must make a foundational showing that the evidence tested was in fact the evidence collected during the investigation of the crime. This showing is essential to establishing the relevance of the forensic science testimony. In California, "[t]he burden on the party offering the evidence is to show to the satisfaction of the trial court that, taking all the circumstances into account including the ease or difficulty with which the particular evidence could have been altered, it is reasonably certain that there was no alteration. The requirement of reasonable certainty is not met when some vital link in the chain of possession is not accounted for, because then it is as likely as not that the evidence analyzed was not the evidence originally received." (People v. Riser, 47 Cal. 2d 566, 580–581, 305 P.2d 1 (1956) (overruled in part by, People v. Chapman, 52 Cal. 2d 95, 338 P.2d 428 (1959)) and (overruled in part by, People v. Morse, 60 Cal. 2d 631, 36 Cal. Rptr. 201, 388 P.2d 33, 12 A.L.R.3d 810 (1964)).)

Chain of custody considerations apply to biological evidence with equal force. In People v. Johnsen (2021) 10 Cal.5th 1116 the California Supreme Court considered a DNA-related chain of custody claim. In processing a murder scene, investigators collected a pair of pantyhose. Upon closer inspection, a criminalist in the Department of Justice's Modesto laboratory discovered a hair in them. (*People v. Johnsen*, 10 Cal.5th at 1159.) After microscopic examination at another laboratory, the hair was placed in a plastic petri dish which was then sealed with tape. (*People v. Johnsen*, 10 Cal.5th at 1159.) Later, the same criminalist inadvertently broke the hair into two pieces when he unsealed the petri dish to photograph the hair. (*People v. Johnsen*, 10 Cal.5th at 1160.) A detective transported the hair evidence to another laboratory for DNA testing. (*People v. Johnsen*, 10 Cal.5th at 1160.) Upon examining the two hair fragments, the DNA lab analyst observed what she thought were two hairs, both of which appeared to have roots. (*People v. Johnsen*, 10 Cal.5th at 1160.) She severed the "root" ends of both hair fragments and combined them for DNA testing. (*People v. Johnsen*, 10 Cal.5th at 1160.) The results of that testing were introduced at trial. (*People v. Johnsen*, 10 Cal.5th at 1160.) On appeal, the defendant argued that, because "it is factually impossible to break a single hair with one root end into two hairs each with root ends. . . the presence of two hairs each with root ends is clear evidence of tampering." (*People v. Johnsen*, 10 Cal.5th at 1161.) The Supreme Court rejected that claim. It held that testimony from the criminalist who accidently broke the hair was "'at least a prima facie showing that the evidence had not been tampered with,' at least not in any way that could alter the subsequent forensic analysis." (*People v. Johnsen*, 10 Cal.5th at 1161.) Aside from the DNA analyst's testimony that she may have seen two root ends, nothing in the record supported the defendant's theory of tampering. (*People v. Johnsen*, 10 Cal.5th at 1161-1162.) The Johnson court concluded the "trial court properly held that testimony about the hair was admissible and that the discrepancies, if any, raised by [the DNA analyst's] visual perception go to the weight of that evidence." (*People v. Johnsen*, 10 Cal.5th at 1162.)

In People v. Jimenez, 165 Cal. App. 4th 75, 80 Cal. Rptr. 3d 579 (5th Dist. 2008), a DNA sample was collected from the handlebars of a bicycle used by a bank robber for his getaway. Investigators instructed an evidence technician to take a buccal (inner cheek) swab sample from suspect Jiminez for case investigation purposes, but the record was insufficient as to who actually took, labeled, and sealed the swabs, how the swabs were transmitted to the crime laboratory, and the condition of the swabs upon arrival at the laboratory. (165 Cal. App. 4th at 80–81.) Accordingly, the Jiminez court held that the foundational showing of an adequate chain of custody had not been made and the trial court abused its discretion in allowing into evidence the reference sample DNA profile for comparison to DNA from the bicycle. (165 Cal. App. 4th at 81.)

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Chapter 11. Admissibility of DNA Evidence at Trial

§ 11:10. Scientific evidence and the confrontation clause

In view of the growing rate of DNA database matches in cold cases that may be many years—if not decades—old, and because DNA casework is increasingly performed by a team of analysts that processes samples in batches along an "assembly line," prosecutors often attempt to present DNA evidence in court in the absence of one or more of the laboratory analysts who physically tested the sample(s) at issue. Whether the defendant has a Sixth Amendment Confrontation Clause right to cross-examine the testing analyst and, if so, under what circumstances have become contentious issues in both state and federal courts nationally.

The United States Supreme Court thus far has issued three opinions addressing the intersection of forensic science and the Confrontation Clause: Melendez-Diaz v. Massachusetts, 557 U.S. 305, 129 S. Ct. 2527, 174 L. Ed. 2d 314 (2009); Bullcoming v. New Mexico, 131 S. Ct. 2705, 180 L. Ed. 2d 610 (2011), and Williams v. Illinois, 132 S. Ct. 2221, 183 L. Ed. 2d 89 (2012). The High Court is sharply divided on these matters, however, with the first two cases decided on a 5-4 split, followed by a 4-1-4 division among the justices in *Williams*. It is very likely that the United States Supreme Court will grant review in additional cases in an effort to provide clearer guidance to lower courts. In the meantime, in light of and following the decision in *Williams v. Illinois*, the California Supreme Court and lower California appellate courts have taken up the issue in a series of decisions.

1) From *Crawford* to *Melendez-Diaz*; *People v. Geier*

The confrontation clause states that "[i]n all criminal prosecutions, the accused shall enjoy the right … to be confronted with the witnesses against him." (U.S. Const., 6th Amend.) Before Crawford v. Washington, 541 U.S. 36, 124 S. Ct. 1354, 158 L. Ed. 2d 177, 63 Fed. R. Evid. Serv. 1077 (2004), was decided, the right to confront prosecution witnesses existed up to the point where out-of-court statements fell within a "firmly rooted hearsay exception" or bore "particularized guarantees of trustworthiness." (Ohio v. Roberts, 448 U.S. 56, 66, 100 S. Ct. 2531, 65 L. Ed. 2d 597, 7 Fed. R. Evid. Serv. 1 (1980) (abrogated by, Crawford v. Washington, 541 U.S. 36, 124 S. Ct. 1354, 158 L. Ed. 2d 177, 63 Fed. R. Evid. Serv. 1077 (2004)).) In Crawford, however, those limitations on the confrontation right were supplanted by a bar on admission of any out-of-court statement classified as "testimonial," unless the declarant is unavailable and the defendant had a prior opportunity to cross-examine the declarant regarding the statement. While Crawford did not provide a comprehensive definition of "testimonial," it set forth various examples of evidence that would fall—or not—into the category of statements from one who "bear[s] testimony. Examples of testimonial evidence, noted the Court, include:

> [*E*]*x parte* in-court testimony or its functional equivalent—that is, material such as affidavits, custodial examinations, prior testimony that the defendant was unable to cross-examine, or similar pretrial statements that declarants would reasonably expect to be used prosecutorially … extrajudicial statements … contained in formalized testimonial materials, such as affidavits, depositions, prior testimony, or confessions … statements that were made under circumstances that would lead an objective witness reasonably to believe that the statement would be available for use at a later trial … .

(Crawford v. Washington, 541 U.S. 36, 51–52, 124 S. Ct. 1354, 158 L. Ed. 2d 177, 63 Fed. R. Evid. Serv. 1077 (2004).) Business records, however, were deemed to be non-testimonial evidence. (41 U.S. at 56.)

In sum, Crawford abandoned considerations of reliability when determining whether the confrontation clause tolerates proffered hearsay statements. Instead, cross-examination of the person who makes a testimonial statement was enshrined as a procedural guarantee. The confrontation clause exists, stated the Court, "to ensure reliability of evidence" by exposing it to the "crucible of cross-examination." (541 U.S. at 61.)

The application of Crawford to situations where a prosecution witness other than the analyst who performed laboratory work testifies to the test results at trial soon became an issue. In some cases, prosecutors would seek to admit the original analyst's report to supplement such testimony, and sometimes would rely on expert witness testimony alone. The California Supreme Court addressed the topic in 2007 in People v. Geier, 41 Cal. 4th 555, 61 Cal. Rptr. 3d 580, 161 P.3d 104 (2007). In Geier, a DNA laboratory supervisor who had not performed the testing but who had reviewed the original analyst's report testified at trial. Geier held that although the DNA analysis report at issue was generated in response to law enforcement requests and for possible use at a criminal trial, it was a "contemporaneous recordation of observable events" and thus distinguishable from testimonial witness statements that recount past events related to criminal activity. (41 Cal. 4th at 605–606.) "[T]he critical inquiry," noted the court, "is not whether it might be reasonably anticipated that a statement will be used at trial but the circumstances under which the statement was made." (41 Cal. 4th at 607.)

The Geier court noted also that the accusatory DNA match evidence was "reached and conveyed not through the nontestifying technician's laboratory notes and report, but by the testifying witness, [the lab director]." (41 Cal. 4th at 607.) "As an expert witness, [the DNA expert] was free to rely on [the testing analyst's] report in forming her own opinions regarding the DNA match." (41 Cal. 4th at 608.) Thus, the witness in Geier was providing evidence of the DNA test results as an independent expert, and not as a mere conduit for another person's scientific conclusions.

A different forensic science scenario, however, was presented in 2009 by Melendez-Diaz v. Massachusetts, 129 S. Ct. 2527, 174 L. Ed. 2d 314 (2009). There, the Court held by a 5-4 margin that admission of a sworn affidavit ("certificate") from a state crime laboratory, identifying a controlled substance seized from the defendant, qualified as "testimonial" evidence that should have been subject to confrontation through "the analysts" who performed the testing. (129 S.Ct. at 2532.) The Melendez-Diaz majority characterized the certificate at issue as "functionally identical to live, in-court testimony," which Crawford had deemed the "'core class of testimonial statements.'" (*Ibid.*) A defendant cannot cross-examine a certificate, however, and thus the defendant was unable to challenge the "honesty, proficiency, and methodology" of the analyst(s) who did the laboratory work in order to "weed out not only the fraudulent analyst, but the incompetent one as well." (129 S.Ct. at 2537, 2538.) A central premise of Melendez-Diaz was that the drug test certificate acted as a direct evidentiary substitute for the analyst's testimony.

Justice Thomas, in a concurring opinion, noted that he had joined the majority because he understood its opinion to address only the constitutional implications of "'formalized testimonial materials, such as affidavits, depositions, prior testimony, or confessions.'" (129 S.Ct. at 2543 (conc. opn. of Thomas, J.).) Justice Thomas did not view the majority opinion as rendering inadmissible any "extrajudicial statements" not "contained in formalized testimonial materials … ."[1] (*Ibid.*)

Finally, Melendez-Diaz emphasized that the drug certificates at issue were "testimonial" in part because Massachusetts law expressly contemplated their preparation for use as evidence at trial. (129 S.Ct. at 2532 [noting that the drug certificates were prepared for the "sole purpose" of prosecuting those accused of drug crimes].) The underlying reason a document is prepared thus became a key criterion in determining its testimonial (or nontestimonial) status. (See also 129 S.Ct. at 2539–2540 ["Business and public records are generally admissible absent confrontation … because—having been created for the administration of an entity's affairs and not for the purpose of establishing or proving some fact at trial—they are not testimonial"].)

2) *Bullcoming v. New Mexico*

In June 2011, the United State Supreme Court decided Bullcoming v. New Mexico, 131 S. Ct. 2705, 180 L. Ed. 2d 610 (2011). Bullcoming involved a New Mexico DUI trial in which the "[p]rinciple evidence" against the defendant was a laboratory blood alcohol concentration (BAC) report generated by an analyst who had been placed on unpaid leave before trial and did not testify. (131 S.Ct. at 2709, 2711–2712.) His BAC report was admitted as a business record. The trial witness was a lab colleague who had not participated in or observed the testing. The New Mexico Supreme Court held that an analyst who had no involvement in the preparation of a forensic alcohol report could testify to the standard procedures used at the lab to record blood-alcohol levels, the testing methods, and defendant's blood-alcohol level at the time of the test without violating the confrontation clause. (131 S.Ct. at 2712–2713.)

The United States Supreme Court disagreed and reversed in a 5-4 opinion. The Court held that the BAC report was the testimonial statement of the original analyst within the meaning of Crawford; thus its admission into evidence in his absence —where there was no showing that the analyst was unavailable and that the defense had a prior opportunity to cross-examine him—violated the defendant's confrontation clause rights. The analyst who prepared the report, observed the Court, was not a "mere scrivener" who simply transcribed machine data. He also made a number of representations about how the test was conducted that were ripe for exploration through cross-examination. (131 S.Ct. at 2714.) In any event, any inherent reliability of transcribed instrument data is still subject to testing in the "'crucible of cross-examination.'" (131 S.Ct. at 2715.) Only four justices signed on to footnote six, which reiterated that the defining characteristic of a testimonial statement is its "'primary purpose' of 'establish[ing] or prov[ing] past events potentially relevant to later criminal prosecution.'" (131 S.Ct. at 2714, quoting Davis v. Washington, 547 U.S. 813, 822, 126 S. Ct. 2266, 165 L. Ed. 2d 224, 70 Fed. R. Evid. Serv. 472, 30 A.L.R.6th 599 (2006).

The Bullcoming Court also pointed out that the trial witness in this case was not able to "convey what [the original analyst] knew or observed about … the particular test and the testing process he employed," or identify failures or fraud on the part of the original analyst. (131 S.Ct. at 2715.) The Court noted, moreover, that the state did not "assert that [the testifying witness] had any "'independent opinion' concerning Bullcoming's BAC." (131 S.Ct. at 2716.) The Court thus drew a distinction between questioning an expert offering an independent opinion, and "questioning one witness about another's testimonial statements … ." (*Ibid*.) The opinion hinged on the fact that the prosecution relied on the original analyst's report as evidence: "In short, when the State elected to introduce [the original analyst's] certification, [the original analyst] became a witness Bullcoming had the right to confront." (*Ibid*.)

Finally, the Bullcoming Court rejected the argument that BAC reports are non-testimonial documents, finding that the report at issue resembled "[i]n all material respects" the drug analysis certificate deemed testimonial in Melendez-Diaz. (131 S.Ct. at 2717.) The fact that the report in Bullcoming was not sworn or notarized was considered immaterial.

Justice Sotomayor filed a concurring opinion in Bullcoming in part "to emphasize the limited reach of the Court's opinion." (131 S.Ct. at 2719.) She highlighted four factual scenarios not presented for consideration nor resolved by the majority's opinion:

1) Where the state contends that an alternate, or even primary, purpose for a report is unrelated to generating evidence for a subsequent prosecution;

2) Where the trial witness actually played a role in the forensic analysis, whether as an observer or supervisor;

3) Where the trial witness provides an independent expert opinion concerning another analyst's reports *not* admitted into evidence. Justice Sotomayor cited rule 703 of the Federal Rules of Evidence, analogous to rule 801(b) of the California Evidence Code, as authority for this circumstance, while emphasizing that in Bullcoming "the State does not assert that [the trial witness] offered an independent, expert opinion about Bullcoming's blood alcohol concentration." "We would face a different question if asked to determine the constitutionality of allowing an expert witness to discuss others' testimonial statements if the testimonial statements were not themselves admitted as evidence;" and

4) Where a machine generated printout of results, such as that from a gas chromatograph, is introduced by itself without the context of a related report.

3) *Williams v. Illinois*

In June 2012, the United States Supreme Court decided Williams v. Illinois, 132 S. Ct. 2221, 183 L. Ed. 2d 89 (2012). There had been widespread hope that *Williams* would bring a measure of clarity to the Supreme Court's Confrontation Clause jurisprudence as it relates to expert witness testimony. It did not. Instead, the decision revealed a severely fractured Court on the issues presented. As Justice Kagan summarized in her dissent, "What comes out of four Justices' [the plurality's] desire to limit *Melendez-Diaz* and *Bullcoming* in whatever way possible, combined with one Justice's [Thomas's] one-justice view of those holdings, is—to be frank—who knows what." (132 S. Ct. at 2277.) Nonetheless, several inferences—albeit limited—can be made about the state of the law in the wake of *Williams*.

In *Williams*, the Illinois State Police DNA Laboratory had outsourced the DNA casework in a Chicago rape case to a private laboratory, Cellmark, located in another state. When a state DNA database hit later identified Williams as the perpetrator, the trial evidence consisted, in part, of a supervisor from the Illinois laboratory testifying about Cellmark's analysis of the crime scene DNA samples. The witness confirmed that she had reviewed the Cellmark DNA analysis, and she described Cellmark's proficiencies, quality controls, and calibration standards. She noted that she had personally developed protocols for Cellmark and that her laboratory staff routinely relied on Cellmark results. Moreover, the Illinois State Police supervisor had scrutinized the test records for contamination and chain-of-custody issues. (132 S. Ct. at 2229–2230.)

A majority of the *Williams* Court (Justices Alito, Roberts, Breyer, Kennedy—the plurality—and Thomas—concurring in the result only—concluded that, given the specific factual circumstances of the case, expert testimony expressly relying upon the contents of a DNA laboratory report prepared by another lab did not violate the defendant's Sixth Amendment right to confront witnesses against him. (132 S. Ct. at 2244, 2255.) Justice Kagan pointed out, however, "in all except its disposition, [the plurality's] opinion is a dissent: Five Justices specifically reject every aspect of its reasoning and every paragraph of its explication." (*Id*. at 2265.) Nonetheless, following *Williams* a forensic science report may or may not be testimonial, depending upon the purpose for which it was made and the degree of formality it embodies.

Five Justices in *Williams* viewed the "primary purpose test" through a similar lens. The dissent drew upon the Court's statement in Davis v. Washington, 547 U.S. 813, 822, 126 S. Ct. 2266, 165 L. Ed. 2d 224, 70 Fed. R. Evid. Serv. 472, 30 A.L.R.6th 599 (2006), that testimonial statements are made "for the primary purpose of establishing 'past events potentially relevant to later criminal prosecution'—in other words, for the purpose of providing evidence." (*Williams*, *supra*, 132 S. Ct. at 2273.) In his concurring opinion Justice Thomas articulated the test as assessing whether the declarant "primarily intend[ed] to establish some fact with the understanding that his statement may be used in a criminal prosecution." (*Id*. at 2261.)

In addition, the more "formal" or "solemn" a laboratory report is, the more likely it will be considered testimonial evidence and thus inadmissible (by itself or through witness references to its contents), absent the opportunity to cross-examine the author. Indicia of formality include the report being a sworn or certified declaration of fact, or where the report attests to or certifies its own truth or accuracy, or where the report is produced in response to formalized dialog with law enforcement. Justice Thomas opined in his concurrence that "the Confrontation Clause reaches 'formalized testimonial materials,' such as depositions, affidavits, and prior testimony, or statements resulting from 'formalized dialogue,' such as custodial interrogation." (*Williams, supra*, 132 S. Ct. at 2259–2260.) The Cellmark report was not formal enough for Justice Thomas to view it as testimonial; hence his concurrence with the plurality in affirming the lower court's judgment. (132 S. Ct. at 2260.)

The four Justices in the plurality did not delve deeply into the question of formality in *Williams* because they agreed that the Cellmark report was not made with the necessary primary purpose that would potentially qualify it as testimonial. (132 S. Ct. at 2242–2244.) They noted, however, that "[t]he Cellmark report is very different from the sort of extrajudicial statements,

such as affidavits, depositions, prior testimony, and confessions, that the Confrontation Clause was originally understood to reach." (*Id*. at 2228.) The reasoning of these four Justices is more apparent based on their views expressed in the predecessor case *Bullcoming*. There, as dissenters, Justices Kennedy, Alito, and Breyer, and Chief Justice Roberts concluded that "impartial lab reports like the instant one, reports prepared by experienced technicians in laboratories that follow professional norms and scientific protocols," are not the products of "formal interrogation in preparation for trial" that the confrontation clause guards against. (*Bullcoming, supra*, 131 S. Ct. at 2726 (dis. opn. of Kennedy, J.); see also *id*. at 2723–2724 [finding significance in the fact that the *Bullcoming* lab report was not a "sworn statement," in contrast to the documents in *Melendez-Diaz*, which were "quire plainly affidavits"].)

In sum, while acknowledging the disparate positions staked out by members of the Court in *Williams*, it is nonetheless likely that some aspects of a report or a lab file are testimonial because they possess both the requisite formality and primary purpose (*e.g.*, a formal conclusion or opinion concerning the significance of the testing), while some aspects are not (*e.g.*, transcription of raw data and bench notes).

Finally, it is a significant development in *Williams* that five Justices (Justices Kagan, Ginsburg, Sotomayor, Scalia—the dissent—and Thomas—concurring with the plurality's result only—also representing a majority of the Court) concluded that when an expert witness repeats statements made by another person as a basis for her opinion, the truth of those statements necessarily matters to the fact finder. (132 S. Ct. at 2257, 2268–2269.)

4) The California Supreme Court: *People v. Lopez*; *People v. Dungo*

In October 2012, the California Supreme Court weighed in with two landmark decisions on the scope of Confrontation Clause protections as they relate to forensic science test results and observations. Both cases, People v. Lopez, 55 Cal. 4th 569, 147 Cal. Rptr. 3d 559, 286 P.3d 469 (2012), petition for cert. filed (U.S. Jan. 12, 2013), and People v. Dungo, 55 Cal. 4th 608, 147 Cal. Rptr. 3d 527, 286 P.3d 442 (2012), as modified on denial of reh'g, (Dec. 12, 2012), hold that some aspects of forensic science and autopsy reports may lack either the formality, the primary purpose, or both necessary to render them "testimonial" within the meaning of *Crawford v. Washington*.

People v. Lopez, *supra*, involved prosecution of a drunk driving manslaughter case pursuant to Penal Code section 191.5, subdivision (b). The blood alcohol analyst was unavailable for trial. Instead, a laboratory colleague testified that he had reviewed the other expert's BAC report "based on his own 'separate abilities as a criminal analyst,'" and agreed with his colleague that the defendant's blood sample contained a .09% blood-alcohol concentration. (55 Cal. 4th at 574.) The trial court admitted the blood alcohol report into evidence. (*Ibid*.)

The *Lopez* court held, first, that whether a statement is a "contemporaneous recordation of observable events," which lay at the heart of People v. Geier, 41 Cal. 4th 555, 61 Cal. Rptr. 3d 580, 161 P.3d 104 (2007), is no longer a relevant mode of analysis. (*Lopez*, *supra*, 55 Cal. 4th at 581.) *Lopez* went on to opine that "critical portions" of the blood alcohol report lacked the requisite formality and solemnity to be testimonial under the United States Supreme Court's string of forensic science confrontation clause cases. (*Id*. at 582.) Such portions included instrument calibration data, gas chromatography quality control information, and raw data printouts from the testing instrumentation. (*Id*. at 583.) Moreover, a chain of custody log sheet linking the defendant to the laboratory's identifying sample number "is nothing more than an informal record of data for internal purposes, as is indicated by the small printed statement near the top of the chart: 'for lab use only.'" "Such a notation," concluded the court, "is not prepared with the formality required by the high court for testimonial statements." (*Id*. at 584.) Accordingly, held the court, admission into evidence of the blood alcohol report in the absence of testimony from the primary analyst did not violate the Confrontation Clause. (*Id*. at 585.)

People v. Dungo, *supra*, involved a murder trial in San Joaquin County. The prosecution elected not to call as a witness the pathologist who performed the autopsy, who had been fired from his most recent position, and had left a prior position in another county "under a cloud." (55 Cal. 4th at 614.) Another pathologist, who owned the company the original pathologist worked

for, testified instead. (*Id*. at 613.) The trial witness offered independent opinions about the cause and manner of death based on observations recorded in the original pathologist's autopsy report—which he relayed to the jury—as well as on photographs taken during the autopsy. (*Id*. at 614.) Significantly, the trial expert opined that the victim had been strangled for more than two minutes because, although she died from asphyxia caused by strangulation, her hyoid bone was not broken. (*Ibid*.) The original pathologist had noted the condition of the hyoid bone, but had not expressed an opinion in his report about the duration of the strangulation. The report itself was not offered into evidence. (*Id*. at 615.)

The California Supreme Court held that the defendant's Confrontation Clause rights had not been violated. In doing so, it parsed the contents of the autopsy report into separate categories. First, the report contained factual statements about the condition of the body, including toxicological tests and microscopic examinations. Second, the report contained conclusions and interpretive findings about the cause and manner of death. (55 Cal. 4th at 619.) Because the trial witness did not reiterate the original pathologist's cause of death conclusions, however, the *Dungo* court did not address the testimonial status of those statements. It did hold, though, that objective observations and measurements recorded in an autopsy report are not testimonial. They are comparable to medical records generated by a treating physician, and thus lack the formality and solemnity required of testimonial statements. (*Ibid*.) Moreover, the primary purposes of autopsy reports are many, and are governed by statutory mandates that require their creation as part of a duty to investigate certain deaths regardless of cause and for reasons—such as public health, insurance claims, and civil liability determinations—that transcend the criminal justice system. (*Id*. at 620–621.) Thus the primary purpose test is not met for objective recordation of physiological facts in an autopsy report. (*Id*. at 621.)

The California Court of Appeal applied and followed *Dungo* in People v. Ford, 235 Cal. App. 4th 987, 185 Cal. Rptr. 3d 898 (1st Dist. 2015), review denied, (July 22, 2015) and petition for certiorari filed (U.S. Oct. 13, 2015). *Ford* involved a 1981 murder. By the time of the 2012 trial, the pathologist who had performed the autopsy was deceased. (235 Cal.App.4th at pp. 989–990.) Consequently, the People presented testimony, over defense objection, from the physician serving as Chief Medical Examiner in 2012. The appellate court, citing *Dungo*, affirmed the trial court's admission into evidence of the 1981 autopsy report. (*Id*. at p. 995.) Notably, the court pointed out that the trial court had redacted the original pathologist's conclusions from the report. (*Id*. at p. 997.) Also, the appellate court confirmed that the descriptions of injuries to the victim observed and recorded by the original pathologist were nontestimonial observations, and not testimonial conclusions. (*Id*. at p. 996.) But in subsequent commentary about the state of confrontation clause jurisprudence, the *Ford* court opined that *Dungo*'s distinction between a pathologist's observations and conclusions "may prove difficult to defend over time and is hardly self-evident." (*Id*. at p. 998.) The court further expressed skepticism of the propositions that scientific or medical observations are inherently less "'formal and solemn'" than attendant conclusions, and that the primary purpose of an autopsy is not to gather evidence for trial. (*Ibid*.) The *Ford* court speculated that "it may well require a change in the composition of the [United States Supreme Court" to clarify "admissibility of expert basis evidence contained in an autopsy report prepared by an absent pathologist," but recommended that experts in pathology nonetheless commence work on "modification of the autopsy protocol that will produce both a more reliable record and one designed to survive even a broad definition of testimonial." (*Ibid*.)

Another California case applying state and federal confrontation clause jurisprudence in a forensic science context is People v. Ogaz (2020) 53 Cal.App.5th 280. In *Ogaz*, a county crime laboratory forensic scientist conducted testing of suspected controlled substances seized by police. (53 Cal.App.5th at 285.) She issued a signed report identifying the substances as heroin and methamphetamine and quantified them. (*People v. Ogaz*, 53 Cal.App.5th at 285) The testing analyst did not testify at trial. Rather, testimony was provided by the laboratory supervisor who had reviewed the testing analyst's report—and that report was received as evidence. (*People v. Ogaz*, 53 Cal.App.5th at 285-286.) The Court of Appeal first held that the testing report was received in error because it was signed by the analyst and "contain[ed] the substantive conclusions [the analyst] reached as a result of the testing she conducted, which is precisely what she would have been expected to testify about had she appeared at trial. It cannot be gainsaid that her report served as the functional equivalent of live, in-court testimony." (*People v. Ogaz*, 53 Cal.App.5th at 291.) Moreover, the primary purpose of the report appeared to be criminal prosecution, rendering the report testimonial for Sixth Amendment purposes. (*People v. Ogaz*, 53 Cal.App.5th at 292.)

The *Ogaz* court held the witness's testimony was also received in violation of the confrontation clause. The trial witness described his own extensive experience in the field, as well as the laboratory methods, procedures, and instrumentation used by the analyst in that case. (*People v. Ogaz*, 53 Cal.App.5th at 285-286.) He offered his opinions that the testing was correctly performed and that he had no "concerns" with the reported results. (*People v. Ogaz*, 53 Cal.App.5th at 286.) That testimony, held the court, violated the confrontation clause:

> [The witness] could not be effectively cross-examined as to what [the analyst] saw or how she interpreted the information her testing produced. [¶] That wouldn't be a problem if [the witness] had formulated his own independent opinions based on the data that [the analyst] produced during the testing process. But this is not a situation where an expert witness reviewed the work of another analyst and came to his or her own conclusion about the matter at hand. [Citations.] [¶] In fact, [the witness] never offered any of his own personal opinions regarding the substances at issue in this case. What he did was simply recite to the jury the results [the analyst] obtained in her testing. In other words, he was a 'mere conduit' for [the analyst's] opinions.

(*People v. Ogaz*, 53 Cal.App.5th at 293.) In sum, the court held that "[w]hile an expert witness who forms his own opinions based on the reports of others creates an original product of substantive evidence that can be tested through cross-examination, that is not the case when, as here, the expert simply conveys the opinions of others." (*People v. Ogaz*, 53 Cal.App.5th at 294.)

5) Other Case Authority

In the wake of *Dungo* and *Lopez*, additional case authority has appeared that addresses the Confrontation Clause implications of forensic science testimony, including testimony from experts who discuss DNA testing performed by a nontestifying analyst.

In People v. Banks, 59 Cal. 4th 1113, 176 Cal. Rptr. 3d 185, 331 P.3d 1206 (2014), the defendant contended on appeal that his Sixth Amendment confrontation right was violated by the testimony of Dr. Robin Cotton of Cellmark Laboratory (incidentally, the same witness and lab at issue in *Williams v. Illinois*, *supra*), who testified about two DNA matches generated by other analysts at her laboratory. (*Id*. at pp. 1165–1166.) The court characterized Dr. Cotton's testimony as follows:

> First, she testified that she had reviewed the X-ray films of the DNA results generated by Cellmark analysts and, based on her independent review of those results, concluded that defendant's DNA matched Latasha W.'s assailant's. Nothing suggests that the X-ray films, which were prepared by other Cellmark analysts, were signed or attested to under oath. Second, Dr. Cotton testified that her conclusions were the same as those reached by the analysts who prepared the X-ray films, although no reports by those analysts were introduced into evidence.

(*Id*. at p. 1167.) Declining to rule on the merits of the confrontation clause claim, the court nonetheless noted that any error was harmless because Dr. Cotton provided independent expert testimony based on her own observations of the X-ray films, or, as the court put it, "objective scientific data." (*Id*. at p. 1168.) "Thus, under *Lopez* and *Dungo*, defendant has not demonstrated that Dr. Cotton's testimony as to her own conclusions based on the X-ray films violated defendant's right to cross-examination." (*Ibid*.)

In People v. Steppe, 213 Cal. App. 4th 1116, 152 Cal. Rptr. 3d 827 (4th Dist. 2013), opinion modified on denial of reh'g, (May 22, 2013) and review denied, (Mar. 26, 2013), the Court of Appeal held that DNA lab reports "lack the degree of formality and solemnity to be considered testimonial for purposes of the confrontation clause." (*Id*. at p. 1127.) As an independent reason for its conclusion that the testimony of a laboratory supervisor about a colleague's DNA analysis did not violate confrontation clause protections, the *Steppe* court cited the witness's role as the colleague's supervisor and reviewer of the results at the time of testing. (*Ibid*.)

In People v. Barba, 215 Cal. App. 4th 712, 155 Cal. Rptr. 3d 707 (2d Dist. 2013), cert. denied, 134 S. Ct. 628, 187 L. Ed. 2d 407 (2013), the Court of Appeal held that the Sixth Amendment's confrontation clause was not violated by testimony of a DNA laboratory director describing testing performed by an analyst who no longer worked for the lab. The witness had reviewed the analyst's test documentation, and then drew independent conclusions "based on her own expertise and training." (*Id*. at p. 718.) Four DNA test reports prepared by the absent analyst were received into evidence. (*Id*. at p. 719.) The court engaged in a lengthy summary of applicable United States Supreme Court and California Supreme Court precedent. It then extracted and applied principles of law to conclude that the witness's testimony, relying upon the absent analyst's DNA test reports, did not violate the confrontation clause because the reports lacked a "primary purpose" that would render them testimonial. (*Id*. at pp. 742–743.) The court listed the following reasons:

> (1) [the reports] were generated by a lab technician pursuant to standardized procedures; (2) even though Barba had been charged with the crime, lab technicians such as Wong have no idea what their results might show, and DNA testing is routinely used to inculpate or exonerate those charged with crimes; and (3) the accusatory opinions came from expert witness Reynolds, who was subject to vigorous cross-examination.

(*Id*. at p. 742.) "[I]t makes no sense," explained the court, "to exclude evidence of DNA reports if the technicians who conducted the tests do not testify. So long as a qualified expert who is subject to cross examination conveys an independent opinion about the test results, then evidence about the DNA tests themselves is admissible." (*Ibid*.) In any event, "defendants who question the validity of DNA test results have an additional safeguard available through their power to subpoena anyone who took part in the DNA testing process." (*Id*. at pp. 742–743.)

In People v. Holmes, 212 Cal. App. 4th 431, 150 Cal. Rptr. 3d 914 (2d Dist. 2012), review filed, (Jan. 25, 2013), the Court of Appeals considered a trial in which three DNA experts offered opinions, "over defense objection, based on DNA tests that they did not personally perform. They referred to notes, DNA profiles, tables of results, typing summary sheets, and laboratory reports that were prepared by nontestifying analysts. None of these documents was executed under oath. None was admitted into evidence. Each was marked for identification and most were displayed during the testimony. Each of the experts reached his or her own conclusions based, at least in part, upon the data and profiles generated by other analysts." (212 Cal. App. 4th at 434.) The court held that the laboratory reports, data, and other materials relied upon by the testifying experts lacked the formality required of testimonial statements. (*Id*. at 436 [referencing "notes, DNA profiles, tables of results, typed summary sheets, and laboratory reports prepared by others"], 438.) Rather, concluded the court, these materials "are unsworn, uncertified records of objective fact." (*Id*. at 438.)

In People v. Huynh, 212 Cal. App. 4th 285, 151 Cal. Rptr. 3d 170 (4th Dist. 2012), review filed, (Jan. 23, 2013), the court considered trial opinion testimony by a sexual assault response team (SART) nurse based on photos taken of victim by a nontestifying SART nurse. (212 Cal. App. 4th at 315–316.) Relying primarily upon People v. Dungo, 55 Cal. 4th 608, 147 Cal. Rptr. 3d 527, 286 P.3d 442 (2012), as modified on denial of reh'g, (Dec. 12, 2012), the court held that "the primary purpose of a particular SART examination is not necessarily for use in a criminal investigation," and thus photos taken and statements recorded during that examination are not testimonial in nature. (212 Cal. App. 4th at 321.) The "particular examination" at issue involved a man who may or may not have been sexually assaulted, and even if he had no suspect was identified. Thus the SART examination could not have been performed for the purpose of generating evidence for a criminal prosecution because there was no "targeted individual" to accuse when the photos were taken. (*Ibid*.)

Footnotes

1 Alternatively, because Justice Thomas was part of the five-justice majority, and because Justice Thomas subscribed to the included yet narrower, factually limited position described in his concurrence, his concurring view established the holding of the Court. It was the only holding to which five justices consented. (See Marks v. U.S., 430 U.S. 188, 193, 97 S. Ct. 990, 51 L. Ed. 2d 260 (1977) ["When a fragmented Court decides a case and no single rationale explaining the result enjoys the assent of five Justices, 'the holding of the Court may be viewed as that position taken by those Members who concurred in the judgments on the narrowest grounds … .'"].)

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Chapter 11. Admissibility of DNA Evidence at Trial

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§ 11:11. Expert witness testimony in the wake of *People v. Sanchez*

1) *People v. Sanchez*

In 2016, the California Supreme Court addressed limitations on admissibility of expert witness testimony related both to state hearsay rules and federal confrontation clause considerations. The case, People v. Sanchez, 63 Cal. 4th 665, 679, 204 Cal. Rptr. 3d 102, 374 P.3d 320 (2016), clarified "the degree to which the *Crawford* [*v. Washington* (2004) 541 U.S. 36] rule limits an expert witness from relating case-specific hearsay content in explaining the basis for his opinion," and "clarif[ied] the proper application of Evidence Code sections 801 and 802, relating to the scope of expert testimony." (*Sanchez*, *supra*, 63 Cal.4th 670.)

Sanchez involved a defendant's conviction for drug, firearm, and gang offenses. (63 Cal.4th at pp. 671, 673.) The gang detective in the case rendered expert opinions at trial about the defendant's gang membership by relating the details of information contained in a police-issued notice of gang involvement, prior police reports prepared by other officers, and a field interview card filled out and maintained as a police department record. (*Id*. at 672–673.) The California Supreme Court first considered whether a gang expert, consistent with California hearsay rules, may properly convey to the jury the factual contents of police reports as justification for his opinion.

Sanchez clarified that a jury must consider for its truth, any expert testimony describing the basis for an opinion, and disapproved prior decisions holding otherwise. (63 Cal.4th at p. 679, 684, 686, fn. 13.) In other words, there is no longer a "not-offered-for-the-truth" limitation on hearsay incorporated into an expert's reasoning. In so holding, however, the court expressly limited its holding to expert basis evidence consisting of "case-specific out-of-court statements." (*Id*. at p. 684; see also, e.g., *id*. at p. 686 ["What an expert *cannot* do is relate as true case-specific facts asserted in hearsay statements, unless they are independently proven by competent evidence or are covered by a hearsay exception"; emphasis in opinion].) Case-specific hearsay statements are those about which the expert has no independent knowledge, that present facts "relating to the particular events and participants alleged to have been involved in the case being tried." (*Id*. at p. 676.) Such facts must be independently established if the jury is to hear them, or if the expert is to assume their existence to answer a hypothetical question. (*Id*. at pp. 676, 677, 685.)

Simultaneously, however, *Sanchez* recognized the "traditional latitude" granted expert witnesses, as "a matter of practicality," to testify to specialized knowledge obtained in the course of their "own experience" as well as to information generally accepted in the area of expertise despite having learned it from hearsay sources such as "conversations with others …." (*Sanchez*, *supra*, 63 Cal.4th at p. 675, 685.) Thus, even if an expert's assertion from the witness stand is "technically hearsay," its admission will not offend state rules of evidence if it is derived from the expert's general subject matter knowledge or personal experience, or is otherwise properly proven. (*Id*. at p. 676, 685; see also *id*. at pp. 677–678.) Accordingly, *Sanchez*

> does not call into question the propriety of an expert's testimony concerning background information regarding his knowledge and expertise and premises generally accepted in his field. Indeed, an expert's background knowledge and experience is what distinguishes him from a lay witness, and, as noted, testimony relating such background information has never been subject to exclusion as hearsay, even though offered for its truth. Thus, our decision does not affect the traditional latitude granted to experts to describe background information and knowledge in the area of his

> expertise. Our conclusion restores the traditional distinction between an expert's testimony regarding background information and case-specific facts.

(*Id*. at p. 685.) In *Sanchez*, for example, the court recognized that the expert's "testimony about general gang behavior or descriptions of the Delhi gang's conduct and its territory … was based on well-recognized sources in [the expert's] area of expertise," and "was relevant and admissible evidence as to the Delhi gang's history and general operations" despite the expert's inevitable reliance on hearsay. (*Id*. at p. 698.)

Further, *Sanchez* distinguished between an expert describing reliance on a type or source of hearsay, and actually articulating for the jury those underlying facts or information on which she relied. (*Sanchez*, *supra*, 63 Cal.4th at pp. 685-686.) The former is permissible, regardless of the nature of the hearsay information: "There is a distinction to be made between allowing an expert to describe the type or source of the matter relied upon as opposed to presenting, as fact, case-specific hearsay that does not otherwise fall under a statutory exception." (*Id*. at p. 685.) Thus, even if an expert cannot repeat case-specific hearsay—testimonial or otherwise—to the jury, she need not excise those facts from the unspoken mental repository of information she calls upon to support an opinion. And, the expert may still "generally describe" the kind of hearsay information relied upon. (*Id*. at p. 686.)

Finally, if case-specific hearsay statements are conveyed to the jury by an expert, the confrontation clause is implicated if those statements are testimonial within the meaning of *Crawford*, *supra*, 541 U.S. 36. (*Sanchez*, *supra*, 63 Cal.4th at p. 685.) The California Supreme Court opined that hearsay information contained in police reports generated "during an official investigation of a completed crime" is testimonial. (*Id*. at p. 694.) The *Sanchez* expert's testimony relaying the contents of those reports as true, violated confrontation clause protections. (*Id*. at pp. 694–695.) In addition, the gang association notice at issue in *Sanchez* was likewise testimonial, having been prepared for the primary purposes of establishing facts for later use at trial and accompanied by an officer's sworn attestation. (*Id*. at pp. 696–697.) The court did not decide the testimonial status of the field interview card because the record was undeveloped as to the circumstances of its preparation. (*Id*. at p. 697.)

In early 2020, the California Supreme Court issued a significant clarification regarding the hearsay implications of *Sanchez* on forensic science evidence. (People v. Veamatahau (2020) 9 Cal.5th 16.) In *Veamatahau*, police seized from the defendant pills wrapped in cellophane. (*Id.* at p. 22.) At trial, a criminalist from the local crime laboratory testified that the pills contained alprazolam (also known as Xanax). (*Id.* at p. 23.) He reached that conclusion based on a visual comparison of the pills and their markings with a reference database listing various pill imprints required by the FDA. (*Ibid.*) The question for the California Supreme Court was whether the witness's description of the contents of the database was inadmissible case-specific hearsay. (*Id.* at p. 24.)

The court held that contents of the reference database, although offered for their truth and thus hearsay, qualified as admissible, non-case-specific, background information within the meaning of *Sanchez*. (*Veamatahau, supra*, 9 Cal.5th at p. 27.) "The database revealed nothing about the particular events. . . in the case being tried,' i.e., the particular pills. . . seized from defendant." (*Ibid.*) Thus, the expert could permissibly rely on those contents, and relay them to the jury as a rationale for his opinion, pursuant to Evidence Code sections 801, subdivision (b), and 802. (*Id.* at pp. 25-27.) "[A]n expert may consult specific sources in a case—a textbook, a treatise, or an academic paper—and supply the information found therein to the jury as background information without running afoul of the hearsay rules." (*Id.* at p. 29.)

Moreover, it is not necessary that, to qualify as admissible background knowledge hearsay, the expert discuss reference material from memory alone, as opposed to consultation in preparation for trial. (*Veamatahau, supra,* 9 Cal.5th at p. 30.) The court explained:

> The focus of the inquiry is on the information conveyed by the expert's testimony, not how the expert came to learn of such information. Thus, regardless of whether an expert testified to certain facts based on composite

> knowledge "acquired from sources too numerous to distinguish and quantify" or if the expert simply looked up the facts in a specific reference as part of his or her duties in a particular case, the facts remain the same. The background or case-specific character of the information does not change because of the source from which an expert acquired his or her knowledge.

(*Ibid.*) At the same time, trial courts retain the ability to vet, screen, or limit proffered expert testimony under Evidence Code sections 720, 801, and 802, to ensure that the "matter" relied upon by an expert is "of a type that reasonably may be relied upon by an expert in forming an opinion upon the subject to which his testimony relates," and that the expert is qualified to render a particular opinion. (*Id.* at pp. 32, 34.) Trial courts may also employ Evidence Code section 352 to "limit[] how much of a hearsay source an expert can relate to the fact finder." (*Id.* at p. 34.) Finally, the opponent of scientific evidence may challenge the trustworthiness of material relied upon by an expert in forming an opinion, either through cross-examination or by calling as a witness the source of the expert's knowledge. (*Veamatahau, supra,* 9 Cal.5th at p. 33, citing Evid. Code, § 804, subds. (a), (d).)

2) Impact on Scientific Evidence

The application of *Sanchez* to forensic science expert testimony continues to evolve, as courts explore the interface of *Sanchez, Dungo,* and *Lopez*. (See, e.g., People v. Lund (2021) 64 Cal.App.5th 1119, 1131-1136.) For confrontation clause purposes, the baseline reference point may be *Sanchez*'s admonition that "only when a prosecution expert relies upon, and relates as true, a *testimonial* statement would the fact asserted as true have to be independently proven to satisfy the Sixth Amendment" (emphasis in opinion). (63 Cal.4th 665, 685.) As discussed *ante*, the California Supreme Court provided detailed guidance to trial courts about what types of opinion basis testimony fall into testimonial and non-testimonial camps when the expert provides evidence of scientific testing, observations, and measurements.

In early 2020, the California Supreme Court issued a significant clarification regarding the hearsay implications of *Sanchez* on forensic science evidence. (People v. Veamatahau (2020) 9 Cal.5th 16.) In *Veamatahau*, police seized from the defendant pills wrapped in cellophane. (*Id.* at p. 22.) At trial, a criminalist from the local crime laboratory testified that the pills contained alprazolam (also known as Xanax). (*Id.* at p. 23.) He reached that conclusion based on a visual comparison of the pills and their markings with a reference database listing various pill imprints required by the FDA. (*Ibid.*) The question for the California Supreme Court was whether the witness's description of the contents of the database was inadmissible case-specific hearsay. (*Id.* at p. 24.)

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(*Ibid.*) At the same time, trial courts retain the ability to vet, screen, or limit proffered expert testimony under Evidence Code sections 720, 801, and 802, to ensure that the "matter" relied upon by an expert is "of a type that reasonably may be relied upon by an expert in forming an opinion upon the subject to which his testimony relates," and that the expert is qualified to render a particular opinion. (*Id.* at pp. 32, 34.) Trial courts may also employ Evidence Code section 352 to "limit[] how much of a hearsay source an expert can relate to the fact finder." (*Id.* at p. 34.) Finally, the opponent of scientific evidence may challenge the trustworthiness of material relied upon by an expert in forming an opinion, either through cross-examination or by calling as a witness the source of the expert's knowledge. (*Veamatahau, supra*, 9 Cal.5th at p. 33, citing Evid. Code, § 804, subds. (a), (d).)

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Chapter 12. Postconviction DNA Testing and Other Postconviction Challenges

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§ 12:1. Overview of postconviction DNA testing

The vast majority of states, as well as the federal government, provide statutory procedures for convicted felons to seek access to DNA testing of biological evidence. California's postconviction DNA testing law is codified in Penal Code section 1405. Section 1405 is a "narrowly circumscribed opportunity to develop new evidence in preparation for a new trial motion based on newly discovered evidence." (Richardson v. Superior Court, 43 Cal. 4th 1040, 1047, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008).) As the Supreme Court of Montana observed recently, "Exoneration of the innocent is the principal purpose of allowing postconviction DNA testing." (Haffey v. State, 2010 MT 97, 356 Mont. 198, 233 P.3d 315, 317 (2010).) A companion law, mandating retention of biological evidence following a felony conviction, is codified in Penal Code section 1417.9.

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§ 12:2. Penal Code section 1405

Postconviction discovery in California criminal cases is exceedingly limited. Section 1405 was enacted as an isolated exception to the general rule that "[n]o order requiring discovery shall be made in criminal cases except as provided in this chapter [i.e., Pen. Code, §§ 1054 et seq.]." (Pen. Code, § 1054.5, subd. (a).) Effective January 1, 2001 and amended effective January 15, 2015, Penal Code section 1405 is California's statutory mechanism for a defendant to request postconviction DNA testing of biological evidence. (Stats. 2000, ch. 821, § 1 as amended by Stats. 2014, ch. 554, § 1 [effective Jan. 1, 2015].) Only defendants convicted of a felony offense and currently serving a term of imprisonment may bring a motion.
Section 1405 contains a number of components, including the following:

• It permits indigent offenders to receive court-appointed counsel to assist with the investigation and filing of a motion for DNA testing. (§ 1405, subd. (b).)

• It provides for discovery of materials related to physical evidence and previous DNA testing. (§ 1404, subds. (c), (e).)

• It sets forth the required contents of the motion for testing itself. (§ 1405, subd. (d).)

• It allows for a hearing on the motion at the court's discretion (§ 1405, subd. (f).)

• It enumerates eight factually-based criteria that must be "established" for the motion to be granted. (§ 1405, subd. (g).)
(See generally Jointer v. Superior Court, 217 Cal. App. 4th 759, 764–765, 158 Cal. Rptr. 3d 778 (4th Dist. 2013) [describing structure and legislative history of section 1405].)

The only other postconviction discovery authorized by statute in this state is limited to cases resulting in conviction for a serious or violent felony, with a sentence of 15 years or more imposed. (Pen. Code, § 1054.9, subd. (a).) Note that, prior to 2020, this provision was even more restrictive, finding application only in death penalty and life imprisonment cases. (See Stats. 2019, ch. 483, § 1, eff. Jan. 1, 2020.) Penal Code section 1054.9 may be utilized in the context of a petition for writ of habeas corpus or a motion to vacate a judgment. (§ 1054.9, subd. (a); see People v. Superior Court (Pearson) (2010) 48 Cal.4th 564, 571-573.) Discovery potentially available under section 1054.9 is limited to "materials in the possession of the prosecution and law enforcement authorities to which the same defendant would have been entitled at time of trial." (§ 1054.9, subd. (c); see In re Steele (2004) 32 Cal.4th 682, 695.) Significantly, section 1054.9 does not overlap with Penal Code section 1405, and cannot be used to obtain postconviction DNA testing. (§ 1054.9, subd. (d) ["The procedures for obtaining access to physical evidence for purposes of postconviction DNA testing are provided in Section 1405, and this section does not provide an alternative means of access to physical evidence for those purposes"]; see Satele v. Superior Court (2019) 7 Cal.5th 852, 858, fn. 3.)

Section 1405, however, does provide a detailed and comprehensive mechanism for seeking postconviction DNA testing. Its components include the following: (Richardson v. Superior Court, 43 Cal. 4th 1040, 1051, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008) ["[T]he trial court does not, and should not, decide whether, assuming a DNA test favorable to the defendant, that evidence in and of itself would ultimately require some form of relief from the conviction."]; see also Jointer v. Superior Court, 217 Cal. App. 4th 759, 768–669, 158 Cal. Rptr. 3d 778 (4th Dist. 2013).)

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§ 12:3. Appointment of counsel

Section 1405 provides for appointment of counsel to assist indigent inmates prior to filing the actual testing motion. (§ 1405, subd. (b).) If the request is made properly and counsel has not been previously appointed, the trial court "shall" appoint counsel "to investigate and, if appropriate, to file a motion for DNA testing … ." (§ 1405, subd. (b)(3)(B).) A proper request for attorney assistance contains (1) a statement by the inmate that he was not the perpetrator of the crime, (2) a statement by the inmate that DNA testing is relevant to his assertion of innocence, and (3) a statement by the inmate concerning previous appointment of counsel under section 1405. (§ 1405, subd. (b)(1); In re Kinnamon, 133 Cal. App. 4th 316, 34 Cal. Rptr. 3d 802 (2d Dist. 2005).)

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§ 12:4. The testing motion

The motion for DNA testing must be filed in the trial court that entered judgment in the case. (§ 1405, subds. (a), (f).) Given the fact-specific nature of the section 1405 inquiry, the judge having the greatest familiarity with the evidence—presented at trial and otherwise—is in the best position to evaluate whether the convicted person has met applicable standards. State law does not bar section 1405 motions in cases where the defendant pleaded guilty, unlike some other state statutes. (Cf. Fuentes v. State, 907 So. 2d 609, 612 (Fla. Dist. Ct. App. 3d Dist. 2005).)

Subdivision (d) of section 1405 sets forth the required contents of the testing motion:

(1) A statement that the petitioner is innocent of the crime.

(2) An explanation of why the identity of the perpetrator was, or should have been, a significant issue in the case.

(3) Identify the evidence to be tested and testing method.

(4) An explanation of how, in light of all the evidence, the requested DNA testing would raise a reasonable probability that the convicted person's verdict or sentence would be more favorable if the results of DNA testing had been available at the time of conviction.

(5) The results of any DNA or other biological testing that was conducted previously by either the prosecution or defense, if known.

(6) A statement whether any motion for testing previously was filed and the results of that motion, if known.

Notice of the motion must be served on the prosecuting District Attorney, the Attorney General, and the court, crime laboratory, or police agency in possession of the biological evidence. (§ 1405, subd. (d)(2).) Any party objecting to the motion for testing has 90 days in which to file a responsive pleading. (*Ibid*.)

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§ 12:5. Adjudication of motion

Subdivision (g) of section 1405 enumerates eight factually-based criteria that all must be "established" for the motion to be granted. (§ 1405, subd. (g) ["The court shall grant the motion for DNA testing if it determines all of the following have been established …"].) They are as follows:

1) The evidence to be tested is available and in a condition that would permit the DNA testing requested in the motion. The initial collection and subsequent handling of the evidence should be scrutinized in light of this requirement. (§ 1405, subd. (g)(1).)

2) The evidence to be tested has been subject to a chain of custody sufficient to establish it has not been substituted, tampered with, replaced or altered in any material aspect. (§ 1405, subd. (g)(2); cf. People v. Catlin, 26 Cal. 4th 81, 134, 109 Cal. Rptr. 2d 31, 26 P.3d 357 (2001), as modified, (Sept. 26, 2001) [holding that a chain of custody objection lacks merit if the proponent of the evidence can show with reasonable certainty that the "evidence analyzed" is the "evidence originally received"].) The California Court of Appeal has emphasized the importance of chain of custody evidence in a DNA case: "Like blood and fingerprint evidence, DNA samples that are relevant to a case are indistinguishable from other samples that have no connection at all to a case. Evidence like that requires expert analysis the accuracy of which is entirely dependent on a proper chain of custody." (People v. Jimenez, 165 Cal. App. 4th 75, 81, 80 Cal. Rptr. 3d 579 (5th Dist. 2008) [and citing section 1405, former subdivision (f)(2), in describing the importance of chain of custody in being able to attribute DNA test results to the relevant source].)

3) The identity of the perpetrator of the crime was, or should have been, a significant issue in the case. (§ 1405, subd. (g)(3).) This requirement may preclude a successful DNA testing motion where the applicant pleaded guilty or offered a consent defense to a sexual assault charge.

4) The convicted person has made a prima facie showing that the evidence sought to be tested is material to the issue of the convicted person's identity as the perpetrator of, or accomplice to, the crime, special circumstance, or enhancement allegation that resulted in the conviction or sentence. (§ 1405, subd. (g)(4).) As a general matter, a prima facie showing may not be founded upon speculation (People v. Gonzalez, 51 Cal. 3d 1179, 1241, 275 Cal. Rptr. 729, 800 P.2d 1159 (1990)) or conclusory allegations. (People v. Duvall, 9 Cal. 4th 464, 474, 37 Cal. Rptr. 2d 259, 886 P.2d 1252 (1995).) Material evidence must "tend to establish guilt" or be "'directly probative of the crimes charged.'" (People v. Bunyard, 45 Cal. 3d 1189, 1212, 249 Cal. Rptr. 71, 756 P.2d 795 (1988), as modified on denial of reh'g, (Sept. 1, 1988), quoting People v. Thompson, 27 Cal. 3d 303, 330–332, 165 Cal. Rptr. 289, 611 P.2d 883 (1980).) A 2015 amendment added that, in addition to being "material to the issue of. . . identity," the petitioner must demonstrate that the desired testing would be "relevant" to that issue. (§ 1405, subd. (g)(4).) The amendment also clarified that, in seeking testing, "[t]he convicted person is not required to show a favorable result would conclusively establish his or her innocence." (*Ibid.*)

5) The requested DNA testing results would raise a "reasonable probability" that, in light of all the evidence, the convicted person's verdict or sentence would have been more favorable if the results of DNA testing had been available at the time of conviction. (§ 1405, subd. (g)(5).) A reasonable probability must represent "a reasonable chance and not merely an abstract possibility … ." (Richardson v. Superior Court, 43 Cal. 4th 1040, 1051, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008).) The California Supreme Court analogized Section 1405's reasonable probability standard to the

reasonable probability standard governing claims of ineffective assistance of counsel under Strickland v. Washington, 466 U.S. 668, 104 S. Ct. 2052, 80 L. Ed. 2d 674 (1984). (*Richardson*, 43 Cal. 4th 1040, 1050.)

a) In assessing whether the "reasonable probability" standard has been met, the trial court in its discretion may consider any evidence whether or not it was introduced at trial. For example, fingerprint evidence, eyewitness testimony, party admissions, modus operandi evidence, videotape evidence, or even other DNA evidence could impact the trial court's evaluation.

b) Trial courts often apply the reasonable probability standard by assuming for the sake of argument that the defendant's DNA profile would not be present on the evidence items tested, and then considering whether such results would have made a difference to the jury and/or judge in terms of verdict or sentence and in light of all the facts of the case. The Richardson trial court engaged in this kind of inquiry in reaching its conclusion. (*Richardson*, 42 Cal.4th at 1048 ["[T]he trial court agreed with the prosecution that … there was no reasonable probability that petitioner would have obtained a more favorable result in light of all the evidence adduced at trial against him, even assuming the testing showed the hairs in question were not his."]; see also Jointer v. Superior Court, 217 Cal. App. 4th 759, 766, 158 Cal. Rptr. 3d 778 (4th Dist. 2013) ["our task is not to speculate about what the results of DNA testing would be, but instead to decide whether a result favorable to defendant could reasonably have impacted the outcome"].)

c) A 2015 amendment added the guideline that adjudication of the testing motion should not consider whether the petitioner would be entitled to "some form of ultimate relief" were the results favorable. (§ 1405, subd. (g)(5).)

6) The evidence sought to be tested meets either of the following conditions (§ 1405, subd. (g)(6)):

a) The evidence was not tested previously.

b) The evidence was tested previously, but the requested DNA test would provide results that are reasonably more discriminating and probative of the identity of the perpetrator or accomplice or have a reasonable probability of contradicting prior test results.

7) The testing requested employs a method generally accepted within the relevant scientific community. (§ 1405, subd. (g)(7).)

8) The motion is not made solely for the purpose of delay. (§ 1405, subd. (g)(8).)

The California Supreme Court has clarified that a postconviction DNA testing order pursuant to Penal Code section 1405 may issue only if and when the statutory criteria set forth in subdivision (g) [formerly (f)] of that statute are satisfied, and no order may issue for the independent purpose of aiding in the litigation of a petition for writ of habeas corpus or other postconviction relief. (*Richardson v. Superior Court*, 43 Cal.4th at 1053, fn. 7 ["To the extent petitioner claims that the DNA testing should have been ordered because the results might be useful to him on habeas corpus or for purposes of executive clemency, we reject the claim. Section 1405 does not require the trial court to order DNA testing because it might be helpful in these contexts but only where the conditions of subdivision (f) are fulfilled."].)

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§ 12:6. Applicability of section 1405 to prior convictions

The question may arise whether a motion for postconviction DNA testing, including a request for appointment of counsel, can lawfully be brought before the trial court that adjudicated a *prior* conviction used to enhance the sentence being served currently. The structure and language of Penal Code section 1405 indicates that such a motion can indeed be properly made.

A motion for postconviction DNA testing is properly brought before the trial court possessing the greatest familiarity with those facts, as various aspects of the statutory scheme demand. The sole function of that trial court is to assess the request under the criteria set forth in Penal Code section 1405, and in light of the facts of the underlying case. If DNA testing is granted, then any remedy based on those test results can and should then be sought from the court that imposed the current sentence – even if it is a trial court in a different jurisdiction.

Penal Code section 1405 is a mechanism for the discovery of new evidence bearing on the identity of "the perpetrator" of a given "crime." (See, e.g., Pen. Code, § 1405, subds. (b)(1), (d)(1)(A), (g)(3).) There is no requirement, however, that the "crime" at issue be the one for which the convicted person is currently incarcerated. In fact, the Legislature expressly recognized that the issue of identity may relate to the truth of an enhancement allegation as opposed to the current criminal conduct. (§ 1405, subd. (g)(4).) In the case of an enhancement allegation, the question then becomes which court should apply the criteria for DNA testing set forth in Section 1405: The trial court that adjudicated the DNA-related crime, or the trial court that imposed the current enhanced sentence based on the prior DNA-related crime?

Some aspects of Section 1405 are ambiguous on this issue. The law states, for example, that a motion for postconviction DNA testing and/or appointment of counsel must be made "before the trial court that entered the judgment of conviction in his or her case …." (§ 1405, subd. (a); see also subd. (e) ["The motion [for DNA testing] shall be heard by the judge that conducted the trial, or accepted the … plea …."].) But, in the context of the rest of the statutory scheme, it is apparent that the Legislature intended the phrase "trial court" to refer to the court that adjudicated the DNA-related crime.

This intent is strongly suggested by the criteria for granting a postconviction DNA testing motion set forth in Section 1405, subdivision (g)(5). First, the trial court that adjudicated the DNA-related crime is in the best position to evaluate whether the evidence is available and in testable condition (§ 1405, subd. (g)(1)) because the evidence is most likely to be in the custody of a local law enforcement agency, crime laboratory, or the court itself if the evidence had been admitted as a trial exhibit.

Second, that original court, having heard the facts of the case, is in the best position to evaluate whether the identity of the perpetrator "was, or should have been, a significant issue in the case." (§ 1405, subd. (g)(3).) Third, that court, having heard the case evidence and having ruled on evidentiary motions, is in the best position to evaluate whether, "in light of all the evidence … whether or not it was introduced at trial," the convicted person demonstrated a reasonable probability that the DNA test results would have aided the defendant at trial had they been available. (§ 1405, subd. (g)(5).) It is difficult to imagine that the Legislature contemplated any court other than the original trial court assessing evidence *not* admitted at trial in ruling on a subsequent DNA testing motion.

Further, if evidence in the disputed-identity case was previously subjected to DNA testing by "either the prosecution or the defense," the court hearing the motion for DNA testing "shall order [that] party" to provide discovery related to the testing. (§ 1405, subd. (e).) A court order to a "party" strongly implies that the court and the party are (or were) participants in the same case rather than in different cases and/or in different jurisdictions. (Cf. Pen. Code, § 1054.5, subd. (b) [providing for a "party" in a criminal matter to seek an order to compel discovery from the trial court].)

Finally, Section 1405 is a postconviction discovery mechanism only. It does not provide for a remedy based on the test results. It does not, therefore, require that the court which would be in position to rule on, for example, a state habeas petition based on newly discovered evidence be the same court which hears the motion for testing. The court hearing the motion for testing should be the court having the greatest familiarity with the facts of the case, and thus best able to render a fact-specific ruling on a fact-specific motion.

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§ 12:7. Appellate review

An order granting or denying a postconviction DNA testing request is not appealable. (§ 1405, subd. (k).) A party dissatisfied with the outcome, however, may petition the Court of Appeal for a writ of mandate or prohibition. The writ petition must be filed within 20 days of the trial court's order. (*Ibid*.) A trial court's ruling on a motion for postconviction DNA testing, brought pursuant to Penal Code section 1405, is reviewed for abuse of discretion. (Richardson v. Superior Court, 43 Cal. 4th 1040, 1047, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008); Jointer v. Superior Court, 217 Cal. App. 4th 759, 765, 158 Cal. Rptr. 3d 778 (4th Dist. 2013).)

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§ 12:8. Case Law

The seminal California case involving postconviction DNA testing is Richardson v. Superior Court, 43 Cal. 4th 1040, 77 Cal. Rptr. 3d 226, 183 P.3d 1199 (2008), as modified, (July 16, 2008). In Richardson, an 11-year-old girl was sexually assaulted and then killed, with her body left in a bathtub. Hairs recovered from debris in the tub were described by prosecution experts at trial as consistent with the defendant. (*Richardson v. Superior Court*, 43 Cal. 4th at 1044.) They were the only physical evidence linking the defendant to the crimes. The defendant was convicted and sentenced to death. (*Ibid*.) Following conviction, the defendant filed a motion under Section 1405 to have the hairs subjected to DNA testing in order to exclude himself as the source. (*Richardson v. Superior Court*, 43 Cal. 4th at 1045.) The California Supreme Court affirmed the trial court's denial of the DNA testing motion on grounds that the hair evidence had not been conclusive on the issue of guilt at trial, and a substantial amount of other evidence linked the defendant to the crime. (*Richardson v. Superior Court*, 43 Cal. 4th at 1051.)

This conclusion was consistent with the reality that "DNA evidence is not a videotape of a crime." (State v. Lotter, 266 Neb. 758, 669 N.W.2d 438, 448 (2003) ["In this case, such testing could show only whose blood is on the items in question, not how the blood was deposited on the items."]. Other cases have affirmed trial courts' denials of requests for postconviction testing on grounds that the testing would not have been favorable to the defendant even if he was not the source of the DNA at issue. (See, e.g., Helton v. State, 947 So. 2d 495, 499 (Fla. Dist. Ct. App. 3d Dist. 2006) [denial of postconviction DNA testing affirmed because testing could not demonstrate how or when DNA was deposited on items of evidence]; Grayson v. King, 460 F.3d 1328, 1330–34 (11th Cir. 2006) [claimant convicted of capital murder after he and a co-defendant raped and killed an elderly woman; postconviction DNA testing properly denied because, even if DNA test results excluded Grayson as the source of blood and semen evidence, it would show only that the accomplice committed the actual rape]; State v. Dupigney, 295 Conn. 50, 988 A.2d 851 (2010) [Postconviction request to conduct DNA testing on hat found near murder scene properly denied; even if he was not source of DNA on hat, no reasonable probability of more favorable outcome at trial]; State v. Riofta, 166 Wash. 2d 358, 209 P.3d 467, 475 (2009) [postconviction testing properly denied "considering the strength of the eyewitness identification, the evidence of motive, and the limited probative value of the DNA evidence sought"]; Haffey v. State, 2010 MT 97, 356 Mont. 198, 233 P.3d 315, 319–320 (2010).)

Numerous examples of meritorious requests for postconviction DNA testing exist as well. In California, Jointer v. Superior Court, 217 Cal. App. 4th 759, 158 Cal. Rptr. 3d 778 (4th Dist. 2013) is a prime illustration. There, the defendant was convicted in 1998 of robbing a grocery store. Before seizing the store's money and food stamps, the robber had purchased a bottle of water and consumed part of it. He left the bottle at the scene as he fled. Evidence at trial included (1) testimony that the defendant's fingerprints were a match to latents lifted from the water bottle; (2) in-court identification of defendant as the robber by a store employee; (3) clothing consistent with the robber's recovered from a search of the defendant's home; and (4) indications that the defendant owned a gun. (*Id*. at pp. 762–763.) Several other witnesses were either ambivalent or unable to identify the defendant as the robber. And, the defendant's nephew was implicated in a bank robbery and had a food stamp in his car when he was arrested. (*Id*. at p. 763.)

In 2012, defendant Jointer brought a postconviction motion for DNA testing of the water bottle from the store. The trial court denied the motion, finding that he had not demonstrated a reasonable probability that the trial outcome would have been more

favorable had the DNA testing been performed then, in view of all the evidence. (217 Cal.App.4th at p. 763.) The Court of Appeal reversed. It reasoned that the trial court's analytical approach should have been to assume favorable DNA test results, and only then inquire whether the trial outcome would probably have been more favorable to the defendant in light of all other available evidence. (*Id*. at p. 766.) Specifically,

> Given the central importance of the water bottle, assuming the DNA test came back favorable for the defendant, there is a reasonable probability of a more favorable verdict for defendant. Although defendant's fingerprints were found on the bottle, the People's expert conceded she could not pinpoint when the fingerprints were put on the bottle. Absent DNA evidence, that bare concession was understandably not enough to create reasonable doubt in the jurors' minds. But combined with favorable DNA results, that otherwise minor gap in the prosecution's logic would take on significantly greater importance.

(*Id*. at pp. 766–767.) The appellate court contrasted this factual scenario with that presented in *Richardson*, *supra*, where "the evidence to be DNA tested was at best a weak link between the defendant and the crime, and was overshadowed by more probative evidence." (*Jointer*, *supra*, 217 Cal.App.4th at p. 767.) Whereas, in *Jointer*, the evidence other than the fingerprints on the water bottle consisted of "fallible eyewitness identifications and relatively weak circumstantial evidence." (*Id*. at p. 768.)

Cases from other jurisdictions provide additional examples of postconviction DNA testing requests that should have been granted. (See, e.g., Ortiz v. State, 884 So. 2d 70, 71–72 (Fla. Dist. Ct. App. 2d Dist. 2004) [DNA testing at trial could have substantiated defense theory]; State v. Gray, 151 Wash. App. 762, 215 P.3d 961, 968 (Div. 1 2009) [postconviction DNA testing would have been probative of the defendant's innocence and should be granted]; Johnson v. State, 356 Ark. 534, 157 S.W.3d 151, 163–164 (2004) [remanding for testing of hairs that, if not the defendant's, would significantly advance his claim of innocence]; People v. Shum, 207 Ill. 2d 47, 278 Ill. Dec. 14, 797 N.E.2d 609, 620–621 (2003) [trial court erred in denying DNA testing because, "[i]f the DNA testing produces results favorable to defendant, this evidence will significantly advance defendant's claim of actual innocence"].)

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§ 12:9. Constitutional implications

Section 1405 represents the California Legislature's effort to address "[t]he dilemma [of] how to harness DNA's power to prove innocence without unnecessarily overthrowing the established system of criminal justice." (District Attorney's Office for Third Judicial Dist. v. Osborne, 557 U.S. 52, 129 S. Ct. 2308, 2316, 174 L. Ed. 2d 38 (2009).) That established system recognizes that, after being lawfully convicted, a defendant possesses a substantially diminished liberty interest, is no longer presumed innocent, is not entitled to discovery of exculpatory or impeaching information within the meaning of Brady v. Maryland, 373 U.S. 83, 83 S. Ct. 1194, 10 L. Ed. 2d 215 (1963), "and has only a limited interest in postconviction relief." (*District Attorney's Office v. Osborne*, 129 S.Ct. at 2320.)

1) *District Attorney's Office v. Osborne*

In District Attorney's Office v. Osborne, the United States Supreme Court held that (1) convicted offenders do not possess a freestanding, substantive due process right to postconviction DNA testing (129 S.Ct. at pp. 2322–2323), and (2) procedural due process protections are violated only if state postconviction procedures—including DNA testing—are "fundamentally inadequate" because they "'offend[–] some principle of justice so rooted in the traditions and conscience of our people as to be ranked as fundamental,'" or "'transgress[–] any recognized principle of fundamental fairness in operation'" (129 S.Ct at 2320 (citing Medina v. California, 505 U.S. 437, 446, 448, 112 S. Ct. 2572, 120 L. Ed. 2d 353 (1992)).) Finally, the Osborne Court noted that "*Brady* [*v. Maryland* (1963) 373 U.S. 83] is the wrong framework" to apply in assessing a prisoner's postconviction right to access biological evidence. (129 S.Ct. at 2320.) In In re Jenkins, 14 Cal. 5th 493, 306 Cal. Rptr. 3d 50, 525 P.3d 1057 (Cal. 2023), the California Supreme Court summarized the constitutional implications, and limitations, of *Osborne*. (14 Cal.5th at pp. 509–511.) It observed that, "[w]hile *Osborne* certainly 'distinguish[es] between the pretrial and the posttrial obligation to provide exculpatory evidence' [citation], we do not understand *Osborne* as holding that the government lacks a duty to disclose, in the postconviction context, *Brady* evidence that was *available* prior to conviction." (*Id*. at p. 510.) The *Jenkins* court further explained that "the *Osborne* court's reason for declining to extend *Brady* to evidence discovered in the postconviction context—namely, that the defendant received 'a fair trial' [citation], also does not apply where the prosecution violates *Brady* at trial." (*Ibid*.)

The United States Supreme Court later described its decision in *Osborne* as one that "severely limits the federal action a state prisoner may bring for DNA testing," and leaves "slim room" for a prisoner to show that the state law governing postconviction DNA testing denies him procedural due process. (Skinner v. Switzer, 131 S. Ct. 1289, 1293, 179 L. Ed. 2d 233 (2011); see also Cunningham v. District Attorney's Office for Escambia County, 592 F.3d 1237, 1269 (11th Cir. 2010) [affirming dismissal of inmate's § 1983 suit because Alabama's postconviction DNA testing procedures were adequate to satisfy fundamental fairness].)

2) *Skinner v. Switzer*

In Skinner v. Switzer, 131 S. Ct. 1289, 179 L. Ed. 2d 233 (2011), the Supreme Court addressed whether that "slim" opportunity for demonstrating that state postconviction testing procedures deny a prisoner procedural due process may be pursued in a civil rights action under 42 U.S.C.A. § 1983, or whether instead such a claim in federal court must be brought instead in a petition for

a writ of habeas corpus under 28 U.S.C.A. § 2254. Following his convictions for multiple murders, Skinner had twice sought postconviction DNA testing under Texas law, but was unsuccessful both times. He then filed a section 1983 action in federal court, alleging that the Texas postconviction DNA testing law, as interpreted by Texas courts, denied him procedural due process protections. Both the federal district court and court of appeals held that Skinner's suit was not cognizable as a section 1983 action, but could only be brought as a habeas petition. The Supreme Court reversed.

It held that Skinner had "properly invoked § 1983," because "[s]uccess in his suit for DNA testing would not 'necessarily imply' the invalidity of his conviction." (Skinner v. Switzer, 131 S. Ct. 1289, 1298, 179 L. Ed. 2d 233 (2011), quoting Heck v. Humphrey, 512 U.S. 477, 487, 114 S. Ct. 2364, 129 L. Ed. 2d 383 (1994).) DNA testing, observed the Court, "may yield exculpatory, incriminating, or inconclusive results … ." (*Skinner v. Switzer*, 131 S.Ct. at 1300.) Related claims, therefore, fall outside the traditional core of habeas corpus. (*Ibid*.) The Court remanded the case to the lower federal court for further proceedings, without commenting on the merits of the criminal defendant's due process claims.

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§ 12:10. The testing order

Once the parties stipulate to postconviction DNA testing under Penal Code section 1405, or once the testing motion is granted over opposition, the court will issue an order setting forth the parameters of the testing to be performed. An appropriate court order should include the following details:

1) An exact description of the evidence items to be tested. For example, do all 20 hairs found in the victim's hand require testing, or is a representative sampling sufficient?

2) The testing technology that will be used (e.g., STRs, Y-STRs, mtDNA).

3) Which laboratory will do the testing, and how evidence will be transported to that facility.

4) Instructions regarding the order in which evidence items will be tested. The items having the highest chance of containing probative and testable biological evidence should be tested first, and the results may eliminate the need for additional costly testing.

5) A provision requiring the testing laboratory to assess the feasibility of testing the evidence before actually proceeding.

6) Acknowledgment that evidence may be consumed in the course of testing. In the alternative, the testing laboratory could be instructed to notify all parties if it appears that testing will consume the entirety of an evidence item.

7) A requirement that the testing laboratory complete the testing of evidence item(s), including dissemination of its report to all parties, before proceeding with the analysis of any relevant reference samples from the defendant, victim, or third parties.

8) All underlying data and laboratory notes will be made available to all parties upon request.

9) Agreement that the defendant will provide new known reference samples upon request for comparative analysis.

10) Permission for the testing laboratory to retest any evidence items it deems necessary.

11) Any DNA testing not contemplated by the order cannot occur without the mutual consent of all parties or further court order. This may include testing the same evidence items using different scientific methodologies.

12) Instructions regarding disposition of the evidence following completion of the DNA testing. Commonly evidence is retained by the testing laboratory or returned to a law enforcement facility.

13) Terms of payment for testing services. If the testing is performed by a private laboratory, the Superior Court ordering the testing will be responsible for payment. (Pen. Code, § 1405, subd. (j)(2).)

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§ 12:11. Preservation and retention of biological evidence

1) Penal Code Section 1417.9

Penal Code section 1417.9, a companion statute to Section 1405, mandates the retention of "all biological material" in felony cases, as long as the convicted person remains incarcerated in connection with the case, in order to preserve the possibility of a motion for DNA testing brought under Section 1405. (Pen. Code, § 1417.9, subd. (a); Stats. 2000, ch. 821, § 2; see 88 Ops.Cal.Atty.Gen. 77 (2005) [misdemeanor convictions do not fall within the evidence retention mandate].)

This mandate was interpreted by a statewide task force as requiring preservation of all items that have a "reasonable likelihood" of containing biological evidence. (Postconviction Testing/Evidence Retention Task Force, *Postconviction DNA Testing: Recommendations for Retention, Storage, and Disposal of Biological Evidence* (2002), at p. 1 http://ag.ca.gov/publications/finalproof.pdf.) The Task Force advised further that, "if there is any reasonable question, the item should be retained." (*Ibid*.) Agencies possessing physical evidence should not be required, however, "to retain material without apparent evidentiary value, or material that is clearly collateral to any question of identity." (*Id*. at p. 6.) Nor should agencies be required to engage in an "unreasonable level of conjecture and speculation about what evidence may or may not constitute biological material." (*Ibid*.) For example, coroners are not required by section 1417.9 to retain human remains to a degree or in a manner inconsistent with standard practices.

Physical evidence falling within the scope of section 1417.9 must be "retained in a condition suitable for deoxyribonucleic acid (DNA) testing." (Pen. Code, § 1417.9, subd. (a).) This means that it should be stored in a dried condition in a controlled —and ideally cold—temperature environment with little or no fluctuation in temperature or humidity. Evidence should not be subjected to repeated cycles of freezing and thawing. Evidence should be stored in such a way as to minimize the chance of contamination from an external source or cross-contamination between two or more evidence items. Accurate and detailed chain of custody records should be maintained for all biological evidence retained in the investigation of a case.

Moreover, use and handling of biological evidence at trial should be minimized. Secondary evidence such as photographs and video should receive preference over the opening of any package containing biological material in a trial court setting. Trial courts should encourage stipulations between parties to promote use of secondary evidence in this context. When biological evidence is brought to court, the court and parties should make every effort to agree that it be returned to an appropriate agency for proper retention and storage following its use. Courthouses are usually a poor choice as facilities for long-term storage of biological evidence.

Biological evidence may be disposed of when all defendants incarcerated in connection with the case are released from incarceration. The agency retaining evidence may contact the California Department of Corrections and Rehabilitation (CDCR) for updates concerning the incarceration status of individuals. When provided with an inmate's name, CDCR number and date of birth, the CDCR's ID/Warrants Unit will provide the necessary information by telephone.

The investigating agency, crime laboratory, or other governmental entity that possesses biological evidence may destroy the evidence before that time, however, under the following conditions and as long as no other provision of law requires its retention:

1) The entity possessing the evidence provides written notification of its intentions to the person or persons remaining incarcerated in the case, all counsel of record, the county Public Defender, the county District Attorney, and the Attorney General. (§ 1417.9, subd. (b)(1).)

2) No motion for postconviction testing, or notification that such a motion will be filed, is received within 180 days following the notification. (§ 1417.9, subd. (b)(2)(A), (B).)

3) No sworn declaration of innocence that has been filed with a court is received within 180 days following the notification. (§ 1417.9, subd. (b)(2)(C).)

In any event, before an agency in possession of biological evidence proceeds with destruction of the items pursuant to the procedures set forth above, it is advisable that the investigating officers of the case be contacted and advised, so that any concerns or objections they have can be considered.

2) Penal Code Sections 680 and 680.3

Penal Code section 680, the Sexual Assault Victims' DNA Bill of Rights, is also a source of rules governing evidence retention by law enforcement. Subdivision (e) of that section requires written notice to sexual assault victims before destruction of evidence in unsolved cases: "If the law enforcement agency intends to destroy or dispose of rape kit evidence or other crime scene evidence from an unsolved sexual assault case, a victim of a violation of Section 261, 261.5, 262, 286, 288a, or 289 shall be given written notification by the law enforcement agency of that intention." (Pen. Code § 680, subd. (e)(1).) Other evidence cannot be destroyed at all: "A law enforcement agency shall not destroy or dispose of rape kit evidence or other crime scene evidence from an unsolved sexual assault case before at least 20 years, or if the victim was under 18 years of age at the time of the alleged offense, before the victim's 40th birthday." (Pen. Code § 680, subd. (e)(2).)

Penal Code section 680.3 creates the "SAFE-T" database, administrated by the Department of Justice, which must be updated by investigating agencies and laboratories to reflect the collection and analysis status of rape kit evidence. (Pen. Code, § 680.3.) The SAFE-T database only contains information about evidence collected on or after January 1, 2018. (Pen. Code, § 680.3, subd. (g).)

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§ 12:12. Database search following testing

Effective January 1, 2015, the Legislature added Penal Code section 1405.1. (Stats. 2014, ch. 554, § 2 [effective January 1, 2015].) This provision permits the court that heard a postconviction testing motion to hold a noticed hearing about whether to order a resulting DNA profile uploaded into state and national DNA databases. (§ 1405.1, subd. (a).) The court "may" order upload only if the requesting party demonstrates that the profile is "attributable to the putative perpetrator of the crime" and meets all technical upload requirements set forth in state and federal policy and legislation. (§ 1405.1, subds. (a)(1), (a)(2).)

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§ 12:13. DNA Test Results as Basis for State Habeas Corpus Relief

Obtaining DNA testing is one thing; using the results to obtain habeas relief is another. In California, Penal Code section 1473 provides a nonexclusive list of statutory bases for seeking a writ of habeas corpus under color of state law. Subdivision (b)(3)(A) of section 1473 provides that a writ of habeas corpus should issue when "[n]ew evidence exists that is credible, material, presented without substantial delay, and of such decisive force and value that it would have more likely than not changed the outcome at trial." "New evidence" means "evidence that has been discovered after trial, that could not have been discovered prior to trial by the exercise of due diligence, and is admissible and not merely cumulative, corroborative, collateral, or impeaching." (Pen. Code, § 1473, subd. (b)(3)(B).) Accordingly, a court considering a state habeas petition premised on postconviction DNA test results "must decide whether the DNA evidence 'would have more likely than not changed the outcome at trial.' (Pen. Code, § 1473, subd. (b)(3)(A).)" (In re Sagin (2019) 39 Cal.App.5th 570, 579.) A changed trial outcome could be an acquittal, but could also be a hung jury. (*Ibid.*; People v. Soojian (2010) 190 Cal.App.4th 491, 521.)

Given the "more likely than not" standard embedded in Penal Code section 1473, an inmate advancing the results of new DNA testing in a state habeas corpus proceeding thus bears the burden of showing that "it is more likely than not the new DNA evidence would have led at least one juror to maintain a reasonable doubt of guilt." (*Sagin, supra*, 39 Cal.App.5th at p. 579.) The *Sagin* court observed that this is a considerably lower bar for habeas relief than was the case before the Legislature amended section 1473 effective January 1, 2017. Before that amendment, the petitioner had to demonstrate that "the new evidence pointed '"unerringly to innocence"' and 'undermine[d] the entire case of the prosecution.' [Citation.] That former standard required a petitioner to conclusively establish innocence. [Citation.] Habeas corpus relief was thus previously reserved for those cases where newly discovered evidence essentially on its own proved a petitioner did not commit the crime." (*Sagin, supra*, 39 Cal.5th at p. 579.) But following changes to section 1473,

> [a] petitioner no longer has to prove innocence but rather must show that the new evidence—viewed in relation to the evidence actually presented at trial—would raise a reasonable doubt as to guilt. The statute creates a sliding scale: in a case where the evidence of guilt presented at trial was overwhelming, only the most compelling new evidence will provide a basis for habeas corpus relief; on the other hand, if the trial was close, the new evidence need not point so conclusively to innocence to tip the scales in favor of the petitioner. The change in the law represents an overall lower tolerance for wrongful convictions. The Legislature has chosen to more closely protect society's interest in ensuring that a person convicted of a crime is the person who committed it.

(*Id.* at pp. 579-580.) In other words, "the relative strength required of new evidence depends on how close the trial was." (*Id.* at p. 580.)

In petitioner Sagin's case, the newly obtained DNA test results were strong enough to merit relief under Penal Code section 1473, given the evidence of his guilt presented at trial. Sagin had been convicted of stabbing a woman to death despite "conflicting" evidence. (*Sagin, supra*, 39 Cal.5th at pp. 575, 580.) Postconviction DNA testing revealed an unknown male's DNA on fingernail

scrapings from the victim. (*Id.* at p. 577.) No DNA matching Sagin was identified on any of the items tested. (*Ibid.*) In assessing the impact of the test results, the Court of Appeal characterized the credibility of witnesses on both sides as "vulnerable" and noted that a key prosecution witness's testimony was "somewhat vague" and "susceptible of alternative explanations." (*Id*. at pp. 580-581.) Ultimately, opined the court, "[t]his case was close. In the end, there was no physical evidence linking Sagin to the crime. The jury therefore had to decide which witnesses to believe, as the prosecutor readily acknowledged in closing argument. Given that context, the ultimate question is whether the addition of the DNA evidence to Sagin's trial would have produced a reasonable doubt in the mind of at least one juror. We believe it would have." (*Id*. at p. 581.) The DNA evidence from the fingernail scrapings was the deciding factor: "Learning that there was DNA from an unidentified male under the fingernails of a victim whose hands almost certainly came into contact with her assailant, together with no DNA results matching Sagin, would have caused the jury to view more favorably the testimony of the witnesses who swore Sagin was nowhere near the crime scene." (*Id*. at p. 582.) Habeas relief followed. (*Ibid*.)

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§ 12:14. Postconviction challenges to scientific evidence received at trial

1) Changed Expert Opinions

In recent years, both California's courts and Legislature have focused increasing attention on the consequences of an expert who, after offering opinion testimony at trial, subsequently recants that opinion. An alternative postconviction scenario, involving habeas petitions premised upon other experts disputing the trial expert's position, has likewise been explored by the California Supreme Court. The long and involved saga of William Richards provides a comprehensive illustration of this trend. It includes two opinions by the California Supreme Court and one major statutory amendment to the statutory grounds for a state habeas petition.

2) In re Richards I

In In re Richards, 55 Cal. 4th 948, 150 Cal. Rptr. 3d 84, 289 P.3d 860 (2012), the California Supreme Court addressed the consequences, for purposes of habeas corpus litigation, of a prosecution expert who changes or recants his or her trial opinion. *Richards* involved a 1993 homicide in San Bernardino County. (55 Cal. 4th at 952.) The prosecution offered bite mark testimony from Dr. Norman Sperber, an expert in forensic dentistry. Dr. Sperber opined that the defendant had an unusual tooth pattern, and testified, "based solely on his experience as a practicing dentist, and expressly without the benefit of any scientific studies, that 'it might be one or two or less' out of a hundred people who would have [that] dental irregularity." (*Id*. at 955.) He then testified, based on a photograph of the victim's hand, that a visible lesion was a human bite mark "consistent with" the defendant's unusual dentition. (*Ibid*.) Ten years later, the defendant sought a writ of habeas corpus in state court and presented new information about the bite mark evidence, including Dr. Sperber's recantation of his trial testimony. (*Id*. at 956–957.) He claimed, consequently, that his murder conviction was based on false evidence, and also that he had discovered new evidence proving his innocence.

California law affords habeas relief on both grounds, among others. The writ may be granted if "[f]alse evidence that is substantially material or probative on the issue of guilt or punishment was introduced against a person at any hearing or trial related to his incarceration." (Pen. Code, § 1473, subd. (a)(1).) The writ may also be granted if the prisoner presents "newly discovered evidence" that both "undermines the prosecution's entire case" and "point[s] unerringly to innocence." (In re Clark, 5 Cal. 4th 750, 766, 21 Cal. Rptr. 2d 509, 855 P.2d 729 (1993).) In *Richards*, the defendant supported his habeas petitioner with a declaration from Dr. Sperber conceding that his statement at trial regarding the percentages of the population having Richards' dental irregularity was "not scientifically accurate," and further conceding that the lesion on the victim's hand may not even have been a bite mark, let alone caused by the defendant. (55 Cal. 4th at 956.) Richards' habeas petition included a declaration from another expert as well, who used "new scientific methods" of removing angular distortion from photographs to generate a better image of the victim's hand, thus permitting "a more accurate comparison between the hand lesion and [Richards's] lower teeth." (*Id*. at 956–957.)

The Court of Appeals denied habeas relief, and the California Supreme Court granted review. The court recognized that expert witnesses "very often testify regarding matters that lie at the frontier of human knowledge about a given subject," and consequently may rely on "evolving theories, assumptions, or methods." (*Richards*, *supra*, 55 Cal. 4th at 962.) Thus, an opinion

expressed in good faith at trial may later be shown objectively false without implicating the expert witness's integrity. Moreover, by its very nature opinion evidence has a subjective component that other evidence may lack; *i.e.*, scientists may reasonably disagree. Given these predicates, the court held that scientific evidence is not "false" for habeas purposes "[w]hen an expert witness gives an opinion at trial and later simply has second thoughts about the matter, without any significant advance having occurred in the witness's field of expertise or in the available technology …. Rather, in that situation there would be no reason to value the later opinion over the earlier." (*Id*. at 963.) Accordingly, a prisoner cannot meet the "false" evidence standard just by pointing to an expert who recants his or her trial testimony, or just by presenting a new expert opinion criticizing or casting doubt upon the scientific evidence at trial.

But, continued the court, if the prisoner can show by a preponderance of the evidence (*i.e.*, more likely than not) "that an expert opinion stated at trial was objectively untrue" due to a "generally accepted and relevant advance in the witness's field of expertise, or when a widely accepted new technology has allowed experts to reach an objectively more accurate conclusion," the false evidence standard does apply. (55 Cal. 4th at 963.) Only in this "narrow circumstance" will habeas corpus relief be granted on grounds of false evidence, and then only when the prisoner shows a reasonable probability that the false trial opinion affected the verdict.

Applying these principles to Dr. Sperber's trial testimony, the *Richards* court held, first, that Dr. Sperber's changed opinions after trial did not make his trial testimony "false" for purposes of habeas relief. (55 Cal. 4th at 964.) He never said that his revised opinions relied upon an advance in photographic technology; he only changed his opinion. (*Ibid*.) Nor, stated the court, does the fact that other experts likewise disagreed with Dr. Sperber's trial opinion make the latter "false." This is the subjectivity of opinion testimony at work; "good faith disagreements among credible experts are commonplace." (*Ibid*.) Further the photographic technique to remove angular distortions from images of teeth did qualify as "a generally recognized and relevant advance in technology," but was not capable of proving Dr. Sperber's statistical population estimate untrue or definitively eliminating the defendant's teeth as a possible source of the mark on the victim's hand. (*Id*. at 965.)

Second, the court held that the evidence presented by the defendant in pursuit of his habeas writ also did not qualify as "new evidence" pointing unerringly to innocence. Although the postconviction expert testimony did undermine Dr. Sperber's trial testimony, there was significant other evidence of Richards' guilt presented at trial. In light of this body of inculpatory evidence, the new evidence involving Dr. Sperber's trial opinion did not unerringly establish Richards' innocence. (55 Cal. 4th at 967–970.)

3) Legislative Response

Effective January 1, 2015, the California Legislature amended Penal Code § 1473 to address the consideration of new or changed or recanted expert opinion following conviction. Now, in addition to providing habeas relief if false evidence was presented that was "substantially material or probative on the issue of guilt or punishment" the statute defines "'false evidence'" as including "opinions of experts that have either been repudiated by the expert who originally provided the opinion at a hearing or trial or that have been undermined by later scientific research or technological advances." (§ 1473, subd. (e)(1).), the statute defines "false evidence" as including expert opinion later repudiated by that expert witness or which has been "undermined by later scientific research or technological advances" (§ 1473, subd. (e)(1)). The revised parameters of false evidence for state habeas purposes do not create new theories of liability for an expert who has repudiated her opinion or whose opinion has been undermined by scientific or technological advances. (§ 1473, subd. (e)(2).)

The California Legislature expressly acknowledged that the amendments to Penal Code section 1473 were responsive to the California Supreme Court's *Richards I* opinion. (Assem. Com. on Public Safety, Analysis of Sen. Bill 1058 (2013–2014 Reg. Sess.) as amended June 4, 2014, p. 5 (Assembly Analysis).) The analysis summarized the facts of the case, set forth the reasoning of the majority and dissent, and stated that the new statute would erase "the distinction between testimony by lay witnesses and testimony of experts created by the *Richards* decision but still requires that the court make a finding that it is reasonably probable that the verdict at trial would have been different without the expert's testimony before granting habeas relief." (Assem. Analysis, *supra*, as amended June 4, 2014, p. 6.)

4) In re Richards II

In the wake of the 2014 (effective Jan. 1, 2015) amendments to Penal Code section 1473, William Richards filed another habeas petition with the California Supreme Court. On May 26, 2016, the court issued a new opinion in the case: In re Richards, 63 Cal. 4th 291, 202 Cal. Rptr. 3d 678, 371 P.3d 195 (2016) (*Richards II*). This time it granted habeas relief and vacated Richards's conviction. In line with the new statutory directive, the court opined that the trial bite mark expert had "clearly repudiated his trial testimony," thus rendering it false for purposes of Penal Code section 1473. (*Id*. at p. 309.) Moreover, held the court, the new photography software developed since trial had permitted more definitive examinations that undermined the expert's trial opinion. (*Id*. at p. 310.)

Then, the 2016 opinion addressed materiality, i.e., whether the false evidence was so significant that there is a reasonable probability it affected the outcome. Despite evidence of guilt it deemed "strong" in its 2012 opinion, the 2016 court concluded that it was not strong enough to render the bite mark opinion less than "substantially material or probative." (*Richards II*, *supra,* 63 Cal.4th at pp. 313-315.) In so doing, the court emphasized the weakness of the prosecution's case against Richards, noting (1) the chronology of events left only minutes in which Richards could have killed Pamela; (2) the absence of shoe prints was unremarkable given the landscape; (3) Richards's familiarity with the crime scene and location of the bloody rocks could be reasonably attributed to his 30-minute wait for the first responding sheriff's deputy; (4) no evidence definitively established Pamela's time of death; (5) Richards had no visible injuries despite the apparent sustained active violence of Pamela's murder; and (6) the size and quantity of blood stains on Richards's clothing appeared inconsistent with what would be expected had he killed her. It was only to the prosecution's bite mark evidence, observed the court, that the defense lacked a substantial response. Accordingly, there was a reasonable probability that the bite mark evidence affected the outcome.

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Forensic DNA Evidence: Science and the Law § 13:1

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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:1. Introduction

Given the rapid pace of development in genetic science, it is easy to be dazzled by the science and recent technological advances to overlook the ethical and pragmatic considerations that are sure to follow. The legal and ethical issues that have emerged in the wake of these genetic advances are difficult and complex, particularly for lawyers and judges. The role of DNA in United States law was limited to matters of identity; it was used to establish paternity or compare blood samples. Today, the legal impact of genetic science extends well beyond the use of DNA evidence to establish identity. Genetic testing is now used to help predict life expectancy or determine the likelihood of someone suffering from a certain disease and perhaps even develop a cure for it. In just the last year, scientists can say that they have likely cured sickle cell anemia.[1] A cure for HIV-1 is now on the horizon.[2] Other outstanding research has also either created, or developed thousands of genetic tests that screen for diseases such as Tay-Sachs, Lou Gehrig's, Huntington's, Gaucher's, cystic fibrosis, inherited breast and ovarian cancer, colon cancer, muscular dystrophy, Li-Fraumeni syndrome, various forms of Alzheimer's,[3] and childhood blindness.[4] A recent study in its early stages uses CRISPR gene editing to help patients who suffer from Leber Congenital Amaurosis, a form of vision loss, to see colors better.[5] Scientists are also continuing to refine sophisticated brain testing techniques that may shed light on the truth of our statements, the contents of our memories, the causes of brain disorders and mood changes, and the motivations of our actions.

These genetic and neurological tests will inevitably raise new legal questions for society. On the one hand are the great benefits, such as more effective disease prevention and treatment through early detection. On the other hand, advances in genetics create risks of privacy invasion, employment discrimination, and denial of health or life insurance. As technology evolves and advances, science and law will become more deeply entwined. Technological strides have forced people to change and expand their ways of thinking about concepts such as privacy, discrimination, and life itself. They also create new avenues for genetic testing fraud and Medicare scams that the Department of Health and Human Services and the Inspector General are targeting on a nationwide basis.[6] To accommodate these developing issues, our legal system must be prepared.[7]

Footnotes

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Health and Human Services, https://repository.library.georgetown.edu/bitstream/handle/10822/512822/SACGHS_oversight_rreport.pdf?sequence=1&isAllowed=y (as of Feb. 12, 2024).

4 Hemant Khanna, Opinion: How gene therapy and CRISPR are helping to cure blindness, (as of Feb. 12, 2024).

5 Rob Stein, NPR, The CRISPR Revolution, A Gene-Editing Experiment Let Patients With Vision Loss See Color Again (September 29, 2021) (as of Feb. 12, 2024).

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Forensic DNA Evidence: Science and the Law § 13:2

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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:2. Genetics and identity

Genetic science has been playing an important role in our legal system for some time. In criminal cases, as this book discusses in detail, DNA has dramatically affected questions of identity.[1] Police, prosecutors, and defense counsel rely heavily on DNA evidence to do their jobs. Throughout the country, huge DNA databanks are being compiled with the genetic information of convicted offenders, arrestees, suspects, victims and their family members, and even witnesses, which can later be tested against samples from crime scenes. Using these databases, law enforcement authorities have been able to make arrests in crimes that have gone unsolved for decades. As of August 2023, the FBI's national DNA database includes genetic profiles of over 16 million offenders, more than 5 million arrestees. "Ultimately, the success of the combined DNA index system, or CODIS, will be measured by the crimes it helps to solve. CODIS's primary metric, the 'Investigation Aided,' tracks the number of criminal investigations where CODIS has added value to the investigative process. As of August 2023, CODIS has produced over 674,405 hits assisting in more than 656,893 investigations."[2]

Local DNA databases are fast becoming a more important tool of law enforcement because they operate largely outside of federal regulation and may therefore contain genetic identifiers not found in the FBI database, i.e., DNA profiles of suspects, victims and their family members, witnesses, and even abandoned biological material.[3] Use of these local databases is a controversial practice. Supporters argue that it "allows police to maximize the potential of genetic surveillance to solve crimes,"[4] but critics assert that it "has unleashed significant negative forces that threaten privacy and dignity interests, exacerbate racial inequities in the criminal justice system, and undermine the legitimacy of law enforcement."[5]

The advancements in DNA technology are possible in part due to large grants from the federal government. Indeed, since 2009, the Department's National Institute of Justice (NIJ) has invested nearly $300 million in its Research and Development funds in Forensic Science to support its Criminal Justice Purposes program—its largest ongoing research initiative—making it a global leader in the advancement of forensic science. "The program spans the breadth of forensic science disciplines from forensic biology, medicolegal death investigation, and toxicology, to trace evidence analysis and more."[6] The state and federal government investments in DNA forensic crime fighting technology will help identify victims, convict perpetrators, improve pathology training, and aid in solving cold cases to promote public safety.[7]

One of the ongoing challenges for law enforcement is how to address the backlog of DNA samples that have been collected over the years. Although it is not known how many Sexual Assault Kits (SAKs) are untested, some have estimated 300,000 to 400,000 untested kits exist. As of January 2022, they have documented nearly 90,000 untested kits in 37 states and Washington D.C.[8] Some call this situation "inexcusable" and ask, "why there is 'no true national outrage over this issue.'"[9]

Progress is being made toward clearing the backlog of untested SAKs. In July 2022, the Bureau of Justice Assistance's Management and Oversight of its National Sexual Assault Kit Initiative released the results of an audit conducted to identify and inventory all unsubmitted SAKs, assess the causes of the backlog and establish a process to ensure the management and oversight of the SAK initiative is accomplishing the Bureau's goals. The audit made several recommendations to improve the entire SAK

identification process, with recommendations that included increased participation from small agencies and providing updated performance metrics, and it is expected that the recommendations will help to address the SAK backlog in the near future.[10]

States are also committed to clearing the SAK backlog. In Memphis, Tennessee, rape victims took action by suing the city and law enforcement officials for failing to test more than 12,000 SAKs, alleging that the city's failure violated their right to equal protection under the 14th Amendment of the U.S. Constitution and allowed their assailants to remain at large and commit more rapes.[11] As a result of such pressure and publicity, several cities implemented more aggressive testing programs, and their efforts bore fruit: testing of old SAKs in Detroit and Cleveland resulted in hundreds of indictments and convictions and identified scores of repeat offenders.[12]

California's mandatory requirements for the submission and testing of sexual assault forensic evidence by law enforcement agencies and public crime labs, went into effect as SB 22 on January 1, 2020, and was codified in 2023 as Penal Code section 680 et seq SB 22 requires a crime lab to process sexual assault evidence and upload profiles to CODIS within 120 days or transfer the evidence within 30 days of receipt to another lab.[13] What this means is that "The first lab has 30 days to transmit the evidence to a second lab, and must upload a qualifying DNA profile to CODIS within 30 days after test results are obtained. (Pen. Code, § 680, subd. (c)(2)(B).) Therefore, if the first lab takes 30 days to transmit the evidence to a second lab, the second lab should take no longer than 60 days to process the evidence in order to ensure that the first lab has 30 days to upload a qualifying probative DNA profile into CODIS."[14]

SB 22 did not exclude cases that have already been solved. "If none of the sexual assault forensic evidence from a sexual assault case has ever been tested, the evidence must still be submitted to a crime lab and a qualifying DNA profile, if found, must be uploaded to CODIS. Even if the DNA evidence is not necessary to identify the suspect or to adjudicate or close the case for which it was collected, it may link the suspect to another case where the offender has not yet been identified."[15]

The California Legislature carved out an exception to the storing of DNA profiles from sexual assault cases when it passed SB 1228 in 2022-2023. Under that provision, the reference samples of DNA from a victim of a crime or samples of an individual's DNA that was voluntarily produced for purposes of exclusion, as well as any profile developed from those samples, may not be included in any DNA database that does not relate to the incident being investigated.[16]

Across the country, much work remains to be done, and there is a great need for additional resources to address this problem, that was officially recognized in 2013 by the United States Congress when it passed the Violence Against Women Reauthorization Act. The Act provides grants to aid local and state governments in conducting audits of the existing backlogs.[17] In 2018, $145 million in federal grants were awarded to help state and local government agencies process untested sexual assault kits.[18] In 2022, the Department of Justice "awarded $51.8 million—a nearly 45% increase in funding from the previous year—to provide victims of sexual assault with services in every state and the District of Columbia, as well as American Samoa, Guam, the Commonwealth of the Northern Mariana Islands, Puerto Rico, and the Virgin Islands."[19]

Scientists can already identify perpetrator DNA from low level samples that are found on crime scene items by using STR mix evidence for probabilistic genotyping.[20] The generally accepted scientific evidence reduces subjectivity in DNA typing results in cases involving several suspects.[21] Scientists are currently working on using a relatively new technology to further isolate and identify sperm cells of individual suspects in sexual assault cases involving multiple possible sperm contributors.[22] The technology, known as DEPArray extraction, enables the separation of cell populations before genetic analysis. It is currently used to isolate cancerous cells in brain tumors and could have a significant impact on the resolution of sexual assault cases with multiple suspects once scientists can prove its reliability and accuracy as a DNA identification tool.[23]

Of course, DNA identity evidence can aid the accused and the already-convicted as well as the accuser. It has, in the words of the United States Supreme Court, the "'unparalleled ability'" both to identify the guilty and to exonerate the wrongly convicted.[24] By April 2020, there had been over 375 postconviction DNA exonerations in the U.S., including 21 people who served time on death row, 44 who pleaded guilty to crimes they did not commit, and 130 who were wrongfully convicted of murder.[25] The average age at conviction was 26.6, and average age at exoneration was 43. Sixty-nine percent of the exonerations involved eyewitness identifications.[26] Fifty-two percent involved misapplication of forensic science, and false or misleading forensic evidence was a contributing factor in 29% of all wrongful convictions nationally.[27] Most recently, the "Innocence Project team helped exonerate nine people in 2023, from Hilo, Hawaii to Syracuse, New York. Together, the nine clients exonerated [last] year persevered through a combined time of 212 years in prison and [were] finally home for the holidays to make up for decades of lost time with their loved ones."[28]

All 50 U.S. states currently give inmates some form of postconviction access to DNA testing. Many of these statues are limited in scope and include substantial hurdles for individuals seeking access.[29] Many of these laws fail to include adequate safeguards for the preservation of DNA evidence and several of them do not allow individuals to appeal denied petitions for testing or allow those who are no longer incarcerated to seek testing.[30]

Although use of DNA evidence to identify and convict criminals is now widespread, a number of legal issues regarding this practice remain. As DNA databases have expanded, suspects increasingly have been identified through "cold hits," meaning that a match turns up when investigators compare the genetic profile of DNA found at a crime scene with DNA profiles in a database. Disputes have arisen in these cases as to the significance of the match. Because even unrelated people share, on average, two or three genetic markers, a DNA match is of little significance absent information about the likelihood the match occurred solely by chance. The smaller the likelihood of a random match, the higher the likelihood the defendant was the source of the DNA found at the crime scene. Using a statistical method called the "product rule," experts determine the rarity of a sample's genetic profile by selecting a set of genetic markers from the sample, estimating the frequency with which each marker appears in the relevant population, and multiplying the frequencies together to produce the complete profile's frequency in the population. This result is often also expressed as the probability that the DNA of a single person selected at random from the relevant population will match the evidentiary sample.[31]

Footnotes

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14 Ibid.

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17 Pub. L. No. 113-4 § 1004.

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Forensic DNA Evidence: Science and the Law § 13:3

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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:3. Cold hit cases

In cold hit cases, a match results not from comparing the crime scene sample to a single DNA profile, but from comparing that sample to many thousands, or even millions, of DNA profiles in a given database. As the number of comparisons increases, the chance of a coincidental match also increases.[1] As a result, defendants sometimes argue that the probability statistic obtained using the product rule in cold hit cases is inadmissible because it does not accurately reflect the probability of a random match. They assert that a different probability statistic should be used to reflect the number of comparisons involved in the database search and the resulting increased likelihood of a match. Of course, many, if not most, of the offenders in a law enforcement database may not be plausible suspects in a given case in view of the age of the crime and/or the appearance of the perpetrator as described by witnesses. Thus, the database probability statistic may not provide the jury with a probative estimate of the chance that a database search identified a coincidental match to an innocent person who is nonetheless plausible as a suspect given the facts of the case. So far, appellate courts addressing this issue have held that, although the product rule probability statistic does not accurately express the probability of a random match in a database search, it nevertheless is relevant and admissible because it accurately expresses the frequency with which a particular DNA profile appears in the general population.[2] The California Supreme Court has confirmed the admissibility of "cold hit" DNA evidence in a death penalty case involving a serial killer defendant, based on the statistical accuracy of the evidence and its relevancy to the defendant's identity.[3] Generally, courts recognize that a probability statistic reflecting the increased likelihood that a database search would produce a match may also be relevant and accepted as scientifically reliable.[4]

There is at least one documented case of an innocent person being charged based on a fluke match from a database search. In 1999, a man in Great Britain was arrested for burglary when a database search showed a match at six loci between his DNA, which had been taken after a prior family dispute, and DNA found at the crime scene.[5] It turned out, however, that the man lived almost 200 miles from the crime scene, had advanced Parkinson's disease, and could barely dress himself.[6] Officials refused to drop the charges until additional testing six months after the arrest at four more loci showed no match.[7] Of course, forensic testing has advanced considerably since 1999; now, techniques such as Y-STR testing, mtDNA testing, and testing of additional STR loci would be far more likely to eliminate a six-locus match before a case was ever charged. Moreover, in the United States, the FBI's National DNA Index System requires a minimum of 20 loci of data for a search.[8]

Other legal issues surrounding use of the product rule in cold hit, database search cases have arisen in the past. In 2001, an analyst running tests on Arizona's DNA database found two men who matched at nine of the 13 loci commonly used to distinguish people.[9] Additional tests showed that among the 65,000 felons in the database, 144 matched at nine or more of 13 tested loci.[10] Subsequent testing in other states has produced similar results; in Maryland, 32 matches of nine or more loci were found in a database with fewer than 30,000 DNA profiles, and 903 such matches were found in an Illinois database with about 220,000 profiles.[11] In the wake of these findings, defense lawyers around the country began asking for searches of their own state DNA databases, igniting a legal fight over whether DNA databases should be open to wider scrutiny.[12] Experts generally agree, however, that most, but not all, of these partial matches were to be expected statistically, because of the way the searches were conducted.[13]

Footnotes

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3 People v. Turner, 10 Cal. 5th 786, 272 Cal. Rptr. 3d 50, 476 P.3d 676 (Cal. 2020) (random DNA match probability calculated by product rule is an expression of DNA profile's statistical rarity, and therefore relevant in cold hit case).

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§ 13:4. Confrontation Clause

In 2012, the United States Supreme Court considered how the Sixth Amendment's Confrontation Clause impacts the use of DNA identity evidence during criminal trials.[1] During a rape trial, a prosecution expert answered "Yes" when asked, "'Was there a computer match generated of the male DNA profile *found in semen from the vaginal swabs of [the victim]* to a male DNA profile that had been identified as having originated from'" the defendant?[2] The defendant claimed this testimony violated the Confrontation Clause insofar as it indicated that one of the test samples came "from the vaginal swabs of" the victim, because the expert had no personal knowledge of that fact.

A divided court rejected the defendant's claim but was unable to produce a majority view explaining why. Four justices—Chief Justice Roberts, Justice Alito, and former Justices Kennedy and Breyer—agreed that the claim failed for two reasons: First, the Confrontation Clause does not apply to out-of-court statements not offered at trial to prove the truth of the matter asserted, and the phrase in question "was not admissible" to prove "the truth of the matter asserted—*i.e.*, that the matching DNA profile was 'found in semen from the vaginal swabs'" of the victim; "[r]ather, that fact was a mere premise of the prosecutor's question, and [the expert] simply assumed that premise to be true when she gave her answer."[3] Second, the DNA lab report, even if admitted into evidence, was "very different from the sort of extrajudicial statements, such as affidavits, depositions, prior testimony, and confessions, that the Confrontation Clause was originally understood reach."[4] From a policy perspective, the four justices who endorsed this analysis also expressed concern that, "[i]f DNA profiles could not be introduced without calling the technicians who participated in the preparation of the profile, economic pressures would encourage prosecutors to forgo DNA testing and rely instead on older forms of evidence, such as eyewitness identification, that are less reliable."[5]

Five justices rejected this analysis. Four of them—former Justices Scalia and Ginsberg and Justices Sotomayor, and Kagan—concluded that the phrase was offered to prove the truth of the matter asserted, and that admission of the testimony thus violated the Confrontation Clause.[6] The fifth—Justice Thomas—concluded that, even though the phrase was offered to prove the truth of the matter asserted, the Confrontation Clause was inapplicable "solely because [the lab's] statements lacked the requisite 'formality and solemnity' to be considered 'testimonial' for purposes of the Confrontation Clause."[7] He therefore provided the fifth vote to reject the defendant's Confrontation Clause claim. The four dissenters predicted that the court's fractured views would produce "significant confusion" about the Confrontation Clause's application in this area.[8]

That prediction, Justice Gorsuch recently wrote, has come true. Dissenting in 2018 from a denial of certiorari, he said the court's 2012 decision, by requiring lower courts to "distill holdings on two separate and important issues from four competing opinions," has "sown confusion in courts across the country."[9] He also said, in urging his colleagues to revisit the issue, that the court "owe[d] lower courts struggling to abide our holdings more clarity than we have afforded them in this area."[10]

Footnotes

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4 Id. at 2228.

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8 Id., at 2277 (dis. opn. of Kagan, J.); see U.S. v. Turner, 709 F.3d 1187, 1194 (7th Cir. 2013) ["the divided nature of the Williams decision makes it difficult to predict how the Supreme Court would treat" the analyst's report].

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§ 13:5. Chimerism

In very rare cases, a condition called chimerism can generate uncertainty in DNA test results. Chimerism exists where some of a person's cells have one DNA signature, and other cells have a completely different DNA signature. It occurs in people who have had bone marrow transplants, because the blood cells that transplanted marrow produce have the donor's DNA and the DNA in the rest of the recipient's body remains unchanged. “Historically, chimerism has been quantified from genomic DNA, but with technological advances chimerism from donor-derived cell-free DNA” is considered especially relevant in solid organ transplantation.[1]

Chimerism can also occur when two fertilized eggs in a woman's womb fuse to make one fetus. In 2005, police in Alaska investigating a sexual assault did a database search and found that the DNA collected at the crime scene matched the DNA in the blood cells of someone who was in jail when the assault occurred.[2] Eventually, they discovered that several years before the crime, the inmate had received bone marrow from his brother, so the DNA signature of his blood cells was identical to his brother's DNA signature.[3] When they tested cells from the inmate's cheek, they found no genetic match with the DNA from the crime scene.[4]

Chimerism also played a role in another unusual case. In 2002, a pregnant woman with two children applied for public assistance in the state of Washington. DNA testing administered as part of the application process indicated that the woman's DNA did not match her children's. After informing the woman that she could not be the children's mother, the state began legal proceedings to determine the children's parentage. The court advised the woman to get a lawyer, but she had trouble finding one willing to fight the power of DNA evidence. The court also ordered that an observer witness the birth of the woman's third child and watch as blood was drawn for another DNA test. The test results were the same; they showed no genetic match. Despite witnessing the birth, state officials suspected that the woman was acting as a surrogate mother, possibly for money. By chance, the woman's attorney heard about a Boston woman whose DNA also did not match her children's. The Boston woman was a chimera, possibly because two fertilized eggs in her mother's womb fused to make one fetus with two distinct genetic codes. Further testing on the woman in Washington showed she had the same condition and that her children were genetically related to her. Based on this testing, and 16 months after the first DNA results put parentage in question, the court found that the Washington woman was the children's mother and dismissed the case.[5] Although chimerism is rare, the Alaska and Washington cases at least raise the question of whether people have been, or could be, either falsely convicted or falsely exonerated based on DNA testing.

Footnotes

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§ 13:6. Indictment by DNA profile

Another issue that has arisen in criminal cases involves the practice of describing a suspect in a criminal complaint or indictment by DNA profile instead of by name. This occurs in cases where authorities recover genetic material associated with a crime but fail to match it to a named individual before the statute of limitations for the crime expires. The federal government and some states have expressly authorized this practice by statute.[1] Defendants are challenging it, arguing that filing charges by DNA profile fails to meet constitutional and statutory particularity requirements. Courts have generally rejected these challenges, at least where the charging document expressly includes or incorporates the suspect's DNA profile.[2]

Footnotes

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§ 13:7. Rapid DNA

DNA testing methods are still being refined and improved. One significant recent advance is something called Rapid DNA Technology, which has shortened DNA testing times from weeks to about 90 minutes.[1] It consists of automated DNA extraction, amplification, separation, detection, and analysis. The only human intervention is collecting a DNA sample— typically a buccal swab—and inserting it into the testing device.[2] Using this technology, several manufacturers have developed machines that can be placed right in the police station with the ability automatically to process a DNA sample taken from an arrestee, produce a DNA profile, compare it to DNA profiles stored in state and federal databases, and report any matches between the arrestee's profile and the stored profiles.[3] The idea is to do in the police station while the arrestee is being processed, what's currently done by outside laboratories in the weeks after an arrest.[4] The ability to perform real-time DNA testing during booking will have obvious and significant benefits for law enforcement officers. It will enable them to determine whether arrestees are connected to other unsolved crimes while they are still in custody.[5] The technology will enhance public safety and, by solving unsolved crimes, help preserve and allocate finite investigative resources. It will also relieve some of the backlog facing overburdened government DNA testing labs.[6]

Police departments across the United States have already been conducting pilot programs to test these mini DNA labs with state DNA databases, and they are reporting positive results.[7] Rapid DNA technology was successfully used for the first time in a criminal investigation in 2013, to apprehend burglars who stole more than $30,000 worth of items from the home of a member of the U.S. military who was away serving in Afghanistan.[8] In Arizona, Rapid DNA technology has been used to solve cases involving burglary, an officer-involved shooting in which the suspect left blood behind at the scene, and a sexual assault case.[9] In the court room, test results using Rapid DNA technology are already being admitted in criminal prosecutions.[10]

The technology is also used to identify victims who are burned beyond recognition following a catastrophic event. In California, Rapid DNA testing was used to quickly identify 58 victims of the 2018 Camp Fire in Northern California's Butte County—"the deadliest wildfire in California history."[11] The same Rapid DNA technology was used to identify 34 victims of the 75 foot Conception dive boat fire that occurred off the coast of Santa Barbara on September 2, 2019.[12]

At the federal level, the FBI has been looking at Rapid DNA technology for over a decade.[13] Its efforts have accelerated since the signing into law of the federal Rapid DNA Act of 2017, which directs the FBI to establish standards and procedures for Rapid DNA testing and allows DNA profiles produced by Rapid DNA machines in compliance with the FBI's standards and procedures to be run through the FBI's DNA database. Under prior law, only profiles produced by accredited labs could be run through that database.[14]

Of course, passage of the federal law does not mean that Rapid DNA testing will magically appear everywhere overnight. It will take time to train law enforcement personnel, to acquire the necessary equipment, and to connect all of the related systems. The FBI began testing its Rapid DNA booking communications structure in 2019 early 2020, and then integrated the technology

with state and federal booking processes.[15] So we will certainly see proliferation of this technology in the coming years. As we integrate artificial intelligence (AI) and machine learning into DNA analysis we could see significant improvements in the use Rapid DNA testing methods and forensic prediction accuracy. And there is both the hope and the expectation that the technology can someday—perhaps even soon—be taken out into the field, so that real time DNA analysis can be performed on site at the crime scene.

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§ 13:8. New investigative tools

As our ability to analyze and understand the impact of DNA advances, we can expect those in law enforcement to find new uses for DNA as an investigative tool. For example, in August 2008, FBI officials announced that they had used new DNA technology to help solve one of the nation's highest-profile cases: the 2001 anthrax attacks that killed five people and sickened 17 others.[1] Using sequencing technology that was not economically viable until 2005, investigators matched the DNA of the anthrax found in one of the victims to a single flask of the bacteria at an Army biodefense laboratory.[2] Using traditional law enforcement tools—interviews, searches, surveillance, and personality profiles—they then determined who had access to that flask, investigated those persons, and identified the alleged perpetrator.[3]

A recently developed research technique known as DNA sorting has matched a defendant's profile to show his DNA contributed to the DNA mixture of DNA found on a gun used to convict him as a felon in possession of a firearm. (United States v. Gissantaner, 990 F.3d 457, 114 Fed. R. Evid. Serv. 1919 (6th Cir. 2021).[4] According to the court, forensic labs are solving crimes by using the sorting process available in "several probabilistic genotyping software programs, including STRmix, LRmix, Lab Retriever, likeLTD, FST, Armed Xpert, TrueAllele, and DNA View Mixture Solution. The product used in [*Gissantaner*], STRmix, was created in 2011 by John Buckleton, a civil servant and forensic scientist who works for the Institute of Environmental Science and Research, a government agency in New Zealand."[5]

A high profile and controversial research tool that uses DNA to identify criminals through their relatives is known as familial database searching.[6] This technique locates profiles in a DNA database that closely resemble, but do not exactly match, the DNA the suspected perpetrator left behind at the crime scene.[7] It is based on the scientific fact that a person's DNA is much more similar to the DNA of the person's biological relatives than to the DNA of unrelated persons. Depending on the degree of the match, a partial match may suggest that the source of the DNA at the crime scene is a biological relative of the person identified from the database search.[8] Police can interview that person's relatives, hoping to identify and find the suspect.

The United Kingdom has been doing familial database searching since 2002, and has used it to solve several sensational crimes.[9] Maryland and the District of Columbia have banned the technique, and Montana requires judicial authorization to search a consumer DNA database but, as of 2018, 12 states permit it.[10] In 2008, California announced its intent to adopt the most aggressive familial database searching program in the nation.[11] Critics of this technique argue that it puts all family members under "genetic surveillance" for crimes they are not even alleged to have committed.[12] Proponents of familial testing counter that family members of those in DNA databases are not under "genetic surveillance" because they are not in any database. Other critics argue that it raises serious privacy concerns because "it turns family members into genetic informants without their knowledge or consent."[13] Some legal scholars assert that a familial database search constitutes an unreasonable, and therefore unconstitutional, search.[14] One constitutional law professor has warned that "if familial searching proceeds, it will create a political firestorm."[15] Because of such concerns, the FBI has so far declined to pursue familial database searching.[16]

In a related technique, investigators are using commercial, publicly available genealogical/ancestry websites to search for genetic relatives of the unidentified person who is the source of DNA found at a crime scene. Through this technique, in 2018, detectives in California arrested a 72-year-old man whom they believe committed a string of rapes and murders in the 1970s and 1980s. They submitted DNA leftover from some of those decades old crimes to a commercial ancestry website and identified the suspect's great-great-great grandparents. They then constructed about 25 distinct family trees of their descendants, located two descendants who were about the age and had ties to the locations of the crimes, surveilled one of those descendants, recovered an item he discarded, and performed DNA testing on the discarded item. The testing produced a match between DNA on the discarded item and DNA recovered at one of the crime scenes.[17] The perpetrator is now serving multiple life sentences without the possibility of parole after pleading guilty to 13 murders and 13 kidnapping-related charges (among other rape and robbery crimes for which the statute of limitations had run), and waiving his right to appeal.[18] Investigators in Minnesota, Washington, Pennsylvania, and North Carolina have since made similar use of genealogical websites to identify suspects and make arrests.[19] The advantages of forensic genetic genealogy used for genealogy research to locate biological relatives "dramatically improves the ability of consumers, including law enforcement, to identify distant relatives and provides investigators with more insight about the degree of relatedness—for example, whether the partial match is a parent, a sibling, or a cousin of the alleged perpetrator."[20]

A recent controversy has developed in California over the use of rape victim DNA to gather evidence in unrelated investigations. Under the California Penal Code, section 297, subdivision (c)(1), crime labs are generally allowed to store and analyze DNA in local databases to help law enforcement solve cases. The practice raises privacy and consent issues with victims and evidentiary issues that defendants convicted under the practice may challenge.[21]

Another emerging technique is using DNA to predict what a perpetrator looks like. In 2007, investigators used DNA analysis to determine whether the perpetrators of the 2004 train bombings in Madrid were of North African or European ancestry.[22] Researchers believe that, based on DNA analysis, they may eventually be able to predict the eye color, hair color, skin color, age, and facial dimensions of persons who leave genetic samples at crime scenes.[23] Criminal investigators are already using this technology to produce composite facial images that generate leads, narrow the list of suspects, and help identify unknown remains.[24] But critics warn that use of this technique "could contribute to racial profiling," and some legal experts say that it raises new Fourth Amendment concerns because it involves DNA linked to personal characteristics.[25]

DNA identification is also being used on the global stage. DNA-Prokids is an international project aimed at combating human trafficking using a worldwide database of genetic information to identify victims, especially children, and their families.[26] In its initial pilot study in 2008, DNA-Prokids successfully used DNA testing to identify 93 missing children and reunite them with their families.[27] In order to be most effective, the program will need DNA analysis to be mandatory globally every time a child is given up for adoption or claimed from an orphanage.[28] "However, the legal and social difficulties that exist for access and disclosure among countries may substantially slow the progress of implementing a comprehensive and effective counter-trafficking system."[29]

In the coming years, the next generation of forensic DNA investigations may increasingly involve the use of nonhuman DNA profiling techniques. In 1996, a man was convicted of murder after investigators used DNA testing to match cat fur found on a discarded jacket—which also was stained with the victim's blood—to the man's cat.[30] Scientists believe it may become commonplace to use DNA testing of fur shed by cats to link perpetrators, accomplices, witnesses, and victims to crimes under investigation.[31] Already, researchers have compiled a database containing almost 1,400 cat DNA sequences.[32] A unique canine DNA database also exists to help law enforcement agencies investigate and combat illegal dog fighting.[33] Eventually, researchers hope to identify criminal suspects based on DNA testing of the bacteria left behind at a crime scene.[34]

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§ 13:9. Genetics and behavior

The impact of DNA evidence in criminal trials is not limited to matters of identity. In a 1998 death penalty case in Georgia, a defendant complained that his counsel conducted an inadequate mitigation defense by failing to pursue genetic testing that might have shown a genetic basis for his violent and antisocial behavior.[1] The highest state court in Georgia affirmed the death sentence, but not because it questioned this use of genetics as mitigation evidence.[2] Twenty years later, in 2018, an appellate court in New Mexico held that a defendant should have been allowed to introduce at his murder trial expert evidence linking one of his genes to low impulse control and aggressive, antisocial behaviors.[3] The New Mexico Supreme Court recently reversed the appellate court to decide against allowing the proposed expert testimony that defendant possessed the so-called "warrior gene" after concluding the testimony was not relevant on the issue of deliberate intent in the absence of evidence that such susceptibility is so well understood as to be an indicator of a specific mental condition.[4] In California, juries convicted two alcoholic lawyers in separate matters for embezzling money from their clients. The attorney who claimed that a genetic disorder caused his alcoholism received a lighter sentence.[5] In another case, a jury found an accused murderer not guilty when her violence was linked to her Huntington's disease.[6]

These cases point to a growing trend involving genetic testing in criminal cases. Increasingly, defendants seek to use their own DNA to deny responsibility for and to mitigate their unlawful actions. They hope to avoid culpability or mitigate their conduct by proving they have a genetic predisposition for violent, impulsive, or antisocial behavior. According to these defendants, their criminal actions are not voluntarily, rather, they claim their actions were caused by their genetically predetermined Antisocial Personality Disorder or ASPD, something over which they have no control. Research may offer support for these claims, through studies showing that up to 62% of antisocial and criminal behavior has a heritable component, and identifying genes associated with violent behaviors and ASPD.[7] If further studies strengthen the links between particular genes and certain behaviors, genetically based defenses may become commonplace. Early research suggested that such defenses may be effective, at least in influencing sentencing judges. In 2012, researchers at the University of Utah reported that judges asked to sentence hypothetical offenders imposed lighter sentences—on average, seven percent shorter—when told that the offender was genetically predisposed to violence.[8] However, another study indicates that genetic evidence is ineffective in reducing judgments of culpability and punishment.[9]

The theory that violent behavior may be beyond a defendant's control because of genetics implicates important philosophical concepts that lie at the heart of our criminal justice system, including culpability, autonomy, and free will. Acceptance of the "DNA defense" would fundamentally change a legal system that, until now, has held almost everyone except the insane and mentally ill accountable for their actions.[10] On the other hand, a "DNA defense" may end up hurting a defendant's case more than it helps. For example, in 2009, a federal district court in New York, in a ruling later reversed on appeal, increased a defendant's sentence for possession of child pornography based on its belief that a gene the defendant was "born with" and could not "get rid of" led to his conduct and would likely cause him to reoffend.[11] Similarly, the Illinois Supreme Court has observed that evidence a defendant's family has a history of violence is not necessarily mitigating; though it may evoke compassion, it may also demonstrate the defendant's potential for future dangerousness.[12]

A 2005 survey of state and federal trial court judges in Maryland offers some insight into judicial perspectives on these issues.[13] Just over half (52.4%) of the respondents said they would admit at trial a positive test for a gene mutation associated with schizophrenia to show that a defendant did not have the criminal intent necessary for conviction.[14] On the other hand, approximately 80% said that, in considering a convicted defendant's future dangerousness during sentencing, they would not order testing to determine whether the defendant has a genetic predisposition to bouts of rage.[15]

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§ 13:10. Genetics in civil cases

We are also likely to see litigants in civil cases attempt to use genetic evidence in a variety of new ways.[1] Defendants in personal injury cases may offer genetic evidence on issues of both causation and damages. For example, in one toxic tort case, a chemical company that was sued on behalf of a child allegedly injured by the company's toxins obtained a court order for genetic testing, hoping to establish that an unrelated genetic condition, rather than the exposure, caused the child's condition.[2] In other toxic tort cases, a defendant may offer DNA evidence of a plaintiff's genetic predisposition to a particular disease, and argue either that there was no causation—because that predisposition, not the defendant's product, caused the disease—or that damages should be reduced because the plaintiff would have eventually developed the disease even without the toxic exposure.[3] A defendant may also offer genetic evidence that the plaintiff was not exposed to the defendant's product; or does not have a susceptibility to disease as a result of the exposure; or has a particular sensitivity, and was actually exposed, to some other product that causes the same disease.[4] To reduce damages awarded for an exposure that causes a lifelong disability, a defendant may even offer DNA evidence to show that, for reasons related to genetics, the plaintiff will live a shortened life.[5] Conversely, plaintiffs in toxic tort cases may offer DNA evidence to show they are genetically predisposed to developing disease from a particular product, and both the fact and extent of exposure.[6] This kind of evidence may be especially useful in "latent risk" cases, where plaintiffs assert that an exposure has increased their risk of developing a disease in the future.[7] In short, genetic evidence has the potential to transform toxic injury litigation.[8]

Maryland trial court judges also addressed these issues in their 2005 survey. Approximately 80% said they would order DNA testing to determine whether a genetic condition either made the plaintiff especially sensitive to pain or was the most likely cause of the plaintiff's injury, and over 70% said they would order such testing to determine whether the plaintiff had a genetic condition necessary for a given toxic exposure to produce disease.[9] Respondents were far more circumspect about genetic evidence of a shortened life expectancy; only about 40% said they would order testing of a 21-year-old plaintiff for the presence of an inherited disorder that caused death, on average, at age 36.[10] Some of those who were troubled about ordering genetic life-expectancy tests expressed concern about the potential psychological and social impacts on the tested plaintiffs and their families.[11] Others asked, "where does this stop?," and wondered, "how far do we go now with trying to predict life expectancy?"[12]

Family court judges also must deal with the impact of genetic evidence. Traditionally, genetic evidence in family law cases has been used to settle paternity questions.[13] Today, family court judges also use it to decide questions about parental rights. In South Carolina, a judge deciding whether to terminate parental rights ordered a mother to be genetically tested for Huntington's disease.[14]

Footnotes

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§ 13:11. Brain evidence in court

Now that courts have largely accepted DNA evidence, the question naturally arises: What will be the next major scientific advance in the legal quest for truth? Many believe the answer lies in the development of two sophisticated technologies for measuring brain activity: functional magnetic resonance (fMRI) imaging and something called "brain fingerprinting."

1) fMRI

fMRI imaging shows changes in the brain's blood flow during some behavior, thought, or activity, which in turn shows which parts of the brain are most active during that behavior, thought, or activity. Essentially, this scanning technology lets us see "what the brain is doing while it does it." Many believe that fMRI technology will someday have a tremendous impact on law and law enforcement. In 2001, researchers reported that "[t]elling a lie produces telltale changes in the brain" that can be detected with functional imaging technology. So, will we be able to use fMRI technology as the ultimate lie detector? Already, two companies are offering commercial lie detection testing using fMRI technology, claiming that their testing is more than 90% accurate for most types of lie detection sessions.[1] More complex technology (fMRI and machine-learning data analysis) has enabled major advances in memory detection and scientific knowledge about the nature of memory. But it has also brought us closer to asking whether the constraints on memory detection may be 'biological problems' as well as technological problems. That is, which limitations on memory detection come from the nature of memory itself?[2] Criminal courts have repeatedly refused to admit fMRI evidence on the grounds that current fMRI lie detection technology fails to meet evidentiary standards.[3] But fMRI technology may become a standard employee screening tool for companies looking to evaluate the trustworthiness of their workers.[4]

Other research also indicates that brain imaging technology can detect bias and distinguish true and false recollections. Such information would be very useful in dealing with witnesses. And, in any particular case, an imaging study can show whether the parts of someone's brain responsible for impulse control, empathy, aggression, and violence are either overactive or underactive.[5] In 2017, researchers reported that they could use brain imaging technology to determine whether subjects were acting intentionally or merely recklessly.[6] It is not surprising, then, that in a number of criminal cases, defendants have offered brain scans to show they could not have formed the mental state necessary for conviction, or to support an insanity defense, or to argue for a reduced punishment. Some of these claims have succeeded; others have failed, either because the courts have kept the evidence from the jury or because the evidence has simply failed to persuade the jurors.[7]

In 2021, the California Supreme Court found that similar brain imaging technology in a defendant's positron emission topography (PET) scan was excludable during the guilt phase of a death penalty case to show a connection between the defendant's temporal lobe epilepsy and her cognitive impairment at the time of her crime.[8] The Court concluded that the evidence was unreliable and would unduly prejudice and mislead the jury.[9] By contrast, some other state defendants have successfully obtained new trials based on a court's refusal to authorize neurological testing or to admit brain imaging evidence.[10]

As these cases show, brain imaging evidence, like genetic evidence, implicates philosophical concepts of culpability, individual responsibility, and free will that traditionally lie at the heart of our criminal law. On the other side of the coin, should prosecutors be allowed to introduce brain scans, either during trial to show that the defendant committed the crime, or during sentencing to show the defendant's future dangerousness? Should parole boards consider this evidence in deciding whether to grant parole?

2) Brain Fingerprinting.

Another technique that has received a lot of publicity and generated controversy, is known as "brain fingerprinting" or iCognative. According to its proponents, brain fingerprinting can tell us whether certain information is present or absent in a person's memory.[11] The technique is based on the principle that when a person recognizes an object or idea, his or her brain will emit an electrical response that is involuntary, distinctive, and measurable using electroencephalogram (EEG) sensors.[12] In theory, by exposing criminal suspects and defendants to crime-related information and measuring their brain responses, we can determine whether they know details of a crime that only the perpetrator could know, or whether they have memories consistent with their alibi.[13] In turn, the science could be used to exonerate the innocent and prevent false accusations.[14] In November 2001, Time Magazine profiled the inventor of brain fingerprinting as one of the 100 innovators who may be "the Picassos or Einsteins of the 21st Century."[15]

There are, however, doubters who say that brain fingerprinting is not ready for forensic use.[16] Some argue that the procedure is too subjective.[17] Others claim we cannot determine how the measured information got into the person's brain as a memory.[18] One researcher, who replicated the procedure in a laboratory using a Homeland Security grant, found that brain fingerprinting only detected 50% of the criminals.[19]

3) Legal Issues in Brain Testing

Significant technical obstacles remain before brain scanning technology can be effective. But even if the technical obstacles are overcome, several legal issues remain. For example, do the constitutional rights of privacy, against compulsory self-incrimination, and against unreasonable searches and seizures limit the use of brain scanning testing? And how will this technology affect the role of the jury? Will courts allow a search warrant for someone's brain?[20] In the United States, determining the credibility of witnesses has traditionally been treated as one of the jury's core functions. Should we allow this function to be taken over—either formally, or in fact, because of the great weight jurors often give scientific evidence—by this kind of brain imaging evidence?

In connection with conventional lie detectors, the United States Supreme Court has grappled with some of these questions. In a 1998 decision, eight of the court's nine justices voted to uphold a military rule of evidence banning the admission of polygraph evidence in court—martial proceedings.[21] Four of those eight argued that the ban serves the government's "legitimate" interest in "[p]reserving" the fact finder's "core function of making credibility determinations."[22] In reaching their conclusion, these four justices expressed "concern[]" that juries might "give excessive weight to the opinions of a polygrapher, clothed as they are in scientific expertise and at times offering … a conclusion about the ultimate issue in the trial."[23] But the four other justices who made up the majority—and the lone dissenting justice, who would have invalidated the categorical ban on polygraph evidence—expressly rejected this view, finding that it "demeans and mistakes the role and competence of jurors in deciding the factual question of guilt or innocence."[24] As it applies to brain scanning imaging, this debate will no doubt intensify if that technology proves to be as accurate as its proponents claim in terms of detecting lying.

Other courts are already grappling with issues related to brain scanning technology. In 2010, courts in New York, Maryland, and Tennessee rejected attempts to introduce fMRI results to show that witnesses—in one case, a criminal defendant—were telling the truth. In the New York case, the court, echoing the concerns of four United States Supreme Court justices in the

1998 polygraph case, reasoned that determining a witness's credibility is both "within the ken of" and "solely for the jury," and that the proffered fMRI evidence would impermissibly "intrude[ ] on" this jury function.[25] In the Maryland case, the court was swayed by testimony that test subjects could fool an fMRI by imperceptibly moving a finger or toe.[26] In the Tennessee case, a federal magistrate found in part that the scientific community had not yet accepted fMRI-based lie detection and believed that fMRI technology was "not ready to be used in real-world lie detection."[27] A federal district court judge later adopted the magistrate's findings and excluded the fMRI evidence. In 2012, the federal Sixth Circuit Court of Appeals affirmed the district court's decision.

To date, there have also been several cases involving brain fingerprinting. In 2000, Terry Harrington, who was serving a life sentence in Iowa for murder, asked for a new trial based on a brain fingerprinting test done more than 20 years after his conviction.[28] He claimed the test results showed that his brain did not contain significant information he would have known had he been at the crime scene, and *did* contain information consistent with the alibi he presented at his trial. After hearing from three expert witnesses, the trial court found that at least part of the science involved in the test was well established in the scientific community.[29] However, the court found that other parts of the test were not well accepted and were subjective.[30] It also expressed a more specific concern about the way the test was administered to Harrington.[31] Without really making a definitive ruling on the admissibility of the brain fingerprinting technique, the court denied Harrington's request for a new trial.[32] In 2003, the Iowa Supreme Court reversed and granted Harrington a new trial, but it based its decision on other issues and expressly declined to consider the brain fingerprinting test.[33]

In 2005, brain fingerprinting was at the center of another post-conviction appeal, this time in a death penalty case. Jimmie Ray Slaughter, who was on death row for murder, asked an Oklahoma court for a new trial based on a brain fingerprint test showing that his brain did not contain significant information about the crime.[34] He submitted an affidavit from the test's inventor detailing the extensive testing and peer-review of brain fingerprinting, its use of objective standards, its very low error rate, and its general acceptance within the relevant scientific community.[35] The court denied Slaughter's request, finding that without corroboration, the inventor's claims, though "interesting," even "startling," were ultimately "unconvincing" and "legally insufficient."[36] In March 2005, with his legal options exhausted, Slaughter was executed.[37]

Although United States courts have so far given brain fingerprinting only a lukewarm reception, law enforcement has embraced it enthusiastically. For example, in 1999, a Missouri sheriff asked the inventor of brain fingerprinting to test J. B. Grinder, who had been a suspect in an unsolved murder case for 15 years.[38] The test results showed that the record stored in Grinder's brain matched critical details of the crime scene that only the perpetrator would have known.[39] When presented with these results, Grinder pled guilty in exchange for a life sentence without the possibility of parole. He later confessed to having committed three other previously unsolved murders.[40] It is important to observe, however, that even though the neuroscience underpinning the technology is generally accepted as valid, the debate over how much deception it can reveal will continue to be the subject of disagreement in the United States.[41]

4) Brain Evidence Outside the U.S.

Outside of the United States, some courts have been more receptive to brain scanning technology similar to brain fingerprinting. Since 2008, several criminal defendants in India have been convicted of murder based in part on brain scans allegedly showing they had experiential knowledge about the crimes that only the killer could possess.[42] Even in India, this forensic use of brain scanning technology is not without controversy. A panel of scientists appointed there to review the technique has concluded that an insufficient scientific basis exists for admitting this type of brain scanning evidence in court.[43] And, in 2010, India's Supreme Court held that compulsory administration of brain scanning tests would constitute cruel, inhuman, or degrading treatment as defined by evolving international human rights norms, and would violate an individual's rights, under India's Constitution,

against self-incrimination, to substantive due process, to privacy, and to a fair trial.[44] In November 2013, a U.S. company announced it had been awarded a contract to train the Singapore Police Force in the use of brain fingerprinting technology.[45]

5) Addiction

Brain scans have also proven useful in terms of another subject that often comes up in criminal law: addiction. Research in neuroscience has enabled us to make much progress in understanding the biological basis for addiction. Based on imaging studies that show what is happening in the brain of someone who is going through withdrawal,[46] neuroscientists have found that "the brains of addicts are different from those of nonaddicts."[47] They have also found that abused substances stimulate the brain's reward system and induce feelings of pleasure that can override the basic survival activities.[48] The hope is that we can use this information to develop pharmaceuticals to effectively treat addiction and the lack of inhibitory control that it causes—and perhaps better address the intractable drug problem that inundates our courts.[49]

6) Civil Uses of Brain Evidence

The usefulness of brain-based technologies in the courtroom is not limited to criminal law. Those involved in civil suits also want to know whether witnesses and possibly even prospective jurors are lying or biased. In tort cases and disability hearings, defendants also want to know whether plaintiffs' claims of physical pain and mental distress are real or feigned. For over a decade, researchers have been trying to use fMRI technology to find objective measures of these traditionally subjective claims.[50] The applications of new scientific technologies ultimately may be limited only by a lawyer's imagination.

7) Outside the Courtroom

There will, of course, also be significant interest in using brain scanning technology outside of the courtroom. Employers may want to use fMRI scans in making hiring decisions. Law enforcement and government intelligence agencies may want to use both fMRI scans and brain fingerprinting to identify terrorists. How will these potential uses of brain-based technologies and the future use of Artificial Intelligence on the fMRI classifications fit with our employment laws and our constitutional guarantees, including our right of privacy, our Fifth Amendment right against self-incrimination, our Fourth Amendment right against unreasonable searches and seizures, and our First Amendment rights?[51]

New developments in regenerative AI are already showing promise for improved DNA and genetic testing. Some of the areas that will benefit from the use of advancements in AI technology include genetic variant analysis, disease risk assessment, data interpretation and genetic counseling. AI will also improve the identification of disease-causing genomic variants and assist development of the next generation of gene editing tools that will follow the use of CRISPR Cas9.[52] We can be sure that GED technology is rapidly changing with integration of AI advancements to create variants of Cas proteins that will help to identify cancer and other disease subtypes, and one day potentially engineer immune cells to target them.[53]

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Forensic DNA Evidence: Science and the Law § 13:12

Forensic DNA Evidence: Science and the Law | June 2024 Update
Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:12. Admissibility of new scientific techniques

Each technological innovation and each novel attempt to use scientific evidence in court will present a new and difficult question of admissibility. In federal court and in states that follow the federal rules, before admitting evidence based on a new scientific technique, a judge must make "a preliminary assessment of whether the reasoning or methodology underlying the [technique] is scientifically valid."[1] California takes a different approach; rather than decide whether a new scientific technique "is scientifically reliable or valid," judges in California must decide whether the technique "is generally accepted in the relevant scientific community."[2] Whichever test applies, new technologies will surely put judges to the test.

Footnotes

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Forensic DNA Evidence: Science and the Law § 13:13

Forensic DNA Evidence: Science and the Law | June 2024 Update
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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:13. Genetic privacy

1) Spectrum of Concerns

The legal implications of genetics extend well beyond evidentiary questions in the courtroom. Genetic privacy is one area of major concern and potential litigation. As James Watson once remarked: "We used to think our fate was in our stars. Now we know, in large measure, our fate is in our genes."[1] DNA is the blueprint of life. A DNA test can reveal an immense amount of very personal information about the person tested. Yet, a person's DNA is extremely accessible. DNA samples can be obtained with relative ease from a wide variety of sources. And, because genetic information is almost always stored electronically in large databases, it is more vulnerable than traditional paper medical records to unauthorized access. In response to such concerns, law enforcement DNA database programs have implemented strict controls and limits on the use and disclosure of DNA information. Moreover, the information stored electronically in these law enforcement databases represents a small fraction of the overall genome.

In addition, because of DNA's unique properties, the privacy implications of genetic testing do not stop with the person tested. DNA is inherited, so a genetic test reveals personal information about not just the person tested, but also that person's close blood relatives. For physicians, this aspect of DNA raises new ethical and confidentiality issues. Some physicians worry about the social and psychological impact of genetic testing of children, as well as their legal duty to disclose such predictive information.[2] When genetic information is medically insignificant but potentially stigmatizing, sharing it with parents and others can be harmful. On the other hand, if a patient refuses to share important genetic information with family members, does or should the law impose on the physician any disclosure obligation with respect to the patient's blood relatives?[3] Should potentially life-saving genetic information obtained from one family member trump doctor/patient confidentiality or implicate the privacy rule standards of the federal Health Insurance Portability and Accountability Act (HIPAA) of 1996, discussed further below?[4] In 1996, one New Jersey court took its turn at answering these questions in a case involving a woman who had colon cancer that spread through her body.[5] When she examined her late father's medical records, she found he had died from the same hereditary condition. She sued her father's physician for failing to warn her of her predisposition to the condition.[6] The New Jersey court found that physicians do have a duty to warn individuals known to be at risk of avoidable harm from a genetic condition.[7]

In 2001, the United States Supreme Court identified one of the key privacy issues associated with genetics: What are the legal "limits" on the "power of technology to shrink the realm of … privacy" guaranteed under the United States Constitution?[8] Answering this question in today's increasingly dangerous world puts our constitutional principles to the ultimate challenge. As one former federal jurist observed in 2001: "New technologies test the judicial conscience. On the one hand, they hold out the promise of more effective law enforcement, and the hope that we will be delivered from the scourge of crime. On the other hand, they often achieve these ends by intruding, in ways never before imaginable, into the realms protected by the Fourth Amendment."[9]

Judges have already been facing this test of conscience in lawsuits by convicted criminals alleging that mandatory collection of blood or, more commonly, buccal (cheek swab) samples for criminal identification purposes violates their Fourth Amendment

right of privacy. Virtually all of these challenges have been rejected, but not without controversy. When 11 judges of the Ninth Circuit Court of Appeals faced the issue in 2004, they could not produce a majority opinion.[10] Six judges voted to uphold the federal government's DNA testing program, but the judge who provided the swing vote wrote a separate opinion using a different analysis and limiting his conclusion to convicted criminals who are still on supervised release.[11] As to those who have completed all aspects of their sentence, he posed this question: "'Should the [DNA profile] be erased'" because of the "substantial privacy interest at stake?"[12] Without sufficient controls, maintaining these profiles implicates our interest in privacy, because, in today's technologically advanced world, "databases can be 'mined' in a millisecond using super-fast computers … extensive information can, or potentially could, be gleaned from DNA," and "this data can easily be stored and shared by governments and private parties worldwide."[13] Four of the dissenting judges sounded this similar warning: "[T]he DNA placed in the [federal] database contains sensitive information, and no one can say today what future uses will be made of it once it is entered into governmental files."[14] "Even governments with benign intentions have proven unable to regulate or use wisely vast stores of information they collect regarding their citizens."[15]

These considerations are reflected in a 2009 federal district court's holding that it violates the Fourth Amendment to include in a DNA database the genetic profile of a criminal victim.[16] In 2000, the defendant in the Maryland case was treated at a hospital as a gunshot victim, and his bloody clothes were collected and retained as evidence.[17] Four years later, he became a suspect in an unrelated murder, and the police retrieved his clothes from the property room and performed DNA testing on the blood stains.[18] The testing excluded the defendant as the perpetrator, but the police then put his genetic profile into its DNA database.[19] Two months later, the defendant's profile registered a "hit" during a database search in connection with another murder.[20] The court held that, on these "rather unique facts," inclusion of the defendant's DNA profile in the database was not "reasonable under the Fourth Amendment."[21] "Were law enforcement permitted to include individuals' DNA profiles in searchable databases under these circumstances," the court warned, "it would open 'a backdoor to population-wide data banking.'"[22]

Privacy concerns about future uses of DNA on file with the government are likely to grow as our technological abilities and understanding increase. To minimize privacy issues, federal authorities, in generating the DNA profiles in their database, primarily use what, at least until recently, has been known as "junk DNA," i.e., noncoding DNA that is not associated with any known physical or medical characteristic.[23] In a 2007 decision, the Ninth Circuit Court of Appeals cautioned that "with advances in [genetic] technology, junk DNA may reveal far more extensive genetic information" than it currently does.[24] The court also cautioned that the Fourth Amendment analysis might change as "the uses to which 'junk DNA' can be put" become "significantly greater."[25] Researchers in 2012 suggested the importance of the court's warning, when they reported that so-called "junk" DNA actually plays a critical role in controlling how cells, organs, and other tissues behave.[26] Other research has linked non-coding DNA sequences to biological processes—like ensuring the proper bundling of chromosomes inside a cell's nucleus and developing opposable thumbs—and even human diseases, including several forms of cancer,[27] and nerve damage that occurs with multiple sclerosis.[28] However, a 2017 study using mathematical models maintains that only 10 to 15 percent of our DNA is functional, with an upper limit of 25 percent.[29]

A more recent study by researchers at University of California, Berkeley, and Washington University "explored the function of one component of this junk DNA, transposons, which are selfish DNA sequences able to invade their host genome. The study shows that at least one family of transposons — ancient viruses that have invaded our genome by the millions — plays a critical role in viability in the mouse, and perhaps in all mammals. When the researchers knocked out a specific transposon in mice, half their mouse pups died before birth."[30] This interesting discovery is the first of its kind to show that junk DNA is critical to the survival of mammals.[31]

Privacy concerns about the use of DNA on file with the government are also likely to grow as DNA database collection and search programs expand. In 2006, following the lead of 13 states, the United States Congress significantly expanded the federal DNA collection program beyond convicted felons, by including "individuals who are arrested, [or] facing charges," and "non-United States persons who are detained under the authority of the United States.[32] Proponents of the expanded program argue that it "will save lives, prevent crimes, and bring justice for victims and their families."[33] Across the country, defendants have challenged the constitutionality of these expanded testing programs, and appellate courts—and often judges within the same appellate court—have reached differing conclusions about whether the Fourth Amendment permits compelled testing of all felony *arrestees*.[34]

In 2013, a 5-4 majority of the United States Supreme Court rejected a Fourth Amendment challenge to a Maryland law requiring the collection and analysis of DNA samples from those arrested for and charged with, but not yet convicted of, a crime of violence or an attempt to commit a crime of violence, or with burglary or attempted burglary.[35] Comparing DNA identification to fingerprinting, the majority reasoned that law enforcement's interest in identifying arrestees outweighs the minimal physical intrusion in collecting a DNA sample by swabbing the inside of a person's cheek.[36] The skeptical dissenters said that analogizing DNA searches to fingerprinting is "apt only to those who know no more than [the majority] has chosen to tell them about how … DNA searches actually work." They also said the majority's view that DNA is being taken, not to solve crimes, but to identify those in the state's custody, "taxe[d] the credulity of the credulous."[37]

In 2018, courts relied on the U.S. Supreme Court's decision to reject state and federal constitutional challenges to a California law requiring the collection and analysis of DNA samples from any felony arrestee.[38] Plaintiffs in these actions argued that the California law was unconstitutional because of three differences between it and the Maryland DNA collection law the Supreme Court upheld in 2013: (1) it applies to *any* felony arrestee, not just those arrested for a crime of violence; (2) it provides for analysis of the DNA sample *before* a judicial finding of probable cause to arrest or the filing of charges; and (3) it does not require automatic expungement of DNA samples and profiles as to arrestees who are never charged, prosecuted, or convicted.[39] A 4-3 majority of the California Supreme Court rejected these arguments and upheld the law—under both the state and federal Constitutions—as applied to someone validly arrested for, charged with, and ultimately convicted of a violent offense.[40] The majority's limited holding expressly left open the question of the law's constitutional validity as applied to those arrested without probable cause, never charged with or prosecuted for a crime, or ultimately exonerated.[41]

Genetic privacy issues have arisen in other contexts. For example, the U.S. Department of Justice announced under the authority of the DNA fingerprinting Act of 2005, title X of Public Law 109-162, that it will collect the DNA of detained immigrants and asylum seekers.[42] With nearly 750,000 samples to be collected, some criticize the plan's utility of taking the DNA of individuals who have never lived in the U.S., and have expressed concerns about the testing's constitutionality.[43] DNA collection is also currently required of the men and women of the United States military, who must give blood and tissue samples to the Department of Defense for its DNA Registry, which helps identify those who are killed in combat.[44] In 1995, two Marines refused to submit DNA to the Registry, because of concern that their genetic information might be used against them in the future. They also argued that the nonconsensual storage and use of their DNA violated their Fourth Amendment rights. They were court-martialed for their stand. A federal district court upheld the DNA sample requirement.[45]

At least one federal court has upheld a person's right to genetic privacy, if only to a limited degree. In 1998, the Ninth Circuit Court of Appeals held that an employer may not test employees for "highly sensitive" medical and genetic information without their consent.[46] The case involved an employer's alleged testing of employees for syphilis, the sickle cell trait, and pregnancy, without their knowledge. According to the unanimous Ninth Circuit panel, "[o]ne can think of few subject areas more personal and more likely to implicate privacy interests than that of one's health or genetic make-up."[47]

2) Federal Legislation

As noted *ante*, at page 27, genetic privacy issues have also been the focus of legislation. The HIPAA's main focus was establishing protections for health insurance coverage, but it also set standards for protecting the privacy of health data. It did not, however, include any specific protections for an individual's genetic information. To fill this gap, the United States Department of Health and Human Services, in promulgating regulations to implement the HIPAA, made clear that the statute's privacy protections extend to genetic information.[48]

In May 2008, the United States Congress passed, and former President George W. Bush signed into law, the Genetic Information Nondiscrimination Act of 2008 (GINA). In terms of privacy protection, the GINA specifically provides that genetic information must be treated as health information under the HIPAA, and that violations of the HIPAA privacy regulations with respect to the use or disclosure of genetic information are subject to the HIPAA's penalties, including civil and criminal monetary penalties up to $250,000 and prison terms up to 10 years, depending on the violator's knowledge and intent.[49]

3) State Legislation

At the state level, as of 2019, every state except Mississippi had enacted laws addressing genetic testing, privacy, or discrimination in some form.[50]

California, Arizona, and Utah recently enacted new privacy laws to address the responsibility of genetic companies to protect individual privacy when collecting DNA samples. In California, the Genetic Information Privacy Act (GIPA)[51] adds several sections to the state Civil Code beginning at section 56.18, part 2.6, and acts in tandem with other consumer privacy laws. It holds genetic testing companies accountable for their data collection practices.[52] The law requires the companies to obtain written consent from individuals when it seeks to use the genetic data and applies to any company that "sells, markets, interprets, or offers genetic testing products or services directly to consumers, analyzes genetic data, or collects and maintains genetic data."[53] California also requires genetic testing companies "to honor a consumer's revocation of consent in accordance with certain procedures, and to destroy a consumer's biological sample within 30 days of revocation of consent."[54] "Vendors must obtain separate consent for the use of genetic data for each purpose before transferring it to other parties or using the data for marketing. Companies are also expected to implement security procedures to protect the data from destruction, unauthorized use, or modification."[55] Any violation of the law is subject to strict fines and penalties for a purposeful violation.[56] The law is an important component of consumer protection in the growing use of DNA technology in both public and private life.

4) DNA Theft

One possible next step is defining the distinct crime of "DNA theft."[57] With the "proliferation of direct-to-consumer DNA tests that are increasingly inexpensive and readily accessible," the risk is ever increasing that "third parties may attempt to collect and analyze anyone's DNA without consent."[58] Legislatures and courts are beginning to address these issues on an increasingly frequent basis.[59]

Footnotes

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Forensic DNA Evidence: Science and the Law § 13:14

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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:14. Genetic discrimination in employment and insurance

1) Legal Issues

Legal issues relating to genetics commonly arise in the context of employment and insurance. A 2002 University of Illinois survey of 84 Fortune 500 companies revealed that 35% used medical records, including genetic information, to make decisions about hiring, firing, and promotion.[1] A similar 1996 survey documented more than 200 instances of workplace discrimination based on the detection of genetic predispositions.[2] For example, in one case, a young social worker who received excellent performance reviews for several months was fired after her employer learned she was at risk for Huntington's disease, a hereditary nerve disorder.[3] In another case, a 53-year-old man explained during a job interview he had a genetic disorder, but that it had not yet caused any symptoms. At his next interview, he was offered the job, but was told that because of his genetic condition the offer did not include health insurance. He said he would accept these terms but was later told that the employer had completely withdrawn the offer, again because of his condition.[4]

Hiring, firing, and promotion are not the only areas in which employers may seek to use their employees' genetic information. In 2001, the Equal Employment Opportunity Commission (EEOC) sued an employer for genetically testing its employees to determine their predisposition to carpal tunnel syndrome. The employer apparently hoped to limit its workers' compensation liability.[5] The case settled, with the employer agreeing to halt the testing and to serve as an advocate in favor of federal legislation prohibiting genetic discrimination.[6]

Health insurance coverage is another area of concern. Although scientists already have a battery of thousands of genetic tests for various diseases and disorders, successful treatments exist for only a very few of these conditions.[7] Thus, insurance companies have a tremendous incentive to consider an applicant's genetic information. Studies have shown that 25% of people in families with a known genetic condition have been denied health insurance coverage because of their genetic status, whether they were sick or not.[8] For example, in one case, a life insurance company denied coverage for two children because one of them had Hurler syndrome, a fatal genetic condition; it offered no reason for refusing to cover the child without the condition.[9] In a 1996 survey of 332 people who either had genetic disorders or had family members with genetic disorders, 43% reported they had been denied health insurance, life insurance, or employment based on disclosure of this information.[10] A 2007 study indicated that individuals with genetic conditions are twice as likely to report having been denied health insurance than individuals with other chronic illnesses.[11] With the rapid progress in genetic technology in just the past decade, a new survey might well show an even higher percentage.

The problem of genetic discrimination in insurance and employment has a number of effects. On the individual level, aside from the obvious unfairness to those discriminated against, fear of genetic discrimination will discourage people from taking genetic tests, thus depriving them of the potential benefits of prevention and early detection. According to Memorial Sloan-Kettering Cancer Center in New York, the fear of genetic discrimination is a leading reason people cancel appointments for tests that detect cancer risk.[12] This obviously has negative ramifications in terms of the possibility, effectiveness, and costs of

treatment should disease eventually develop. Of course, these negative effects impact not just the individual, but society at large. In addition, fear of genetic discrimination discourages people from participating in medical research studies, which prevents us from fully realizing the benefits genetic science has to offer.

2) Federal Legislation

After considering legislation dealing with these issues for over a decade, the U.S. Congress passed the Genetic Information Nondiscrimination Act of 2008 (GINA) to address genetic discrimination in health insurance and employment.[13] By amending several federal statutes, the GINA imposed new restrictions on the collection, use, and disclosure of genetic information by covered employers and insurers.[14] In general, it bars health insurers from denying coverage or adjusting premiums based on a person's predisposition to a genetic condition; prohibits employers from discriminating on the basis of predictive genetic information; prohibits employers (with limited exceptions) from requesting, requiring, or purchasing "genetic information" about employees or their families; prohibits employers from retaliating against anyone for opposing a prohibited act of genetic discrimination; and prohibits both employers and insurers from requiring applicants and their family members to submit to genetic tests.[15] Notably, "genetic information" under the GINA includes not only genetic test results, but also information regarding family history of disease.[16]

On the employment discrimination side, the remedies and enforcement provisions under the GINA are the same as those under Title VII of the 1964 Civil Rights Act, and include both government (e.g., EEOC) and private actions for reinstatement, back pay, front pay, injunctive relief, and compensatory and punitive damages.[17] However, the GINA expressly prohibits the "disparate impact" theory of liability, although it provides for reevaluation of this prohibition based on further developments in genetic science.[18] On the insurance discrimination side, the GINA provides for substantial monetary penalties and injunctive relief, including retroactive reinstatement of health care coverage.[19]

One of the GINA's congressional sponsors called it "the first major new civil rights bill of the new century."[20] In passing it, Congress noted our nation's checkered past with regard to genetic science, including forced sterilization of those with certain presumed genetic defects and discrimination against members of racial and ethnic groups with which particular genetic conditions and disorders were principally associated.[21] Congress also found that because the "existing patchwork of State and Federal laws" regarding genetic discrimination was "confusing and inadequate," "[f]ederal legislation establishing a national and uniform basic standard [was] necessary to fully protect the public from discrimination and allay their concerns about the potential for discrimination, thereby allowing individuals to take advantage of genetic testing, technologies, research, and new therapies."[22] In other words, as another of the legislation's sponsors remarked, Congress hoped that the GINA, "by alleviating the most common fear about genetic testing," would "accelerate research," "unlock[] the great promise of the Human Genome Project," and enable "Americans to finally realize the benefits and health care savings offered by gene-based medicine."[23]

Probably the most notable component of the statutory "patchwork" that predated the GINA is the Health Insurance Portability and Accountability Act (HIPAA) of 1996, discussed earlier. The HIPAA was the first federal law specifically to address genetic discrimination in health insurance.[24] It precludes group health insurers from using genetic information as a basis for denying or limiting eligibility for coverage, or from treating genetic information as a preexisting condition where there is no current diagnosis of any associated condition or illness.[25] It also prohibits group insurers from charging a different premium to a particular individual within the insured group based on that individual's genetic information.[26] The HIPAA does not, however, prohibit covered insurers from raising premiums for everyone in an insured group based on genetic information, from seeking genetic information, or from requiring genetic testing. It also does not apply to private individuals seeking health insurance in the individual market; it covers only employer-based and commercially issued *group* health insurance.[27] Because of these

features, the HIPAA left significant gaps in protection. The Americans with Disabilities Act may also provide some protection against genetic discrimination in employment, but both the existence and scope of the protection is open to legal question.[28]

In 2010, the U.S. Congress passed the Patient Protection and Affordable Care Act (ACA), which amends the Public Health Services Act (PHSA), in part, to increase protection of genetic information.[29] The ACA prohibits insurers from denying coverage to individuals due to pre-existing conditions,[30] which precludes them from denying coverage based solely upon genetic information. It also precludes insurers from basing coverage eligibility on an applicant's "health status-related factors," which expressly includes "genetic information."[31] It provides for "guaranteed issue" of insurance policies and requires insurers to accept every individual or group, subject to certain conditions.[32] It also provides for "guaranteed renewal," which requires insurers to renew policies when they expire, absent certain conditions, such as nonpayment of premiums.[33] Thus, insurers may not decline to issue or renew policies based upon genetic information. Finally, the ACA prohibits insurers from varying rates, absent specified factors such as tobacco use, age, or geographic area.[34] Genetic information is *not* one of the specified factors, so insurers may not raise premiums based on recently discovered genetic information. Many of these protections may overlap with protections under the GINA.[35]

3) State Legislation

At the state level, as of January 2017, 49 states and the District of Columbia had some sort of law pertaining to the use of genetic information in health insurance,[36] and 34 states and the District of Columbia provided some level of protection against genetic discrimination in employment.[37] The employment laws all prohibit discrimination based on genetic test results; many extend protection to inherited characteristics, and some include family members' test results, family history, and information about genetic testing, such as the receipt of genetic services.[38] Most also restrict employer access to genetic information, with some prohibiting employers from requesting, requiring, or obtaining genetic information or genetic test results, or directly or indirectly performing or administering genetic tests.[39]

The discrimination protections are extremely important now that precision medicine is improving its ability to determine unique genetic factors that make up individual genetic characteristics. According to the US National Institutes of Health (NIH), "precision medicine is 'an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person'. Many rare diseases are caused by a single gene defect. More common diseases such as diabetes and heart disease are polygenic and complex in nature, but scientists are identifying genetic factors that predict the risks of these diseases with greater precision and accuracy. Other genetic research is aimed at strengthening the predictive power of genome-wide polygenic scores for specific measures of intelligence (and/or educational attainment) and athleticism." Thus, although the future of disease cure and genetic characteristic determination looks promising, equally important is keeping the legal protections in place so the genetic information does not get into the wrong hands.[40]

4) GINA and Covid-19 Vaccines

The advent of the Covid-19 pandemic gave rise to new questions about GINA's application when employers administer the Covid-19 vaccine to employees or require employees to show proof that they received the vaccine before allowing them to return to work. The general consensus is that either administrating the vaccine to employees or requiring proof of vaccination before allowing employees to return to work once the pandemic waned does not implicate GINA because it "does not involve the use of genetic information to make employment decisions, or the acquisition or disclosure of 'genetic information' as defined by the statute. This includes vaccinations that use messenger RNA (mRNA) technology."[41] On the other hand, if employees are required to answer pre-vaccination screening questions that inquire about family genetic history, such inquiries might violate GINA.[42]

The science used to develop and administer the mRNA vaccines has raised other questions about genetics. These questions focus on "whether such vaccines modify a recipient's genetic makeup and, therefore, whether requiring an employee to get the vaccine as a condition of employment is an unlawful use of genetic information. The CDC has explained that the mRNA COVID-19 vaccines 'do not interact with our DNA in any way' and 'mRNA never enters the nucleus of the cell, which is where our DNA (genetic material) is kept.' Thus, requiring employees to get the vaccine, whether it uses mRNA technology or not, does not appear to have violated GINA's prohibitions on using, acquiring, or disclosing genetic information."[43] A recent California Court of Appeal opinion implicitly adopted that position when it held that the necessity exception to the Confidentiality of Medical Information Act (CMIA) shielded a public elementary school, school district, and principal from liability for an employee's claim for discrimination after she was terminated for refusing to authorize release of her COVID-19 vaccination status or get tested weekly for COVID-19 in compliance with a state public health order (Cal. Civ. Code § 56.20(b).) (Rossi v. Sequoia Union Elementary School, 94 Cal. App. 5th 974, 996–997, 312 Cal. Rptr. 3d 738, 420 Ed. Law Rep. 511 (5th Dist. 2023), review denied, (Dec. 13, 2023).).

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Forensic DNA Evidence: Science and the Law § 13:15

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Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:15. Medical issues

1) Gene Therapy

For about 30 years, scientists and researchers have been trying to develop gene therapy techniques to treat a host of diseases and conditions. Using recombinant DNA technology, gene therapy involves the insertion of normal DNA into cells to treat medical conditions caused by mutated genes.[1] In gene therapy studies, a carrier called a "vector" is used to insert a normal gene into the genome as a replacement for an "abnormal" disease-causing gene. Typically, vectors are some kind of virus, because viruses have evolved a way of encapsulating and delivering their own genome into our cells. Geneticists take advantage of this capability, but only after using recombinant DNA techniques to eliminate the virus's own disease-causing features. In place of the harmful viral genes, the human therapeutic gene of interest is inserted into the viral genome.

After a gene therapy vector is prepared, it is inserted into the patient's target cells, such as lung, liver, or bone marrow. The vector then unloads its genetic material. When the process is successful, generation of a functional protein from the therapeutic gene restores the target cells to a normal state. The goal with gene therapy is not simply to treat the symptoms of the disease, but to fix the problem at its core by inserting a healthy gene into a person's cells, which then produces the correct protein.

In 1995, researchers reported what is generally agreed to be gene therapy's first clear clinical success: treatment of children with severe combined immunodeficiency (SCID), which is more commonly called "bubble boy syndrome."[2] Since then, progress has been slow, and there have been numerous setbacks. But in 2017, there were several important breakthroughs. In the last quarter of that year, the U.S. Food & Drug Administration (FDA) announced its first approvals of gene therapy products: one to treat a form of leukemia, another to treat a form of lymphoma, and a third to treat a rare eye condition that destroys cells in the retina needed for healthy vision.[3] In December of that year, researchers conducting a clinical trial announced a major advance in a gene therapy for a blood-clotting disorder (hemophilia B).[4] Recently, however, the gene therapy developer has been exploring whether a volunteer's liver cancer was caused by the therapy or an unrelated mechanism.[5] In 2019, researchers reported promising results with a gene therapy product to treat sickle cell disease, but that trial was halted this year as a cautionary measure after two patients developed cancer.[6] Despite these setbacks, scientists are optimistic about the future of gene therapy as a medical revolution that will eventually offer a cure—not just a treatment—for a broad range of ailments, including cancer and AIDS.[7] Most recently, Science Daily reported that scientists from Nagoya University in Japan have found that the drug Fasudil reverses key symptoms of schizophrenia in mice (February 17, 2023), and the University of London is developing a gene therapy that controls gene expression in overactive cells that may suppress excessive activity of a small number of brain cells that cause epilepsy (November 3, 2023).[8] Both studies provide insight into the rapidly changing landscape in DNA technology.[9] Although the FDA has approved only a limited number of gene therapy products by the end of 2022, scientists anticipate many more approvals in the coming years.[10]

2) Germ Line Editing

Current gene therapy techniques involve modifying the DNA of somatic cells, which are cells other than sperm and egg cells. Genetic alterations in somatic cells are not passed on to future generations through reproduction. But a groundbreaking technique that makes DNA editing much easier and more precise—known as CRISPR-Cas9—has brought new focus to the possibility of producing genetic changes that are inheritable.[11] Two scientists, Emmanuelle Charpentier of the University of Vienna (now with the Max Planck Institute for Infection Biology) and Jennifer Doudna, of UC Berkeley—known as the CVC Group, first filed for a CRISPR patent in 2012. They received the 2020 Nobel Prize in Chemistry for their work in developing the CRISPR-Cas9 gene editing tools.[12]

Other scientists, however, including Feng Zhang and George Church, who are members of the Broad Institute from Harvard and MIT, also contributed to CRISPR's development, and have been engaged in a prolonged patent dispute with the UC and Vienna Nobel Prize winners over who's discovery was the most important and commercially lucrative.[13] The Broad Institute said its later 2014 patent was distinct from the original 2012 invention of Charpentier and Doudna because it concerned the use of CRISPR in eukaryotic cells—those with membranes—for gene-editing and other purposes. The Broad Institute claims that its patent for the CRISPR technology is more important, and more commercially valuable as a license, because cells in the human body are eukaryotic.[14]

In the latest round of patent litigation, an appeals board of the U.S. Patent and Trademark Office (USPTO) held that the Broad Institute had made the "'actual reduction to practice' of CRISPR's ability to edit eukaryotic cells, including humans. This means companies developing CRISPR-based medicines must now negotiate with Broad and its partners, Harvard University and the Massachusetts Institute of Technology, for the use of the editor."[15] The CVC is attempting to determine how to successfully appeal the USPTO's findings and it appears the patent fight will continue unless the Broad Institute and the CVC can negotiate a shared access to their technology.[16]

Now that the Broad Institute owns the US patent on editing human cells with CRISPR Cas9, it has licensed its product to Editas Medicine to develop a treatment for sickle-cell anemia.[17] Competitor company Vertex, in partnership with CRISPR Therapeutics owned by Charpentier and Doudna, has access to the competing intellectual property that could prove useful in developing the sickle cell treatment. Whether these two companies will settle the license wars in order to speed development for a sickle cell cure is unknown, but an agreement to work together toward a common goal could be beneficial to both sides.[18]

What is the fight over? Potentially billions of dollars.[19] "CRISPR, short for clustered regularly interspaced short palindromic repeats, is a microbial 'immune system' that prokaryotes — bacteria and archaea — use to prevent infection by viruses called phages. At its core, the CRISPR system gives prokaryotes the ability to recognize precise genetic sequences that match a phage or other invaders and target these sequences for destruction using specialized enzymes."[20] In the technique, a single-cell, fertilized, pre-implantation embryo is injected with an enzyme complex designed to target and splice a problematic gene.[21] The spliced gene is replaced or repaired by a separate, simultaneously injected molecule.[22] Theoretically, all cells formed through division of the altered, single-cell embryo will have the replaced or repaired gene.[23] Because the changes would be inheritable, use of this technique would produce changes to the human genome pool.[24] The first report of this technique's use with human embryos appeared in April 2015.[25] Researchers in China applied the technique to non-viable pre-embryos—those that could not result in a live birth because they had an extra set of chromosomes—hoping to edit the gene that causes a potentially fatal blood disorder.[26] They were largely unsuccessful. About 20% of the embryos did not survive.[27] Of those that did, only about half were successfully spliced, and only a fraction of those had the repaired or replacement gene.[28] Moreover, there were a number of mutations in non-targeted genes found in other parts of the genome.[29] Faced with these results, the scientists suspended their research, concluding that the technique was "too immature."[30]

Nevertheless, in early 2016, researchers in England obtained permission to use the technique to study the genetic switches involved in a fertilized egg's movement through its first few divisions.[31] They hope to find genetic modifications that will serve, not themselves as a basis of therapy, but as an aid in developing treatments for infertility.[32] In September 2017, they announced that they had used CRISPR to disable a gene thought to play a key role in early development, and confirmed the gene's importance.[33] Approval of this work by the UK Human Fertilisation and Embryology Authority may have been the world's first endorsement of this kind of research by a national regulatory authority, and was expected to provide encouragement to scientists around the world who are interested in pursuing embryo-editing research.[34] That expectation became reality in 2017, when researchers announced they had used CRISPR to successfully edit disease-causing mutations out of viable human embryos.[35]

In late 2018, a scientist in China announced the birth of the world's first genetically edited babies: twin girls whose genes had been altered with CRISPR to make them resistant to HIV infection.[36] He also announced that a second pregnancy involving a gene edited embryo was in progress.[37] His work has not been published or reviewed, but official investigators in China reportedly have confirmed his claims.[38] Also in 2018, a published study reported that CRISPR caused more damage to DNA than previously thought, by "disrupt[ing] healthy genes when it is meant only to fix faulty ones."[39] However, scientists are optimistic that ongoing efforts to increase CRISPR-Cas9 specificity through improved base editing[40] and use of the bacterial ubiquitin transferase machine that could be programmed (as Cap3) to edit out problem proteins, will further hone the CRISPER technology to treat formerly evasive disease in humans while avoiding potential damage to healthy genes.[41]

In an effort to facilitate public discourse on these challenges, experts in Crisper-Cas-9 editing participated in the Third International Summit on Human Genome Editing in March 2022.[42] Stakeholders from across the world discussed the current state of the science, including important ethical and cultural considerations that are developing along with the fast-moving technology.[43]

In the past year, advancements in CRISPR Cas9 technology have accelerated. The USDA recently approved a groundbreaking cure for sickle cell anemia with the use a CRISPR-based gene editing therapy from Vertex Pharmaceuticals and CRISPR Therapeutics. The therapy is known as "exagamglogene autotemcel, or exa-cel" and has demonstrated proven results back to the first patient, Victoria Gray, who was provided the first dose in 2019.[44] Scientists are even planning to expand access to the therapy to Africa, where the first SCD mutation "arose more than 7000 years ago."[45]

In addition to developments in sickle cell cure therapies, the "FDA has granted fast track designation to Excision Biotherapeutics' CRISPR-based, multiplexed in vivo gene editing therapy EBT-10 for the potential cure of virus type HIV-1.[46] The disease affects million worldwide and 1.1 million in the US, where current lifelong antiretroviral therapy (ART) is the standard of care. EBT-1-1 is a potentially curative 1-time treatment which uses adeno-associated virus (AAV) to deliver CRISPR-Cas9 and dual guide RNAs" to remove the HIV genome and prevent viral escape and reproduction.[47]

Base editing therapies have also been in the 2023 CRISPR spotlight. "Base editors have been proposed as safer alternatives to traditional CRISPR-Cas9 editing, particularly for therapeutic purposes. This is primarily because they do not induce double-stranded breaks in the genome, which can have unintended consequences such as chromothripsis."[48] Additionally, CRISPR-Cas12a "is a new RNA guided endonuclease that has been recently harnessed as an alternative genome editing tool, which is emerging as a powerful molecular scissor to consider in the genome editing application landscape."[49] CRISPR-Cas13 can effectively extract nucleic acids from biological samples to aid in the accurate "diagnosis of microbial infections."[50]

Another fast-moving change involves the startup Verve Therapeutics, which has targeted base editing treatments for cardiovascular disease to treat conditions caused by elevated levels of low-density lipoprotein cholesterol (LDL-C). Eli Lilly

and Company recently acquired Beam Therapeutics' opt-in rights to Verve's gene therapy programs for cardiovascular disease. Beam Therapeutics is also engaged in using base editors to target several forms of cancer, including T cell acute lymphoblastic leukemia, and T cell lymphoblastic lymphoma. All are in clinical trials this year.[51]

3) Cloning and Stem Cell Research

Two other areas of global importance are cloning and stem cell research. Cloning is a process for producing an embryo by inserting the nucleus of a mature body cell into an egg cell whose nucleus has been removed.[52] Theoretically, the process can be used for either reproductive or therapeutic purposes. For example, scientists have already successfully cloned the CH2 homozygous genome-edited cat using cytoplasm injection clone technology. They have created hypoallergenic cats using the CRISPR-Cas9 system—a significant step forward because these cats can safely approach allergic patients.[53]

In January 2009, the United States Food and Drug Administration approved the world's first human tests of a therapy derived from human embryonic stem cells.[54] In therapeutic cloning, stem cells are harvested from the cloned embryo for purposes of medical research and treatment. Embryonic stem cells are unspecialized cells that can differentiate into almost all of the cells in the human body, including the cells that make up our organs. Stem cell research advocates believe these cells will be useful in developing treatments for a wide range of ailments and degenerative diseases, like Parkinson's disease or spinal cord injuries.[55] Research in this area has taken off since 1998, when human embryonic stem cells were first isolated.[56] In the short term, scientists hope to use stem cell therapies to repair or replace damaged tissues and organs like the kidneys, heart or liver.[57] They also hope that someday, patients will be able to repair their own organs using stem cells from cloned embryos that genetically match the tissues in their bodies, thus avoiding rejection problems.

4) Personalized Medicine

DNA and genetics have also ushered in a new era in the ability of physicians to diagnose and treat their patients. When researchers finished decoding the human genome, the search for better, faster, and more effective medications began in earnest.[58] Increasingly, scientists armed with our genetic blueprint can identify the individual molecules that make us susceptible to a particular disease.[59] With this information, and some high-speed silicon-age machinery, they can build new molecules that hone in on their targets like well-aimed arrows.[60] For example, in 2012, a California biotech company obtained FDA approval of a drug that successfully treats the most common form of skin cancer—basal cell carcinoma—by targeting the biologic pathway implicated in more than 90% of basal cell carcinoma cases. This drug, taken orally, offers new hope to those with advanced stages of the disease, and to those with a rare genetic disorder that can give them thousands of skin cancer tumors during their lifetimes.[61]

In the new era of genomic medicine, doctors will treat diseases like cancer and diabetes before symptoms even begin and will use medications and treatment plans that are tailored to a patient's unique genetic code.[62] As the director of the National Human Genome Research Institute has explained, “[t]he whole idea here is to take medicine” from “a generalized one-size-fits-all approach, and really make it appropriate for the individual.”[63] In December 2016, President Obama signed the 21st Century Cures Act, which secures $4.8 billion in federal funding for infrastructure to advance biomedical research into precision medicine.[64]

According to some, in 2007 alone, we had “more breakthroughs in understanding the pathways of disease and health than we [had] had in decades,” and in the future, “[t]he way we give medicine today will be considered the dark ages.”[65] DNA sequencing technology has already yielded tangible clinical results. For example, by using sequencing technology to compare the complete genetic sequence of a patient's cancer cells to the complete genetic sequence of her healthy cells, physicians at

Washington University School of Medicine in St. Louis were able to identify the mutation that caused the patient's cancer and to determine that she needed chemotherapy instead of a stem cell transplant.[66] In 2017, researchers conducting two small clinical trials reported that vaccines tailored to a person's unique cancer mutations had warded off tumors in a small pool of patients.[67] Also in 2017, a large medical group started offering a $179 gene test that helps doctors determine the best medication for a patient.[68] In a 2018 survey, about two-thirds of participating oncologists reported they already use DNA testing to identify the best treatment options for cancer patients.[69] In 2020, Researchers at Tel Aviv University (TAU) "demonstrated that the CRISPR/Cas9 system is very effective in treating metastatic cancers, a significant step on the way to finding a cure for cancer. The researchers developed a novel lipid nanoparticle-based delivery system that specifically targets cancer cells and destroys them by genetic manipulation. The system, called CRISPR- LNPs, carries a genetic messenger (messenger RNA), which encodes for the CRISPR enzyme Cas9 that acts as molecular scissors that cut the cells' DNA."[70] In 2022, it was announced that scientists using genetic sequencings had identified shared ancestry in autism spectrum disorder variants that could lead to revolutionary treatment for the brain type.[71]

Scientists envision that within the next 20 years, a doctor, during a routine office visit, will be able to swab a patient's cheek and get a read out of that patient's entire genome.[72] And a newborn will get a full genome scan that "could provide a kind of medical road-map for life, outlining which diseases are most likely to be a concern for that baby as it grows up," and "tell[ing] doctors which medications and treatments and screenings will work best for that child, as a child and then as an adult."[73] Already, all 50 states and the District of Columbia require newborn screening for more than 20 genetic disorders.[74] Advancements have occurred in this area as well. In a cohort study in China in 2021, scientists applied gene panel sequencing as a first-tier newborn screening test for 29, 601 newborns. The result was that the sequencing of 128 diseases identified 59 more patients (1 in 500 newborns). "Of these, 20 patients were affected by disorders screened by both biochemical and gene panel sequencing and 39 patients were affected by disorders screened solely by gene panel sequencing." The result provides an evidence-based suggestion that genomic screening could be considered as a crucial method for first-tier screening of all newborns.[75]

The pace of progress has been nothing short of amazing. It took 13 years and $3 billion to sequence the first genome in 2003.[76] Less than four years later, using new technology, it took only two months and $1 million to sequence the genome of James Watson, co-discoverer of DNA's structure.[77] In March 2008, a California company announced it had lowered sequencing costs for one individual's genome to less than $60,000.[78] Three years later, another California company began offering complete DNA sequencing commercially for as little as $4,000, and California researchers announced they had reduced sequencing times to under three minutes.[79] Just three years after that, in 2016, the $1,000 barrier was broken, when a Massachusetts company began offering complete genome sequencing—including screening, analysis, and genetic counseling—for $999.[80] In 2019, the company lowered the cost to $599 and said it hoped to reach the $100-$200 range within two years.[81] Most recently, scientists using genetic sequencing have identified shared ancestry in autism spectrum disorder variants. As a result of these advances, our ability to determine DNA sequences is beginning to outrun our ability to store, transmit, and analyze the data, creating a data handling bottleneck that could delay the use of DNA sequencing as a routine part of medical treatment.[82]

5) Public Health

Advances in genetic technology have expanded opportunities for personalized medical treatment. They have also affected the management of public health issues, both nationally and globally. Since 1996, the U.S. Centers for Disease Control and Prevention have operated a system called PulseNet, which uses DNA fingerprinting of bacteria in cases of foodborne illness to detect disease outbreaks at local and multistate levels.[83] PulseNet International, the global health arm of PulseNet, operates in over 80 countries to facilitate "early recognition of foodborne disease clusters that may represent common source outbreaks."[84] In 2008 the U.S. Food and Drug Administration created the GenomeTrakr network, which stores genomic sequencing and

geographic information from public and university laboratories in a single database.[85] Both the CDC's and the FDA's networks allow governmental organizations to monitor disease outbreaks and reduce the harmful effects of foodborne pathogens.

5) Legal and Ethical Issues

These advances pose new ethical and legal challenges. For example, a problem that medical professionals will increasingly face is deciding which of the hundreds of available genetic tests are most useful for any given patient. Some medical professionals argue that testing for every known genetic condition, even those that are rare, is unjustified in terms of the public health expense.[86] Other testing decisions may be ideologically motivated; for example, doctors might not test for deafness in the face of arguments that deafness is not a disease.[87] In choosing among the available tests, doctors must continue to balance the risk of a malpractice suit and the likelihood that a particular test will reveal something material to a patient's health.

Moreover, companies already are selling directly to the public genetic test kits that indicate whether someone has a gene linked to some disease. Millions of these kits have reached the market in just the past few years. Companies selling the kits claim the tests can help predict and diagnose illnesses and conditions like cancer, Alzheimer's, and bipolar disorder. Some even claim they can predict athletic ability. Experts caution that the tests receive almost no government oversight, and they question whether telling people their genetic information will really make any difference.[88] Some experts argue that test results may prompt consumers to make negative choices about their health.[89] Proponents of these tests characterize this view as "paternalistic" and argue that individuals have the right to know their genetic makeup, even if the data are not 100% correct.[90]

The FDA has indicated that it intends to regulate direct-to-the-consumer genetic testing. In May 2010, it notified a company that its genetic test kit "appeared to meet the definition of a medical device" under the Food, Drug, and Cosmetic Act, which would give the FDA jurisdiction to regulate.[91] The FDA subsequently sent out 19 similar letters to other companies marketing genetic test kits.[92] One at-home test for colon cancer has received FDA support.[93] Meanwhile, in June 2008, after investigating complaints about the accuracy and costs of genetic tests being marketed directly to the public, California's Department of Public Health demanded that 13 companies halt sales of such tests until they comply with California law, which prohibits testing absent a physician's order and requires both laboratory certification and test validation for clinical utility and accuracy.[94] The New York State Department of Health took similar action in November 2007.[95] Some companies complied, some stopped selling in certain jurisdictions, and others went out of business.[96] At the end of 2011, regulation in this area remained uncertain at best.[97] Despite this uncertainty, or perhaps because of it, at least one company decided to work with the FDA instead of fighting it; in 2012, it applied for FDA approval of its personalized DNA test kit.[98] Unsatisfied with the company's subsequent showing, in November 2013, the FDA ordered the company to discontinue marketing the test kit until obtaining FDA approval.[99] In response, the company continued to market the test, but it removed all health-related results from its reports and started offering only genetic analysis of ancestry.[100] In April 2017, the company finally obtained FDA approval to market tests that provide genetic risk information for 10 diseases or conditions.[101] The FDA continues to be very active in this area. In April 2019, it issued a warning letter to a company for illegally marketing a genetic test kit with the claim that it could predict responses to specific medications based on genetic variants.[102] In February 2020, it released a table of scientifically supported gene-drug interactions for use in deciding whether to use DNA testing in making treatment decisions for particular patients.[103] At the same time, it announced a new and stepped-up effort to evaluate commercial claims of links between genes and drug responses.[104] The FDA said it was taking this step because companies were continuing to market DNA tests with linkage claims that were not adequately supported by sound science.[105]

The advent of the COVID-19 pandemic highlighted the FDA's ability to expedite testing and grant emergency use authorization (EUA) for public vaccines and testing kits. While several vaccines are in use—the newest ones can even target specific variants

of the COVID-19 virus—in 2021, "the U.S. Food and Drug Administration issued an emergency use authorization (EUA) for the Cue COVID-19 Test for Home and Over The Counter (OTC) Use. The product is a molecular nucleic acid amplification test (NAAT) that is intended to detect genetic material from SARS-CoV-2 virus present in the nostrils. The test has provided tremendous support in detecting the COVID-19 virus and was the first molecular test authorized for at-home use without a prescription." The FDA's continued vigilance in the wake of the worst pandemic, and rapid development of similar tests for consumer use in over a century underscores the importance of the FDA's oversight and continued assurance that the products we use will be reliable and safe.[106]

The federal government has also become involved in personalized medicine as a direct contributor to genetic research. As part of the Million Veteran Program, the Department of Veterans Affairs (VA) has created a database of volunteer participants to study their genetic data, military exposure, and general medical information in order to improve care and integrate it with insurance services.[107] Over 1,000,000 veterans have enrolled in the program since its launch in 2011, making it the world's largest genomic database tied to a health care system.[108] Because the VA already possesses extensive data security and legal infrastructure, it has so far avoided the obstacles to conducting large scale research that private companies face. In 2015, through the Precision Medicine Initiative, President Obama announced plans to create a parallel database in the public sector.[109] The initiative aims to apply genetic and health data in more innovative and efficient ways by bringing together healthcare providers, governmental agencies, private researchers, and one million volunteers.[110] The Health IT Now Coalition and the Center for Data Innovation subsequently released recommendations for addressing potential privacy and consent issues related to the initiative.[111]

Social critics fear that the identification of genetic differences between people of separate continental origins could undermine the presumption that all human beings are fundamentally equal. In turn, this could potentially instigate a new era of racism.[112] As a result of these genetic differences, people in the medical community are marketing certain drugs and tests to certain populations more at risk of certain medical ailments.[113] Scientists argue that acknowledging such differences is crucial to understanding the genetic basis for disease, although they do worry that as their data are extended beyond the medical context, their field is entering a "dangerous time."[114]

Several ethical and legal issues have already come up in connection with gene therapy research. In 1999, Jesse Gelsinger, an 18-year-old volunteer for a university's gene therapy study, who was in relatively good health at the time despite a metabolic condition, died from a reaction to a gene therapy treatment only four days after receiving it. Investigations into Gelsinger's death revealed some troubling information: The university failed to exclude him from the study as it should have based on his ammonia levels at the time of the treatment; it failed to mention, as part of the informed consent process, that monkeys given a similar treatment had died; and it failed immediately to report that two patients had experienced serious side effects from the gene therapy. More broadly, the investigations revealed that gene therapy researchers in general were substantially underreporting adverse events associated with gene therapy trials, that some scientists were asking that problems not be made public, and that there may have been at least six unreported deaths attributed to genetic treatments.[115]

A lawsuit in Massachusetts demonstrates another kind of disclosure issue associated with gene therapy. Roger Darke agreed to participate in an experimental gene therapy treatment for chronic heart disease, which required injection of a healthy gene directly into his heart. Less than 24 hours after undergoing the procedure, he died. A lawsuit was later filed alleging that the doctor performing the procedure and the hospital where it was performed were liable because they failed to disclose a financial stake in the gene therapy treatment that gave them an incentive to encourage patients to submit to the treatment. The doctor and the hospital argued that this theory was legally invalid because the doctrine of informed consent only requires disclosure of medical information. The Superior Court of Massachusetts disagreed, finding that the informed consent doctrine is "broad enough" to require a doctor to disclose "he has a financial interest in the treatment that he recommends."[116]

The principle of informed consent raises additional issues when children are involved. By 2005, gene therapy had restored the immune systems of over 40 children with Severe combined immunodeficiency (SCID), a rare genetic disorder that causes life-

threatening immunodeficiency.[117] However, five of the children participating in early gene therapy trials developed leukemia; one died in 2004. It was believed that the vector—the virus used to deliver the healthy gene—accidentally activated a cancer-causing gene.[118] In early 2003, just after the first leukemia cases were reported, the FDA placed a temporary hold on all United States gene therapy trials involving the technique used in the SCID trials: use of a retrovirus to insert new genes in blood stem cells.[119] Later that year, the FDA allowed trials not involving SCID to resume, so long as additional warnings regarding the risks of cancer were provided. It permitted SCID trials to resume only where there were no other treatments options to preserve the patient's life.[120] The FDA again temporarily halted SCID trials in 2005, after another child in a SCID trial developed leukemia.[121] Recent trials with new vectors have offered promise of gene therapy for SCID that is both effective and safe.[122] Scientists now have gene therapy for at least three SCID conditions and the genetic editing is promising. "In addition, the prospect of genome editing based on the CRISPR-Cas9 technology, or likely even better, on base or prime genome editing of mutated SCID genes could offer additional advances in the treatment of SCID. There is even the prospect that the later technologies might be used without *ex vivo* cell handling."[123]

All of this raises questions about the ability of parents to make informed decisions about gene therapy trials when their child suffers from a rare genetic disease. In 2019, in order to enhance knowledge of the issues of pediatric genetic testing and genomics,[124] The Working Group on Pediatric Gene Therapy and Medical Ethics was created as part of the Division of Medical Ethics at NYU Grossman School of Medicine.[125] The group plans to "study ethical issues surrounding research in genetic interventions for pediatric populations."[126] Complicating the issue is the fact that most gene therapy trials are early phase studies that focus on safety, not treatment or efficacy. Thus, at this point, "[t]he potential for benefit" from participating "is very low."[127] Making this fact clear to parents has been identified as a "key concern" of gene therapy researchers.[128] As one medical ethicist put it, "[p]arents will always have hopes for their sick children, but participation in gene transfer research should not be offered in ways that exploit those hopes."[129]

In the sports world, gene therapy and gene editing raise an entirely different kind of problem: gene doping. Using gene therapy, researchers have been able to genetically engineer mice with super strength. Their goals are to find a way to treat muscle-wasting diseases like muscular dystrophy, and to counteract the muscle weakening that happens to us all as we age. But so far, the greatest interest in their research has come from the world of sports. Some athletes who want to achieve optimum muscle speed and agility to gain a competitive advantage over opponents might be tempted to search for ways to use the CRISPR/Cas technology to alter their genes.[130] According to one researcher, in the six years after he published his first results, he received an average of three emails a week from athletes and coaches looking for a competitive edge; "[t]he inquiries surge every time another advance is announced."[131] As one sportswriter put it, genetic modification through gene therapy "looms as the ultimate supplement. Improvement seems guaranteed and permanent, and there is no test to catch users."[132]

In the eyes of many, gene doping could result in "the death of sports as we know it."[133] Unfortunately, most experts also agree that it is not a question of whether, but when; if gene doping has not already occurred, it almost certainly will, and probably soon.[134] For this reason, in 2002, the World Anti-Doping Agency began trying to develop a test to detect gene doping. In 2003, it added gene doping to its list of prohibited methods, and in 2017, it added gene editing to the list.[135] In 2004, during congressional hearings on steroid use in baseball, Don Fehr, the Executive Director of the players union, testified that gene doping is "something which bears the closest scrutiny."[136]

Although scientists are close, so far, there has been little success in developing a precise one-size-fits-all test to detect gene doping. In September 2010, two groups of scientists announced they had each developed a gene doping test that could be ready by the 2012 Olympic Games in London.[137] The tests were not ready, and, at the 2012 London Games, there were plenty of gene doping allegations, but no proof.[138] According to the World Anti-Doping Agency (WADA), a test now exists and will be

retroactively used for samples collected from athletes during the 2016 Olympic Games in Rio de Janeiro.[139] In 2017, 4,913 samples were analyzed at the Brazilian Doping Control Laboratory, and the presence of a prohibited substance was confirmed in 29 specimens.[140] In February 2018, WADA announced that it was considering another tool to detect gene doping: a sort of "biological passport" for athletes, who would have their genomes sequenced to help regulators look for illegal modification.[141] Scientists are trying to stay ahead of successful doping efforts and recently announced that they are closer to detecting gene doping in "both human plasma and in live mice."[142]

The answer may be on the horizon, however. Scientists have recently turned to CRISPR-deadCas9 as a method for detecting genetic doping. Although CRISPER-Cas technology is well known for its gene editing functions, one group of scientists has "successfully completed the detection of exogenous human erythropoietin gene doping based on CRISPR/deadCas9. Under optimal conditions, the developed assay successfully achieves highly sensitive detection of gene doping in a whole blood sample" although "neither CRISPR-Cas13 nor CRISPR-Cas13a have been reported for use in gene doping detection. This may be due to the fact that CRISPR-Cas13 and CRISPR-Cas13a are primarily applied to shear against RNA."[143]

There is no doubt that the announcement in April 2015 of efforts to edit the human germ line rekindled a smoldering debate over the safety, wisdom, and morality of altering the human genome. Proponents argue that such gene editing can potentially eliminate devastating diseases before a child is even born.[144] But critics charge that it "crosses an ethical line" and, by producing inheritable germ line modifications, "could have an unpredictable effect on future generations"[145] and "alter the nature of the human species."[146] Critics also warn that it could start us down a "slippery slope towards unsafe or unethical uses of the technique"[147] and be "exploited" for non- therapeutic genetic changes, like enhancing physical and mental traits.[148] And in 2016, the U.S. Director of National Intelligence identified germ line editing as a potential weapon of mass destruction.[149] About 40 countries ban or discourage human germ line editing.[150] In December 2015, an influential international group of scientists—including national scientific academies in the United States, China, and England—called for a voluntary moratorium on use of the technique on human embryos.[151] Aside from the safety and ethical issues, they argue, there currently is "no pressing medical demand" for editing the human genome because few diseases are caused by a single defective gene and in vitro fertilization can often be used to produce healthy embryos for those with a gene linked to one of the rare diseases that are so caused.[152] But in February 2017, the National Academies of Science and Medicine endorsed the use of germ line editing to cure genetic diseases for future generations, provided it is done only to correct disease or disability, not to enhance people's health or abilities.[153]

Against this backdrop, the announcement in late 2018 that twin girls had been born with CRISPR altered genes to eliminate the HIV virus in the embryos created a firestorm. Scientists around the world condemned it, noting that there are other ways to address the medical concern—the risk of HIV infection—that motivated the alteration.[154] China suspended the scientist's work, saying that his conduct was both unethical and in violation of Chinese law.[155] It later sentenced him to three years in prison and fined him over $400,000 for carrying out the illegal practice of medicine.[156] One of CRISPR's co-inventors said that the development "reinforces the urgent need to confine the use of gene editing in human embryos to settings where a clear unmet medical need exists, and where no other medical approach is a viable option."[157] But a few prominent scientists came out in support of the work.[158]

Further studies on the CRISPR twins indicates they might have had their brains inadvertently enhanced by deleting a gene called CCR5—a process that has been shown to make mice smarter and also improve human brain recovery after a stroke.[159] The exact effect on the girls is impossible to predict at this time, however, so further studies will be needed to determine whether the effect will be permanent or is even related to the CRISPR gene editing.

Several prominent groups are already intensely considering germline editing and its implications. In 2019, sparked by the developments in China, a separate International Commission on the Clinical Use of Human Germline Genome Editing was convened by the U.S. National Academy of Medicine, the U.S. National Academy of Sciences, and the Royal Society of the United Kingdom, with participation by science and medical academies from around the world.[160] Its mission is to develop a framework for potential clinical applications of germline editing.[161] After examining the scientific and ethical issues, the expert panel issued a report observing that at this point in time, "heritable human genome editing is too technologically unreliable and unsafe to risk testing it for any clinical application in humans at the present time. The report cited the potential for unintended off-target DNA edits, which could have harmful health effects, such as cancer, later in life. Also noted was the risk of producing so-called mosaic embryos, in which the edits occur in only a subset of an embryo's cells. This would make it very difficult for researchers to predict the clinical effects of heritable genome editing in human beings."[162] The panel concluded that "heritable gene editing, if ever permitted, should be limited initially to serious diseases that result from the mutation of one or both copies of a single gene.

The first uses of these technologies should proceed incrementally and with extreme caution."[163] This report was sent to the World Health Organization committee to serve as an important resource for human genome editing research and clinical trials.[164]

Meanwhile, in June 2019, a Russian scientist announced plans to move forward with germline editing to produce gene-edited embryos that are more resistant to the HIV virus when implanted into women who are HIV positive.[165] However, wary of the fate of the scientist in China, he also announced he would not proceed without express approval from several government agencies, including the Russian health ministry.[166] That approval appears unlikely to happen any time soon, In October 2019, the Chinese health ministry said that any clinical use of genome-editing technologies on human embryos is "premature," and expressed full support for the World Health Organization's position against altering the human germline until the "implications have been properly considered."[167] Thus, even if refinements in the technology address the safety issues, the complex and difficult ethical questions surrounding this area remain.

Recognizing that it is important to establish international guidelines for genome editing, the WHO recently issued two companion reports that provide the first global recommendations to assist in establishing an emphasis on "safety, effectiveness and ethics."[168] WHO's goal is to minimize the inherent risks created in human genome editing.[169] The WHO report "delivers recommendations on the governance and oversight of human genome editing in nine discrete areas, including human genome editing registries; international research and medical travel; illegal, unregistered, unethical or unsafe research; intellectual property; and education, engagement and empowerment. The recommendations focus on systems-level improvements needed to build capacity in all countries to ensure that human genome editing is used safely, effectively, and ethically."[170]

Stem cell research is also very controversial, principally because most techniques for obtaining stem cells involve destroying an embryo in the process—an action that is becoming more divisive in contemporary political arenas.[171] Another new controversial technique for producing embryonic stem cells involves "injecting human DNA into a hollowed- out animal egg cell" to create "hybrid human-animal embryos" that are 99.9% human and 0.1% animal.[172] Opponents of this research say it is unnatural and unethical, while proponents tout the possible medical ramifications.[173] And efforts to create patient specific embryonic stem cells that genetically match a patient's DNA involve attempts to clone human embryos. Thus, both cloning and stem cell research present us with difficult moral choices.

In February 2002, the United Nations Ad Hoc Committee On The Convention To Ban Human Cloning met for the first time, and heard experts testify about the science and ethics involved.[174] Singapore, Great Britain, Taiwan, and Germany ban cloning and allow limited stem cell research. In 2008, Great Britain's House of Commons failed to pass a bill that would have banned

the creation of hybrid embryos—part human and part animal—for scientific research.[175] Currently, licensed British scientists may harvest stem cells from hybrid embryos. However, research on embryos that are over fourteen days old is prohibited.[176]

In the United States, as of 2015, 17 states had laws prohibiting human reproductive cloning, and at least seven of those states had also outlawed human cloning for research (or any other) purposes.[177] State laws relating to embryonic stem cell research vary widely; some encourage it, some restrict the use of state funds for the research or the use of stem cells from particular sources, and some strictly forbid research on embryos regardless of source.[178] Californians recently passed Proposition 14, which authorizes the state to issue $5.5 billion in bonds to support the Institute for Regenerative Medicine, the state's stem cell funding agency.[179]

At the federal level, since 1998, the Food and Drug Administration (FDA) has claimed authority to regulate clinical research using cloning technology to create a human being.[180] Since 1997, over 44 bills have been introduced in the United States Congress seeking to ban or regulate cloning research.[181] All of these attempts failed because of disagreements over whether to allow cloning for research purposes.[182] Since 1996, Congress has prohibited the use of federal funds to create cloned embryos for stem cell research or for research in which embryos are destroyed, discarded, or knowingly subjected to risk of injury.[183] In 2001, President George W. Bush authorized the use of federal funds for research on existing stem cell lines.[184] In 2006, and again in 2007, the United States Congress passed bills to expand federal funding for stem cell research. President Bush vetoed both bills, as he had promised to do well before they passed.[185] In March 2009, President Barack Obama signed an executive order permitting federal funding for stem cell research on stem cell lines other than those that existed in 2001. The National Institutes of Health later issued funding guidelines to implement President Obama's order. Litigation was then filed challenging the guidelines as being contrary to Congress' still-intact statutory ban on federal funding for stem cell research.[186] In 2012, a federal appellate court rejected the challenge and, in 2013, the United States Supreme Court declined to review the decision.[187] In September 2018, the Trump administration announced that it had started a "comprehensive review" of all federally funded research that uses fetal tissue "in light of the serious regulatory, moral, and ethical considerations involved."[188] Based on that review, in June 2019, the administration announced a severe cut back on federal spending for medical research using tissue from aborted fetuses, including cessation of fetal—tissue research within the National Institutes of Health and cancellation of a $2 million-per-year research contract with the University of California, San Francisco.[189]

President Biden's past voting record shows that although he supports stem cell research, he opposes cloning.[190] His administration, however, acted to lift the previous administration's restrictions and implement new rules for fetal tissue research—a sea change in administrative policy.[191] Still, cloning and stem cell research are likely to remain contentious subjects for quite some time because they raise for some the same spiritual and ethical issues that fuel the debate over abortion.[192]

Ultimately, there may be a nonjudicial, scientific light at the end of this tunnel. In late 2007, two research teams working independently in Japan and the United States announced a new technique for transforming ordinary adult human skin cells into cells that look and behave much like embryonic stem cells. The technique involves introducing three or four genes that code for stem cell transcription factors into skin cells, and does not require use of embryos.[193] In January 2008, scientists in Southern California announced that by extracting a single cell from an early stage human embryo, they could create a new human embryonic stem cell line without destroying the embryo.[194] In November 2011, the Oregon Health & Science University secured a patent for a unique method of transforming a person's own skin cells into stem cells without using embryonic stem cells.[195] In May 2013, the University, along with the Oregon National Primate Research Center, announced they had successfully reprogrammed human skin cells to become embryonic stem cells capable of transforming into any other cell type in the body.[196] In 2018, researchers in Japan announced that they had created stem cells from human blood cells.[197] Just last year, a Singapore scientist reported on a new method to generate large quantities of red blood cells from "pluripotent stem cells" for use in blood

transfusions and other therapeutic applications.[198] These stem cells have been reprogrammed from a differentiated state back to an embryonic-like state.[199] Questions of scale remain, and scientists need to determine how to mass produce the blood in factories in order for the technology to have a measurable effect.[200] Although these techniques may avoid contentious issues involving the destruction of embryos, they raise other ethical considerations, such as the possibility of creating human-animal chimeras by injecting human stem cells into animals to make human organs.[201] These concerns led the inventor of one new technique to remark that "the science has moved too far ahead of talk of ethical issues."[202]

Advances in genetic research that involve stem cells and human tissue also pose a host of other new legal questions. As products of human genome research move into the marketplace, how does society address attempts to commercialize products developed from an individual's genetic information? How do the laws of intellectual property apply? Do donors have a right to know that their tissue and cells are being used? Do they have a privacy interest in this material? Do they have an ownership right in this material, or in any discovery or product derived from research on this material?

One famous ownership case lies in the story of Henrietta Lacks, a young Black woman who was diagnosed and died at the age of 31 from an aggressive form of cervical cancer in 1951.[203] Samples of her cells were taken during a biopsy at Johns Hopkins University Hospital without her knowledge, a practice that was legal at the time. Although Johns Hopkins never claimed ownership over the cells, they were used in various forms of scientific research, and remarkably, today, "these incredible cells —nicknamed 'HeLa' cells, from the first two letters of her first and last names — are used to study the effects of toxins, drugs, hormones and viruses on the growth of cancer cells without experimenting on humans.[204] They have been used to test the effects of radiation and poisons, to study the human genome, to learn more about how viruses work, and played a crucial role in the development of the polio and COVID-19 vaccines."[205]

In 2021, Lacks' estate sued the manufacturing giant Thermo Fisher Scientific that used her cells in research and development.[206] The Lacks' estate was paid a settlement for unjust enrichment for the unconsented taking of her cells for research.[207] In 2023, the Lacks estate also sued Ultragenyx Pharmaceutical Inc. for unjust enrichment after it was discovered that the company used Lacks' cells for four approved therapies in the treatment of rare diseases.[208] Today, most research labs turn away from ownership and instead practice informed consent so the individual from whom the cells are taken is at least aware that their cells might be used for research purposes.[209]

Other than the Lacks' cases, courts that have addressed more recent tissue research consent issues have held generally that a person has no ownership or proprietary interest in tissue and cells that have been either donated for research purposes or removed from the body during the course of medical treatment.[210] However, in 1990, when the California Supreme Court first reached this conclusion, it also held that physicians who perform medical procedures for therapeutic purposes may be civilly liable for failing to disclose research or economic interests that may affect their professional judgment.[211] Thirteen years later, a federal court applying Florida law held that as to tissue donated strictly for medical research, outside of any therapeutic relationship, researchers have no duty to disclose their economic interests.[212]

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Forensic DNA Evidence: Science and the Law § 13:16

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Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:16. Genetics and reproductive science

Similar legal issues involve ownership of donated reproductive cells. In 2003, an English judge ruled that the legal father of a woman's twins was not her husband, with whom she was raising the children, but the man whose sperm was mistakenly used to fertilize her eggs.[1]

In Massachusetts, a woman who was artificially impregnated with her deceased husband's sperm had twin daughters, and then applied for mother's and children's Social Security survivor benefits.[2] A key to resolving this issue was whether state law permitted the twins to inherit from the deceased husband, and on this question, a Massachusetts court held that they could if the woman established their genetic relationship to her former husband and that before his death, he consented to support any children reproduced posthumously.[3] In May 2012, the United States Supreme Court held that, as a matter of statutory interpretation, posthumously conceived children are not eligible for survival benefits if state law precludes them from inheriting from the deceased biological parent.[4]

In New Jersey, a divorced man sought to have a surrogate mother bear a child using cryogenically preserved pre-embryos he had created with his former wife while married. The New Jersey Supreme Court refused to allow the procedure, finding that it would violate the former wife's fundamental right not to procreate.[5] Texas, Tennessee, and Massachusetts have similarly recognized this right.[6] As of 2015, 20 states had passed statutes dealing with issues relating to posthumously conceived children.[7] For example, California enacted legislation in 2004 to allow a decedent's heirs to include posthumously conceived children who are in utero within two years of the issuance of the decedent's death certificate (or an earlier entry of judgment to determine the fact of the decedent's death) as long as the decedent authorized the posthumous conception in writing.[8]

In 2005, a "new frontier" potentially opened in the legal landscape involving preserved embryos when a judge in Chicago ruled that because a pre-embryo is a human being, a fertility clinic that accidentally destroyed a frozen embryo could be sued for wrongful death.[9] The judge based his ruling on an Illinois statute that says an "unborn child is a human being from the time of conception and is, therefore, a legal person."[10] The ruling, had it stood, could have had tremendous legal repercussions, not just for United States fertility clinics already storing an estimated half million frozen embryos, but for everyone involved in genetic research.[11] However, in 2008, an Illinois appellate court reversed the decision, holding that there is no wrongful death cause of action or recovery under state law for loss of an embryo that was never implanted into the mother.[12]

Similar issues were recently litigated in a Missouri divorce case involving the fate of frozen embryos created during a couple's marriage. The former wife wanted to use the embryos to give birth to children, but the former husband did not want any more children with his former wife. Third parties appeared in the case asserting that the embryos should be considered children and were entitled rights, including the right to be born. A Family Court commissioner ruled that the embryos were not children under Missouri law, and were to be treated as marital property.[13] In November 2016, a divided appellate court affirmed the ruling, the majority concluding that forcing the former husband to procreate against his wishes would violate his constitutional right to

privacy, and that the frozen embryos were, marital property of a special character.[14] By contrast, the dissent found it "abundantly clear" under state law that the embryos were "human beings with protectable interests in life, health, and well-being," and that the Thirteenth Amendment to the U.S. Constitution "removes all human beings from the category of property."[15]

Issues have also arisen when one woman was "mistakenly" implanted with another couple's embryo.[16] The woman decided to carry the baby to term and, after giving birth, gave the child to his "genetic parents." As DNA technology continues to advance, courts are able more precisely to identify a child's genetic origins, increasing the tension between biological and social theories of parentage.[17] Cases involving artificial insemination and parental rights seem to be becoming more frequent and will undoubtedly pose unique legal and ethical questions.[18] Other cases question what happens to embryos that have been stored for decades and the facility's responsibility for their disposal or return to their original donors.[19]

The availability of more information during pregnancy can also have major repercussions. DNA blood tests may give women a new option for prenatal screening, offering a less invasive test than amniocentesis, which involves inserting a needle into the womb.[20] Noninvasive prenatal genetic testing (NIPT) uses a simple blood test on the mother to analyze cell-free DNA from the fetus.[21] Application of these prenatal screening procedures, however, raise issues concerning genetic privacy and provider liability.[22] Suppose a woman who is considering pregnancy is tested to determine whether she carries genetic traits that could harm her child. The test is negative and the woman becomes pregnant, but the child is born severely deformed. The laboratory made a mistake. The woman sues the laboratory, claiming she based her decision to have a child on the results of the testing. Is the laboratory liable? Is the answer different if the test, even when done properly, correctly identifies harmful traits only 30% of the time? What about the parents who learn shortly before birth, through an abnormal fetal ultrasound, that the implanted embryo has observable genetic differences?[23]

In a related context, what are the child's rights; can he or she sue for so-called "wrongful life" injuries?[24] A child with a genetic disorder who files a "wrongful life" claim may allege that the doctor did not properly conduct genetic screening tests that would have revealed hereditary genetic defects. As one appellate court in Maryland put it, a "wrongful life" claim is based on the premise "that an impaired existence is worse than nonexistence," that "being born, and having to live, with the affliction is a disadvantage and thus a cognizable injury, when compared with the alternative of not having been born at all."[25] Many courts characterize this kind of claim as being "nearly theological [in] nature."[26] Only a handful of states recognize any form of recovery for "wrongful life"; most prohibit recovery, either by statute or case law.[27]

In August 2002, a California appellate court was presented with an unusual variation of the typical "wrongful life" claim in a case involving a child, a sperm bank, and several different aspects of genetic technology. The child sued the sperm bank, alleging that its improper screening of the donor who provided the sperm her parents used to conceive her resulted in her birth with a genetic kidney disease. Finding that her claim was essentially one for "wrongful life," the court followed the California rule that applies in "wrongful life" cases, which prohibits recovery of general damages, including lost earnings and pain and suffering, but allows recovery of extraordinary expenses to treat the hereditary ailment.[28]

These cases demonstrate the difficult challenges confronting us as genetic technology progresses. We will no doubt see more of these claims as our ability to predict genetic disorders continues to improve.[29] Unfortunately, few standards exist for this kind of testing. We need guidance sooner rather than later because we are already facing questions that only a few years ago seemed unimaginable—and we are grappling for answers.

Other complex and difficult issues relating to reproduction are just off the horizon. For example, we now know that certain disorders are caused by mutations found in mitochondrial DNA, outside of the cell's nucleus. To eliminate these disorders, scientists in England, with governmental support, have developed a technique for extracting nuclear DNA from a mother and

father, and injecting it into a donor egg from another woman. This process, known as mitochondrial DNA replacement therapy, can produce an embryo that essentially has three parents.[30] In 2016, the first child with DNA from three people was born after a U.S.-based team working in a Mexican fertility clinic used the technique to prevent transmission of Leigh Syndrome, a rare and fatal disorder associated with genes in mitochondrial DNA.[31] And, in several labs around the world, researchers are trying to make genetically male cells develop into eggs, and genetically female cells into sperm. If they succeed, lesbian and gay couples may someday be able to have children who are genetically related to both partners. There are, however, significant safety issues associated with using artificial chromosomes, and some argue that the experiments needed to address these issues would constitute "unethical human experimentation."[32] Others argue that even if the safety issues can be solved, same-sex reproduction would be politically controversial.[33]

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Forensic DNA Evidence: Science and the Law § 13:17

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Justice Ming W. Chin, Michael Chamberlain, Amy Rojas

Chapter 13. Science and the Law: DNA Evidence and Beyond

§ 13:17. Agricultural and environmental biotechnology

Genetic science is also having a tremendous impact in agriculture, through increasing use of genetically modified organisms (GMOs). Existing organisms can be endowed with new properties by giving them a gene from another organism.[1] We have already seen crops genetically modified to survive better in droughts or frosts, to stay fresh longer, to resist insects and diseases, and to tolerate herbicides, which allows farmers to spray weed killer on fields without crop damage.[2] Common examples of this process include delayed-ripening tomatoes and rice enriched with vitamin A.[3] Eventually, genetically modified microorganisms may be developed that increase the geographic range of crops by helping control soil conditions.[4] The same biotechnological tools can be used with livestock to produce animals that are healthier, more disease resistant, and faster growing, and to improve the quality, quantity, and nutritional value of milk, eggs, meat, and wool.[5]

Although only a few types of GMO crops are grown in the United States, some of the GMOs that are grown make up a significant percentage of the crop (i.e., soybeans, corn, sugar beets, canola, and cotton).[6] "In 2020, GMO soybeans made up 94% of all soybeans planted, GMO cotton made up 96% of all cotton planted, and 92% of corn planted was GMO corn."[7] These genetically engineered crops comprise a staggering about of available farmland—about 60 million acres of United States farmland were covered with genetically engineered crops.[8] By 2018, the number had more than tripled, to 185 million acres.[9] In 2019, genetically engineered crops accounted for 94% of United States cotton acreage, 94% of United States soybean acreage, and 92% of United States corn acreage.[10] Worldwide, in 2004, 167 million acres were planted with genetically engineered crops.[11] By the end of 2018, the number had increased to over 473 million acres in 26 different countries by 17 million farmers.[12]

Another major development has been China's 2009 approval of genetically modified rice, which is perhaps the most important food crop in the world.[13] The Chinese government declined to renew the approval when it expired in 2014,[14] but in January 2018, the FDA approved the sale in the U.S. of genetically modified rice developed by Chinese researchers.[15]

Proponents argue that in addition to the obvious benefits of increased food production, use of genetically modified crops will help reduce greenhouse gases and mitigate climate change through, among other things, increased production of biofuels to replace fossil fuels.[16] They also argue we are already seeing socio-economic benefits associated with biotech crops, including higher school enrollment and better access to medical care. These benefits are said to result from the increased wealth biotech crops generate.[17]

Scientists are also developing a process called molecular farming, or "biopharming."[18] In this process, plants are genetically engineered to contain drugs that can either be extracted and given to a patient or delivered directly simply by having the patient eat the plant. Biopharming is far less costly than current laboratory techniques, and its global implications are significant.[19] If made widely available, genetically engineered pharmaceuticals and medical treatments can potentially improve the health and well-being of millions of people worldwide who suffer from treatable diseases and conditions.[20] "Plants such as tobacco, for

example, can be genetically engineered to produce therapeutic proteins, monoclonal antibodies and vaccines to treat cancer, inflammatory diseases and other life-threatening or debilitating conditions."[21]

Scientists are using similar techniques to produce "biopharm" animals.[22] These animals are genetically modified to produce substances for treating disease in humans.[23] In February 2009, the United States Food and Drug Administration issued its first approval for a drug produced from biopharm animals: goats genetically engineered to produce in their milk a human protein used to treat patients at high risk of developing blood clots because they lack the protein.[24]

Biotechnology may also have other significant environmental benefits. In 1980, Dr. Ananda Chakrabarty obtained a patent for genetically modified bacteria capable of digesting oil.[25] Released into an oil spill, Dr. Chakrabarty's bacteria contain and degrade the environmental hazard faster and more efficiently than naturally occurring bacteria by feeding on the oil and simultaneously breaking down several of its components.[26]

Since Dr. Chakrabarty designed his bacteria, thousands of useful microbes have been isolated and used to treat domestic sewage, industrial wastewater, and other environmental pollutants. For example, in 1990, after the Exxon Valdez's oil spill in Alaska, microbe-enhanced fertilizers were used to help clean oil debris from beaches and shorelines. In a process called bioremediation, the microbes essentially fed upon large, complex, harmful molecules, and broke them down into smaller, harmless ones.[27] Because of bioremediation's great potential to enhance environmental safety more efficiently and at a lower cost than traditional clean-up methods, scientists are looking for ways to genetically engineer bacteria for greater reliability and to expand the number of pollutants we can treat with this process.

Precision gene editing in miscanthus, a promising perennial crop for bio energy production, is currently in the works.[28] Biologists used CRISPR Cas9 technology to edit three miscanthus species and hope to enhance the crop's source as a biofuel, renewable byproduct, and carbon sequestration so that we can one day reduce our reliance on petroleum-based energy.[29]

Genetically modified animals, insects, and plants also may provide environmental and health benefits. Using genetic engineering, scientists hope to produce food animals that grow more quickly, require less feed, and leave behind less environmentally damaging waste.[30] They also hope to reduce the use of pesticides in agriculture crops and plants. For example, in 2017, researchers in New York hoping to stem the estimated $5 billion yearly crop loss caused by diamondback moths, began field testing moths genetically modified to self-destruct through infusion of DNA designed to kill female larvae.[31] Researchers also hope to combat painful, mosquito-borne diseases by releasing mosquitoes with a specially made gene that kills their offspring after they mate in the wild.[32] Using the mosquitoes against themselves is beneficial, proponents argue, because it delivers the correct chemicals without causing collateral damage to beneficial animals. Genome editing "using CRISPR/Cas and related systems (e.g., base editors) has been used lately for almost all studies and a rising number of market-oriented traits have been addressed by the technology."[33] In 2021, scientists created newly engineered variants of CRISPR-Cas9 they've labeled SpG and SpRY, that remove the barriers of what can and can't be targeted for genome editing and making the technology more efficient and flexible for targeting nearly any genomic sequence in plants for potential mutation.[34]

Despite these potential benefits, agricultural and environmental uses of modern biotechnology remains highly divisive. In 2007, the California Legislature passed SB 63 that would have required food processors to label products that contain ingredients from cloned animals, but the Governor vetoed it, finding the bill "premature" before the FDA had a chance to weigh in on the controversial subject.[35]

The FDA currently does not require labeling.[36] The public and many scientists fear that genetic engineering poses unprecedented risks to the environment and to human health and safety.[37] For example, concern exists that a previously benign microbe might

accidentally be transformed into a human pathogen that produces dangerous toxins or causes cancer.[38] Concern also exists that genetically engineered animals, insects, and crops, if released into the environment, could out-compete native species and reduce biodiversity, interbreed and pass on their genetically engineered traits to organisms that are not genetically engineered, unintentionally harm other insects and wildlife, or disrupt natural ecosystems.[39] These concerns are heightened because, unlike hazardous chemicals or wastes, genetically modified organisms can both spread—because they have "legs"—and proliferate.[40] For example, critics have voiced concern that genetically engineered fish kept in net pens might escape and interbreed with or overwhelm wild fish populations,[41] and that pollen from genetically engineered trees carried hundreds of miles by the wind could fertilize wild forests.[42] As opponents of genetically modified mosquitoes have put it, once the insects are released, "[t]he genie will be out of the bottle, and you can't stuff it back in."[43] From a human health perspective, many fear that genetically engineered foods, which some critics derisively refer to as "Frankenstein Foods" or "Frankenfoods," could contain new allergens or toxins, or produce harmful and unforeseen secondary effects, such as resistance to antibiotics.[44] Some critics of genetically engineered animals also cite ethical objections and raise concerns about animal health and welfare.[45]

Because of public concern, in 2001, United States producers agreed not to introduce meat or milk from clones or their progeny into the food supply until the FDA could further evaluate the issue.[46] In January 2008, the FDA announced that meat and milk from cloned cows, pigs, and goats are as safe to consume as food from conventionally bred animals.[47] At the same time, it recommended that food from clones of other animals, such as sheep, not be introduced into the food supply because of a lack of information regarding safety.[48] Moreover, despite the FDA's action, the United States Department of Agriculture asked farmers to continue observing the existing voluntary "moratorium" on commercial sales of food from cloned animals until the controversy subsides.[49]

In January 2009, the FDA issued final recommendations for regulating genetically modified animals.[50] Unlike the broad safety endorsement it issued one year earlier for food derived from certain cloned animals, the FDA is requiring case-by-case safety approval of any food derived from genetically modified animals.[51] According to the FDA, this difference in approach is necessary because, unlike cloned animals, genetically modified animals have intentionally been changed, and these changes may impact food safety.[52] Regarding labeling, the FDA's view is that although food marketers may voluntarily label their products as coming from genetically modified animals, they are not required to do so unless that food is different from its nonmodified counterpart.[53] The mere fact that genetic engineering is used to produce the food is not, by itself, material information that must be disclosed.[54] In November 2015, the FDA gave its first approval of a genetically modified food: an Atlantic salmon with genes from a Chinook salmon that allow it to grow rapidly.[55]

In 2011 and 2012, nineteen U.S. states considered or passed labeling legislation for genetically modified foods.[56] In 2014, another twenty states considered the issue, with three in the northeast passing laws requiring labeling.[57] But some of those laws take effect only if similar legislation is passed in neighboring states.[58] Meanwhile, the push from voters and interest groups for labeling requirements continued to swell, with polls showing that over 90% of Americans want GMO foods labeled.[59] In response, the FDA announced it would work with states interested in enacting labeling laws. But in 2016, the federal government essentially put an end to these state efforts, by enacting legislation that gave the U.S. Secretary of Agriculture two years to establish a national disclosure standard for bioengineered foods and that precluded states from having a different labeling requirement.[60] In December 2018, the Secretary of Agriculture fulfilled his duty by releasing the National Bioengineered Food Disclosure Standard, which becomes mandatory on January 1, 2022.[61] Supporters of the law have hailed it as a victory for consumers, but critics have called it "the DARK Act" because it allows companies to provide GMO information indirectly through a scannable bar code on the product instead of listing GMO ingredients directly on the label.[62] The law also does not address gene-edited foods—made with tools, like CRISPR, that snip and tweak genes at precise locations, instead of adding

genes from other organisms—creating what some argue is a potentially large loophole in labeling requirements.[63] The Biden administration is now moving to strengthen FDA regulatory oversight over genetically modified animals.[64]

Many biotechnology companies, their trade associations, United States government officials, and others interested in using biotechnology such as farmers, doctors, and industrial waste managers, assert that current regulation in the United States is adequate to protect human health and the environment.[65] Others assert that the existing regulatory framework was not created with genetic engineering in mind and is inadequate to deal with the potential risks of this new technology.[66] The regulatory challenge is to control the potential risks without unduly burdening biotechnological development.[67]

In 2015, the U.S. government launched an effort to update its Coordinated Framework for regulating genetically modified crops and other biotechnology products. The old Framework, which was last updated in 1992, involved a confusing patchwork of overlapping regulation by three federal agencies: The Department of Agriculture, the Environmental Protection Agency, and the Food and Drug Administration. The complexity of this system negatively impacted both the public's understanding of how biotechnology products were evaluated for safety and the ability of companies to navigate the regulatory process.[68] The stated goal of the new update effort was to promote public confidence in government oversight of biotechnology products and to establish transparent, coordinated, predictable, and efficient practices by the involved federal agencies while maintaining high standards that are based on the best available science and that appropriately protect health and the environment. To achieve these ends, a Biotechnology Working Group was set up to clarify the regulatory roles and responsibilities of the involved federal agencies, to develop a long-term strategy for ensuring that the regulatory system can efficiently assess the risks of future biotechnology products, and to commission an expert analysis of the future landscape of such products.[69] In September 2016, the Working Group completed the first two of these tasks, proposing an Update to the Coordinated Framework that outlines the roles of the FDA, the USDA, and the EPA, and releasing a National Strategy that lists regulatory objectives.[70] The final Update was released in January 2017.[71] A few months later, in March 2017, the third task was completed with the release of a report entitled, “Preparing for Future Products of Biotechnology.”[72]

President Biden signed an executive order to advance U.S. biotechnology and biomanufacturing by prioritizing research and innovation in a variety of fields, including food. The initiative is structured to help the U.S. be dominant in the space, but also to be more competitive on a global scale, enhance national security, and grow the economy. According to the executive order, it will improve and expand biomanufacturing production capacity and process, train a biotech workforce, expand market opportunities for the crops and food products, and streamline regulation.[73]

In Europe, battles over genetically modified crops have been fought for many years.[74] In countries that are members of the European Union (EU), each genetically modified product must be individually approved for use and distribution.[75] By the end of 1997, the EU had issued approvals for a handful of genetically modified products.[76] However, between 1998 and 2004, no new approvals were issued and several EU members banned crops the EU had already approved.[77] The United States, Canada, and Argentina successfully challenged these actions before the World Trade Organization, leading to a change in EU policy.[78] Despite this policy change, the use and acceptance of genetically modified crops and foods remain both problematic and controversial in the EU. Applicants for new approvals face a rigorous approval process, and must prove that the genetically modified product poses no threat to human health or to the environment.[79] Distributors of approved products must comply with strict tracing and labeling laws designed to enable authorities to trace a genetically modified product back to its source and to inform consumers that genetic engineering was part of the production process.[80] Moreover, although the EU, as a body, has approved a number of new applications since 2004,[81] many of its member states continue to ban approved products.[82] Given this background, it is not surprising that, as of 2015, only two forms of genetically modified crop were currently being grown commercially in the EU, and only in five of the 27 EU member states.[83] In 2015, the EU amended its legislation to give

member states more power in deciding whether to allow the cultivation of GM crops, using a principled approach that requires significant assessment.[84] In Switzerland, which is not a member of the EU, voters in 2005 approved a five-year ban on the farming of genetically modified crops.[85] The Swiss Parliament has extended the ban three times, first until 2010,[86] then until 2014, and then until 2021.[87] In 2014, Russia announced that it would no longer import GMO products.[88]

In the context of food imports from cloned animals, in March 2011, the European Parliament could not agree on regulations aimed at imports into Europe of meat and dairy products from cloned animals.[89] Consequently, farmers in other countries, such as the United States, that produced food from cloned animals, as well as food manufactures, were not burdened with costly regulation and labeling requirements for imports into Europe.[90] But in 2015, the European Parliament voted to ban the cloning of all farm animals and the sale of cloned livestock, their offspring, and products derived from them.[91]

China has also weighed in on GMOs. It does not allow commercial cultivation of any GMOs except papaya and cotton.[92] It does, however, allow 16 GMO crop varieties to be imported as raw materials for processing into cooking oils and for animal feed.[93] And in January 2019, it approved the importing of five types of genetically modified crops: two types of canola, two varieties of soybeans, and one variety of corn.[94] In step with these policies, China is among the over 60 nations that require labeling of importable GMOs.[95] At the same time, wary of dependence on Western nations to feed its population of 1.3 billion, it has been experimenting with genetically modified crops that can survive its arid lands.[96] This potential policy shift has given rise to intense internal debate within China.[97] Nevertheless, in late 2019, China took new steps towards commercialized domestic cultivation of GMO crops, issuing biosafety certificates for genetically modified corn and soybean.[98]

The next generation of genetically modified animals and crops is raising new regulatory questions. Using new techniques, companies have begun directly editing the genes of animals and crops instead of adding foreign genes from another organism. Hundreds of acres of gene-edited crops have already been grown in the U.S., including wheat with greater resistance to fungal diseases and mushrooms and potatoes that resist turning brown. And farmers are producing hornless dairy cattle, which could reduce the use of surgical "dehorning," a controversial practice that implicates animal welfare.[99] Food companies hope these animals and crops will be more acceptable to consumers, because gene editing does not involve mixing the genes of separate organisms. But critics are skeptical the public will see a difference and warn that the food industry is ignoring potential safety issues, making the same mistakes it made with existing GMO foods. It is unclear how these gene-edited foods fit within the existing U.S. regulatory framework. In December 2016, the FDA released for public comment a draft rule that would regulate gene-edited animals as if they contain new animal drugs.[100] The public comment period is now closed and the FDA will now be deciding how to promulgate the new regulations.[101]

In December of 2020, the FDA approved the first genomic alteration of domestic pigs for human food and potential therapeutic uses.[102] The FDA stated that "This is the first IGA in an animal that the FDA has approved for both human food consumption and as a source for potential therapeutic uses. The IGA in GalSafe pigs is intended to eliminate alpha-gal sugar on the surface of the pigs' cells. People with Alpha-gal syndrome (AGS) may have mild to severe allergic reactions to alpha-gal sugar found in red meat (e.g., beef, pork, and lamb)."[103]

Despite the FDA's deliberative approach to genetically modified foods, there is still growing concern in America over its consumption. In a campaign called "Just Label It," studies show that over 90% of Americans favor the use of mandatory labeling of genetically modified foods.[104] Overseas, there is an ongoing—some say bitter—debate over whether gene-edited animals and crops should be regulated as GMOs.[105] in July 2018, the European Court of Justice, which is the highest court in the European Union, ruled that organisms produced with gene editing techniques are in principle subject to the same regulations

as GMOs.[106] There is little doubt that the EU's concern over the unintended effects that might occur with genome editing will require further risk assessment to address the techniques used before the technology gains widespread acceptance.[107]

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