CHAPTER 13 Admissibility of DNA Evidence in Court

F orensic DNA typing has existed since the late 1980s, and has been admitted in court cases as evidence of identity since the late 1980s (Kaye, 2010, pp. 60–63). Some DNA evidence admissibility questions are now relatively uncontroversial (such as a "match" between robust single-source polymerase chain reaction-short tandem repeat (PCR-STR) profiles), and others are still contentious (such as results of "low-copy-number" testing and interpretations of complex mixtures by expert systems). This chapter offers a brief overview of the legal rules governing the admissibility of forensic DNA typing results, primarily in US court cases.

Any discussion of the admissibility of DNA in court, it should be said, is really a discussion of several different questions of admissibility. Before introducing evidence of a DNA profile "match" at trial, for example, the proponent must show not only that the DNA typing method is reliable, but also that the method of interpreting the results and calculating the statistical significance of the results is reliable. Thus, in a case involving a complex DNA mixture in which the prosecution alleges that a suspect is a likely contributor and seeks to introduce a likelihood ratio (LR) reported by a probabilistic genotyping software program like TrueAllele, the prosecution might be called upon in a pretrial reliability hearing to establish the reliability of (1) the PCR-STR method used to compare alleles among various potential contributors to a mixture; (2) the reliability of the expert system in estimating the number of contributors and whether a peak is a true allele or an artifact; and (3) the reliability of the statistical method the system uses to generate the LR, along with the reliability of the LR itself as an expression to the jury of the statistical significance of the results.

It is also worth noting that even where forensic DNA typing results are admissible as an evidentiary and constitutional matter, their meaning and probative value might be vigorously contested at trial by the opponent. The parties might disagree over whether a peak is a true allele or artifact and offer conflicting expert testimony on the matter; whether a match statistic is grossly overstated and offer conflicting expert testimony on the matter; the relevant population of potential contributors to a mixture; and the prevalence of phenomena like DNA transfer, which might offer an alternative innocent explanation for the presence of a person's DNA at a crime scene. An opponent might also question the qualifications or conclusions of a DNA expert, even if that expert succeeds in testifying. In short, the admissibility of DNA—that is, whether a judge or jury determining the facts of a case is even allowed to hear the results of forensic DNA typing—is only the first of many questions related to how the legal system treats DNA evidence in court.

THE BASIC LEGAL RULES GOVERNING ADMISSIBILITY OF DNA EVIDENCE

To be admissible in a civil or criminal trial in the United States, forensic DNA typing results must comply with the jurisdiction's rules of evidence (each state, as well as the federal system, has its own rules of evidence), as well as provisions of the US Constitution that give certain trial rights to those accused of a crime.

This section focuses on the rules of admissibility of DNA evidence applicable *at trial*. Although not all court cases involving DNA go to trial, the rules related to admissibility of evidence at trial loom large over settlement or plea negotiations, which are conducted in the shadow of a trial. And while DNA typing results might also be offered in legal proceedings beyond trial, such as sentencing proceedings, the rules governing admissibility of evidence at sentencing are generally both simple and permissive. For example, the US Sentencing Guidelines state that sentencing courts "may consider relevant information without regard to its admissibility . . . at trial, provided that the information has sufficient indicia of reliability" (U.S.S.G. § 6A1.3(a)).

Reliability Requirements for Expert Testimony

The first set of legal rules governing the admissibility of DNA relate to the requirement, under statutory or common law rules of evidence, that expert testimony based on scientific methods be reliable. Nearly all DNA typing results offered to prove identity are presented through one or more expert witnesses: laboratory technicians, DNA analysts, statisticians, population geneticists, and the like. As a result, the admissibility of DNA will turn in part on the rules of evidence governing expert witness testimony. In particular, nearly every state, as well as the federal system, requires that expert testimony be based on reliable methodology.

Some courts—following the so-called *Frye* standard—delegate the question of reliability of DNA to the scientific community, allowing the admission of expert testimony based on DNA typing and interpretation methods so long as those methods are "generally accepted" within the relevant scientific community. Before the 1920s, scientific evidence was treated like most other evidence, subject only to the usual requirements of relevance, witness competence, and the like (*Spring Co. v. Edgar*, U.S., 1878). But in 1923, the D.C. Circuit Court of Appeals in *Frye v. United States*

held that a criminal defendant accused of murder, James Frye, could not offer the expert testimony of Dr. William Moulton Marston—who would later create the character *Wonder Woman*—that Mr. Frye had taken and passed a polygraph examination (*Frye*; Lepore, 2015). According to the *Frye* court, a novel scientific methodology like the polygraph should not be admitted unless it is "sufficiently established" as a method "to have gained general acceptance" among the "authorities" in the field (*Frye*, p. 1014). Because the polygraph "ha[d] not yet gained such standing and scientific recognition," it was properly excluded by the trial court. The *Frye* "general acceptance" standard was highly influential and ultimately became the dominant standard in US courts for admissibility of expert testimony based on such methods.

Not until 1993, with the US Supreme Court's decision in Daubert v. Merrell Dow Pharmaceuticals, would the Frye test's dominance be challenged. In Daubert, the Court held that the federal rule of evidence governing admissibility of expert testimony—Rule 702—did not require that an expert's method be "generally accepted." The rule's language required only that an expert's "scientific" or other technical or specialized knowledge be helpful to the jury, which in turn required only that a method—if purportedly scientific—be scientifically valid (Daubert). And like all preliminary questions related to admissibility of evidence, the scientific validity of an expert scientific method must be determined by the trial judge, not by the scientific community. Thus, the Court reasoned, expert testimony is admissible so long as the expert is qualified and her method, if scientific, is deemed by the trial judge to be sufficiently reliable. In setting forth the factors to be considered by trial judges in determining scientific validity, the *Daubert* Court relied heavily on Karl Popper's view of the scientific method (Daubert, p. 593). Influenced by Popper's preoccupation with the concept of falsifiability, the Daubert Court set forth the following nonexhaustive list of factors to be considered by a judge in determining reliability of an expert method: (1) whether the method "can be (and has been) tested"; (2) whether the method "has been subjected to peer review and publication"; (3) the method's "known or potential rate of error"; (4) "the existence and maintenance of standards controlling the technique's operation"; and (5) whether the method is generally accepted in the "relevant scientific community."

In two subsequent decisions, the Supreme Court held that the *Daubert* reliability test applies not only to the method an expert uses but also to the expert's application of that method (*General Electric Co. v. Joiner*, 1997) and that *Daubert* applies not only to "scientific" methods but to all expert testimony, including nonscientific "technical" fields like tire-tread analysis (*Kumho Tire Co. v. Carmichael*, 1999). Together, *Daubert*, *Joiner*, and *Kumho Tire* are typically called the "*Daubert* trilogy" (Bernstein & Jackson, 2004). The language of Federal Rule of Evidence 702 has been amended to reflect the trilogy's holdings and now requires both that the "testimony is the product of reliable principles and methods" and that "the expert has reliably applied the principles and methods to the facts of the case" (F.R.E. 702(c),(d)). Courts applying *Daubert* to scientific methods continue to apply the nonexhaustive *Daubert* factors (testability, peer review, existence and extent of error rate, existence of standards to govern the method, and general acceptance in the scientific community) set forth in *Daubert* itself (see, e.g., Moss, 2015).

Today, most states and the federal system have shifted to the *Daubert* standard, either through court decisions or through passage of a statute or rule similar to Federal Rule of Evidence 702. Still, a significant minority of states, including New York and California, continue to adhere to *Frye* in determining admissibility of novel scientific evidence such as DNA (Jurilytics, 2017). Thus, in relying on precedent related to admissibility of a particular DNA method, litigants should be aware of which standard—*Frye* or *Daubert*—governed the precedential decision and which standard governs in the litigant's jurisdiction.

The Evidentiary Rule against Hearsay and the Constitutional Right of Confrontation

The second set of rules that might preclude admission of DNA typing results is the rule against "hearsay" and its corresponding constitutional rule, the confrontation clause of the Sixth Amendment to the US Constitution. For better or worse, the Anglo-American system prefers that the claims of human witnesses, if offered for their truth, be made live, in court, subject to the oath, physical confrontation, and cross-examination. Thus, the Federal Rules of Evidence exclude "hearsay"—an out-of-court statement offered "for the truth of the matter asserted in the statement"—as presumptively inadmissible (F.R.E. 801(c), 802). All 50 states have an analogous rule (Broun, 2013, § 244). Hearsay is thus inadmissible unless the proponent lays a foundation for admissibility under an applicable exception to the rule against hearsay, such as for "business records," "statements against penal interest," or "dying declarations" (Broun, 2013, § 245 et seq.). Even if a hearsay statement is admissible as an evidentiary matter under an exception, its admission in a criminal case against the accused might still violate the confrontation clause if it is the "testimonial" hearsay of a nontestifying declarant. Hearsay is generally "testimonial" if it is a sufficiently solemn statement that is either facially accusatory or created with the help of government officers, such as a stationhouse police confession of a defendant's alleged accomplice (Crawford v. Washington) or a formal affidavit of a forensic chemist about the presence of a drug in a tested substance (Melendez-Diaz v. Massachusetts).

In the context of DNA, these two rules arise most often when a testifying DNA expert determines a match or calculates a match statistic based in part on the hearsay report of another DNA expert who does not testify at trial.

The Fourth Amendment

The Fourth Amendment to the Constitution also gives rise to potential admissibility challenges to DNA evidence in court when offered in a criminal case against the accused. The Fourth Amendment protects against "unreasonable searches and seizures" and prohibits the issuance of a search or arrest warrant unless supported by "probable cause" (U.S. Const. amend. IV). Police may therefore apply for a search warrant to obtain a nonconsensual DNA sample from a criminal suspect only if they have probable cause to believe the DNA will show that the suspect has committed a crime. Police can also obtain DNA from a suspect by consent without violating the Fourth Amendment (*Schneckloth v. Bustamonte*; Will, 2003). To the extent forced DNA sampling in the absence of any individualized suspicion to believe the suspect is engaged in a crime is unconstitutional, any DNA test results stemming from such a Fourth Amendment violation may be inadmissible under the "exclusionary rule" as the "fruit" of a constitutional violation (*Mapp v. Ohio; Maryland v. King*). As discussed further later in the chapter, the primary context in which criminal defendants have argued that evidence of a DNA match violates the Fourth Amendment is in database "cold hit" cases.

THE STATUS OF RELIABILITY-BASED ADMISSIBILITY CHALLENGES TO DNA EVIDENCE

This section explores the status of reliability challenges to various forms of DNA evidence, setting forth both areas of consensus, in which the reliability of DNA typing results will not likely be disputed, and areas of controversy, in which the reliability of DNA typing results or statistical methods is more contentious.

Single-Source PCR-STR Testing Results and Random Match Probabilities (RMPs)

Some forms of DNA evidence are now universally accepted as evidence of identity in US courts as a matter of reliability. The original forms of forensic DNA testing and interpretation used in the 1980s and early 1990s were subject to much criticism during the "DNA Wars," the history of which has been ably told by others (Kaye, 2010; Lynch et al., 2008; see chapter 1). But these earlier techniques have been replaced in forensic DNA analysis by PCR-based STR discrete-allele typing. Courts now universally accept as generally reliable both the PCR process for amplification of DNA and the STR-based system of identifying and comparing alleles (Kaye, 2010, pp. 190–191).

The most common PCR-STR-based kits used in forensic analysis in criminal cases in the United States are those manufactured by Applied Biosystems (such as ProFiler/CoFiler, testing 13 core STR loci, including amelogenin, or sex; IdentiFiler, testing 16 loci, including amelogenin; and, most recently, GlobalFiler, testing 24 loci)) and Promega's PowerPlex kits (FBI, n.d.). These are the primary kits accepted by the Federal Bureau of Investigation (FBI) for uploading to the Combined DNA Index System (CODIS) for comparison purposes (FBI, n.d.). All new reference samples taken by convicted or arrested persons for upload to CODIS must contain 20 "core CODIS loci" and thus must be tested using the most recent, most highly discriminating kits (FBI, n.d.). All evidence samples from crimes or missing persons inquiries must be at least tested for the core CODIS loci, though results at all 20 loci are not necessary for comparison purposes (FBI, n.d., §§ 19, 20).

In addition, the use of the RMP to express the statistical significance of a match between two PCR-STR single-source (non-mixture) profiles has also been universally accepted by US courts.¹ In general, evidence of a DNA match is inadmissible without a corresponding match statistic expressing the statistical significance of the match to the factfinder.² In the words of one court, "[w]ithout the probability assessment, the jury does not know what to make of the fact that the [DNA] patterns match: the jury does not know whether the patterns are as common as pictures with two eyes, or as unique as the Mona Lisa." (United States v. Yee, 1991). The RMP is the product of the probabilities of a person having each of the alleles represented in a singlesource PCR-STR profile (Butler, 2009, pp. 229–230). While the RMP has been the subject of some academic debate because its accuracy rests on the assumption of statistical independence among the STR loci and minimal population substructure, courts have universally accepted it as a reliable expression of the statistical significance of a match between two single-source samples under both *Frye* and *Daubert* (see, e.g., Mueller, 2008). Only where the RMP has been mistaken by a prosecutor as the chance of the defendant's innocence—the "prosecutor's fallacy" or "fallacy of the transposed conditional"—have courts commented on its potential for undue prejudice.³ Moreover, while expert witness assertions of source attribution based

1. See, e.g., *State v. Roman Nose*, 667 N.W.2d 386, 398 (Minn. 2003) ("[A] random match probability statistic [product rule] is scientifically acceptable when applied to a known single source sample."); and *People v. Smith*, 132 Cal. Rptr. 2d 230, 233 (Ct. App. 2003) ("Defendant concedes, 'It is generally accepted the [polymerase chain reaction and short tandem repeats] can be completely accurate in typing genetic material from single source samples."). Cf. *United States v. Silva*, 889 F.3d 704, 718 (10th Cir. 2018) (expert described single-source sample analysis "as easy as you can get").

2. See, e.g., *State v. Tester*, 968 A.2d 895, 909 (Vt. 2009) ("[A]dmission of DNA match evidence, without additional evidence of the frequency with which such matches might occur by chance, is error."); *Deloney v. State*, 938 N.E.2d 724, 730 (Ind. Ct. App. 2010) (deeming DNA evidence inadmissible without "accompanying testimony explaining the statistical significance of those non-exclusion results"); *United States v. Davis*, 602 F. Supp. 2d 658, 673 (D. Md. 2009) ("DNA evidence cannot be admitted in a vacuum; the Government must also present some additional information with which a jury can accurately assess the significance of the consistency between a defendant's DNA profile and that of the evidence."); and *Commonwealth v. Mattei*, 920 N.E.2d 845, 858 (Mass. 2010) ("The challenged expert [DNA] testimony concerning the nonexclusion results should not have been admitted without accompanying statistical explanation of the meaning of nonexclusion."). But see *State v. Hummert*, 933 P.2d 1187, 1191 (Ariz. 1997) (noting that in Arizona, no numerical statistic is required as foundation for expert testimony on a DNA match).

3. The "prosecutor's fallacy," or fallacy of the transposed conditional, occurs when a lawyer (or judge or juror) mistakes the RMP (e.g., one in a million) for the probability that the defendant is not the source. Put differently, the person hearing the statistic mistakes one conditional probability (the chance the defendant would match the profile, given that he is not the source of the DNA, or the RMP) for its transposed conditional (the chance the defendant is not the source, given that he matches). See, e.g., *McDaniel v. Brown*, 558 U.S. 120 (2009) (noting that the prosecutor and the government's DNA expert both engaged in the fallacy of the transposed conditional in their statements before the jury); and (Roth, 2010), explaining the fallacy in laypersons' terms. ().

on RMPs have been the subject of some defense challenges, courts generally allow DNA experts to testify to their opinion, based on an exceedingly small RMP, that the DNA profiles share a common source. For example, FBI analysts commonly testify to source attribution above any RMP threshold of 1 in 300 billion (1,000 times the US population) (Butler, 2009).

Y-STR and Mitochondrial DNA (mtDNA) Testing Results

Litigants have also made reliability challenges to Y-STR and mtDNA testing results, with little success. While forensic PCR-STR typing looks at short repeated sequences of DNA on the "autosomal" (nonsex) chromosomes (Butler, 2009), forensic Y-STR typing looks at certain short repeated sequences on the Y chromosome in male DNA samples. Men inherit the Y-STR profile of their father, and the profiles are not believed to change much over generations. Thus, the statistical significance of a Y-STR match is not calculated by an RMP; the allelic frequency tables that generate RMPs for traditional PCR-STR profiles assume statistical independence of the STR markers. In Y-STR typing, in contrast, analysts use a "counting method" to generate a match statistic. That is, they look for the Y-STR profile or *haplotype* in a database of Y-STR profiles from a relevant population, take the resulting number of "hits" (say, zero or one), and build a confidence interval around that number to express the chances of seeing additional matches in a larger population sample. Thus far, courts appear to have universally accepted Y-STR typing results as reliable when offered by the government in a criminal case, both under $Frye^4$ and Daubert.⁵ Notably, courts have excluded Y-STR typing results in certain circumstances when offered by a criminal defendant in postconviction proceedings as evidence of innocence, even while acknowledging that Y-STR typing is generally accepted.⁶ One recent court also

5. See, e.g., *People v. Tunis*, 318 P.3d 524, 528 (Colo. Ct. App. 2013) (holding as an issue of first impression that Y-STR is reliable under *Daubert*); *People v. Wood*, 862 N.W.2d 7, 24 (Mich. Ct. App. 2014), *judgment vacated in part on other grounds*, 498 Mich. 914, 871 N.W.2d 154 (2015) (trial court did not abuse its discretion by admitting expert testimony on Y-STR after holding *Daubert* hearing); and *State v. Maestas*, 299 P.3d 892, 934 (Utah 2012) (same).

6. See, e.g., *Commonwealth v. DiCicco*, 25 N.E.3d 859, 869 (Mass. 2015) (holding that the trial judge did not abuse her discretion by excluding defendant's proffered Y-STR expert witness, because the Y-STR exclusion was based on a single potential allele, a method that is discouraged, though not prohibited, under the SWGDAM Y-STR guidelines); *People v. Stoecker*, 10 N.E.3d 843, 849 (Ill. 2014) (holding that, given the DQ alpha testing done

^{4.} See, e.g., *People v. Zapata*, 8 N.E.3d 1188, 1195 (Ill. Ct. App. 2014) (holding that no new *Frye* hearing was required because Y-STR was already generally accepted); *State v. Calleia*, 997 A.2d 1051, 1065 (N.J. Ct. App. 2010), *rev'd on other grounds*, 206 N.J. 274, 20 A.3d 402 (2011) (ruling that Y-STR is generally accepted); *Commonwealth v. Jacoby*, 170 A.3d 1065, 1095 (Pa. 2017), *petition for cert pending* (ruling as a matter of first impression that Y-STR is generally accepted); *State v. Bander*, 208 P.3d 1242, 1255 (Wash. Ct. App. 2009) (no new *Frye* hearing required because Y-STR is already generally accepted); and *People v. Stevey*, 148 Cal. Rptr. 3d 1, 12 (Ct. App. 2012) (no new *Kelly-Frye* hearing required because Y-STR is already generally accepted).

excluded evidence of Y-STR results in a (currently pending) Texas murder trial, but only apparently because the results did not incriminate the defendant other than the tendency to show that the DNA was male (Winkle & Goard, 2018).

Challenges to mtDNA typing results have been similarly unsuccessful. Unlike Y-STR typing, mtDNA typing isolates a long sequence of DNA in a particularly hypervariable region of DNA found in the mitochondria of one's cells (outside the nucleus). Like Y-STRs, mtDNA is not recombinant; we inherit our mtDNA sequence from our mothers, and mtDNA sequences (like Y-STRs) are not believed to change much over generations. As with Y-STR haplotypes, the statistical significance of a match between mtDNA sequences is expressed through the *counting method*, building a confidence interval around the number of matching haplotypes found in a relevant mtDNA population database. To be sure, mtDNA match statistics have been criticized for being misleading and inaccurate, given the amount of "clustering" of haplotypes based on migration patterns (Kittles et al., 2006). Nevertheless, most if not all challenges to mtDNA typing results or match statistics in US courts have been unsuccessful under *Frye*⁷ and *Daubert*,⁸ with very few challenges even being brought in the last decade.

Admissibility Challenges to "Low Copy Number" DNA Typing Results

The primary context in which admissibility challenges to single-source nuclear DNA comparison results are still successful is low copy number (LCN) DNA testing. Many laboratories have a different set of protocols for testing DNA samples involving an amount of input DNA lower than 1 nanogram, a level below which the identification

before trial, there was no "reasonable likelihood of more probative results" using Y-STR typing after conviction); and *People v. Barker*, 1-12-3238, 2015 WL 2069736, at *8 (Ill. App. Ct. Apr. 30, 2015) (same).

7. See, e.g., *People v. Stevey*, 148 Cal. Rptr. 3d 1, 11 (Ct. App. 2012) ("mtDNA evidence . . . has also gained general acceptance within the scientific community"); *People v. Klinger*, 713 N.Y.S.2d 823, 831 (N.Y. Co. Ct. 2000) (holding that mtDNA is generally accepted and reliable based on holdings in a number of other jurisdictions); *Magaletti v. State*, 847 So. 2d 523 (Fla. Ct. App. 2003) (same); *State v. Pappas*, 776 A.2d 1091, 1108 (Conn. 2001) (same); and *People v. Holtzer*, 255 Mich. App. 478 (2003) (same).

8. See, e.g., *State v. Brochu*, 949 A.2d 1035, 1049 (Vt. 2008) ("Although mtDNA evidence is relatively new, all jurisdictions to have considered the issue have uniformly found mtDNA to be reliable."); *United States v. Beverly*, 369 F.3d 516, 531 (6th Cir. 2004) (holding that trial court did not abuse its discretion in admitting mtDNA evidence because the "scientific basis for the use of such DNA is well established"); *United States v. Coleman*, 202 F. Supp. 2d 962 (E.D. Mo. 2002) (holding mtDNA admissible under *Daubert*); *Wagner v. State*, 864 A.2d 1037, 1044 (Md. Ct. App. 2005) (same); and *State v. Council*, 515 S.E.2d 508, 518 (S.C. 1999) (same). Cf. *State v. Griffin*, 384 P.3d 186, 203 (Utah 2016) (noting, while discussing probative/prejudicial balancing, that "every state that has been confronted with the question of whether mtDNA is admissible under its applicable rules of evidence has answered the question in the affirmative").

and interpretation of alleles becomes more difficult and controversial (Butler, 2015, pp. 159–160; ISHI Conference, 2017). Several trial and appellate courts have ruled LCN testing reliable, under both *Frye*⁹ and *Daubert*.¹⁰ Nonetheless, at least a handful of courts have excluded LCN testing results on reliability grounds.¹¹

Admissibility Challenges to Mixture Interpretations by Human Analysts

Criminal defendants in the United States challenging the admissibility of DNA typing results have perhaps had the most traction in cases involving DNA mixtures and the presentation of a match statistic called the combined probability of inclusion, or CPI, to the factfinder.

Because DNA mixtures involve more than one contributor, it may be difficult for analysts to determine how many contributors there are to a mixture, and which alleles at each locus belong to which contributor. As a result, a simple calculation of an RMP using allelic frequencies and the product rule, as analysts do for singlesource sample comparisons, is not possible in mixture statistics. And while new probabilistic genotyping software programs hold great promise for mixture deconvolution and the calculation of highly discriminating match statistics based on the consideration of thousands of permutations, analysts are more limited in their mixture interpretation abilities. Thus, analysts calculate a match statistic in mixture cases by (1) identifying all alleles at all loci, (2) determining whether the reference sample of interest (such as a criminal suspect) has alleles that are consistent with the alleles

9. See, e.g., *Phillips v. State*, 226 Md. App 1 (Md. Ct. Spec. App. 2015) (holding LCN DNA analysis admissible under *Frye* and that any attack on its reliability went to its weight rather than admissibility); *People v. Garcia*, 963 N.Y.S.2d 517 (N.Y. Sup. Ct., Bronx County 2013) (holding both that LCN DNA testing is not a novel science that would require a *Frye* hearing before being admissible and that LCN DNA testing conducted by the OCME in New York is generally accepted); and *People v. Megnath*, 898 N.Y.S.2d 408 (N.Y. Sup. Ct., Queens County 2010) (holding that LCN DNA testing as conducted by the OCME is admissible under *Frye*). Cf. *People v. Lazarus*, 190 Cal. Rptr. 3d 195, 239 (Ct. App. 2015) (holding that LCN was not generally accepted).

10. See, e.g., *United States v. Morgan*, 53 F. Supp. 3d 732 (S.D.N.Y. 2014), *aff'd*, 675 F. App'x 53 (2d Cir. 2017) (holding that the OCME's LCN testing methodology is reliable under *Daubert*); and *United States v. Barton*, 8:14-CR-496-T-17AEP, 2016 WL 4921036, at *6 (M.D. Fla. Sept. 14, 2016) (holding that magistrate did not abuse its discretion in denying *Daubert* challenge to LCN results). *Cf. United States v. Sleugh*, 14-CR-00168-YGR-2, 2015 WL 3866270, at *3 (N.D. Cal. June 22, 2015), *appeal pending* (holding that no *Daubert* hearing was necessary to introduce LCN results).

11. See United States v. McCluskey, 954 F. Supp. 2d 1224 (D.N.M. 2013) (excluding LCN testing under Daubert because the New Mexico Department of Public Safety laboratory used different procedures and methods than the New York OCME, and there was no evidence that the NM procedures and methods would yield reliable results); and People v. Collins, 15 N.Y.S.3d 564 (N.Y. Sup. Ct., Kings County 2015) (holding LCN testing using the OCME's "FST" software was not admissible under Frye).

in the mixture, and (3) if so, calculating the chance that a randomly selected person would also be consistent with the combination of alleles present in the mixture—the CPI (sometimes referred to equivalently as the "random man not excluded" statistic) (Bieber et al., 2016; Butler, 2015).

The CPI has been the subject of considerable criticism, from both sides of the American criminal justice system. On the one hand, the CPI is a much less discriminating statistic than the RMP and tends to ignore a significant amount of relevant information about likely number of contributors and likely contributor profiles (Curran & Buckleton, 2008). At the same time, some argue that the CPI carries too great a risk of falsely inculpating innocent suspects, because it removes any loci from its statistical calculation that exhibit signs of "allelic dropout": based on a suspect's allele being absent from the mixture, rather than considering the possibility that the absence of the suspect's allele reflects that the suspect is simply not a contributor (Murphy, 2015, pp. 92–94; Butler, 2015; Curran & Buckleton, 2010).

In 2010, in response to the critiques of the CPI from the scientific community, the Scientific Working Group on DNA Analysis Methods (SWGDAM) changed its DNA mixture interpretation guidelines to require laboratories to remove certain loci from their CPI calculations. SWGDAM's concern was with peaks that were above the profiling system's "analytical threshold" (AT) (the height below which a peak carries too great a risk of being an artifact rather than genetic material) but below the system's "stochastic threshold" (ST) (the height above which stochastic effects,¹² such as allelic dropout, are unlikely to occur). The new guidelines required laboratories to remove any locus from the CPI calculation that contained any peak above the AT but below the ST.¹³In 2016, a distinguished group of scientists reiterated this call to remove any locus from the CPI calculation where any peak was within a certain range (Bieber et al., 2016; PCAST, 2016, p. 78 (citing Bieber et al. 2016)). And later in 2016, the President's Council of Advisors on Science and Technology (PCAST) concluded that the CPI method is "clearly not foundationally valid" under *Daubert* (PCAST, 2016, p. 78).

While the CPI has been introduced as a valid match statistic under both $Frye^{14}$ and

13. See Scientific Working Group on DNA Analysis Methods, "SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories" (approved January 4, 2010, § 4.6.3) ("When using CPE/CPI (with no assumptions of number of contributors) to calculate the probability that a randomly selected person would be excluded/included as a contributor to the mixture, loci with alleles below the stochastic threshold may not be used for statistical purposes to support an inclusion. In these instances, the potential for allelic dropout raises the possibility of contributors having genotypes not encompassed by the interpreted alleles.").

14. See, e.g., *State v. Bigger*, 227 Ariz. 196, 205, 254 P.3d 1142, 1151 (Ariz. Ct. App. 2011) (CPI is "generally accepted," even when applied to LCN samples); and *Phillips v. State*, 126 A.3d 739, 751 n.11 (Md. Ct. Sp. App. 2015), *aff'd on other grounds*, 152 A.3d 712 (Md. 2017) (holding in footnote that the use of a CPI statistical computation for a steering wheel DNA sample was admissible because the laboratory "analyzed the steering wheel sample in a generally accepted manner.").

^{12.} Stochastic effects are those due to sampling issues caused by the low number of events.

Daubert¹⁵ in numerous criminal trials in the United States, at least one recent court has rejected the CPI as unreliable,¹⁶ and other courts have recently reversed convictions based on the presentation of mixture statistics to a jury that, viewed in retrospect, are vastly more inculpatory—sometimes by several orders of magnitude—than they would have been under the post-2010 guidelines (see, e.g., Moran, 2017; Texas Forensic Science Commission, 2015). Moreover, some courts have excluded a CPI on undue prejudice grounds in cases where the statistic is only minimally discriminating (such as excluding only 50% of the population).¹⁷ Litigants involved in DNA mixture cases should therefore be aware of the guideline change and how it might affect match statistics presented at both past and current trials.

Admissibility Challenges to Complex Mixture Interpretations by Expert Systems

Some laboratories have begun to address the problems of the CPI by employing expert systems to interpret DNA mixtures. Unlike human analysts, expert systems, or probabilistic genotyping software (PGS) in this case, can consider much more information, including data sets estimating allelic dropout averages at various loci, than human analysts can. Instead of calculating the CPI, these expert systems calculate an LR or similar statistic that purports to compare the probability of seeing the mixture given the competing hypotheses that the suspect (or other person of interest) is or is not a contributor to the mixture. The resulting LRs tend to be much more discriminating than the CPI; a typical LR reported by the program TrueAllele would state, "A match between Mr. [Defendant] and the fingernails is 189 billion times more probable than a coincidental match to an unrelated Caucasian." (Perlin, 2010). Expert systems have also been wielded by lawyers for criminal defendants as evidence of innocence in high-profile exonerations (see, e.g., McCall, 2018). While some PGS are open source, most are proprietary. One proprietary program, the "FST" software developed by New York's Office of the County Medical Examiner (OCME), was excluded by one trial judge under *Frye*, prompting the OCME to both make the source code public and shift to using a different program (Jacobs, 2016). Now, the two main

15. See, e.g., *State v. Haughey*, 3 A.3d 980, 992 (Conn. Ct. App. 2010) (defendant could not demonstrate that the trial court abused its discretion in admitting CPI evidence).

16. *United States v. Williams*, 3:13-CR-00764-WHO-1, 2017 WL 3498694, at *13 (N.D. Cal. Aug. 15, 2017) (excluding DNA analysis from the SERI laboratory, which used a "suspect-centric" form of CPI analysis "not based on sound methodology."). Cf. *People v. Smith*, C062513, 2011 WL 4528254, at *22 (Cal. Ct. App. Sept. 29, 2011) (unpublished) (holding that "the CPI was an improper statistical analysis to be used in this case because [the expert] knew he was dealing with a mixture that had significant allelic dropout," but finding no prejudice).

17. See, e.g., *People v. Pike*, 53 N.E.3d 147, 170 (Ill. App. Ct. 2016), *reh'g denied* (May 2, 2016), *appeal denied*, 89 N.E.3d 761 (Ill. 2017) (holding that it was error, but not plain error, for the trial court to admit a "50% inclusion probability statistic" derived from CPI calculations "because the statistic was irrelevant").

programs used in forensic DNA testing in the United States are TrueAllele, owned by the Pittsburgh, Pennsylvania, company Cybergenetics; and STRMix, owned by the New Zealand research institute ESR (PCAST, 2016, p. 80).

The 2016 report of the President's Council of Advisors on Science and Technology (PCAST) cited expert systems as an improvement over existing human analysis of complex mixtures, concluding that such methods have been established as foundationally valid for mixtures with three or fewer contributors, where the minor contributor constitutes at least 20% of the intact DNA in the mixture and the DNA amount exceeds the minimum required by the method for analysis (PCAST, 2016, p. 82). The report suggested, however, that use of the software beyond its empirically established range could be problematic. To be sure, the PCAST report has itself been subject to criticism both for failing to more fully solicit the participation of forensic examiners and law enforcement and for placing a premium on properly designed "black box" validation studies as a prerequisite for foundational validity (National District Attorney's Association, 2016; Budowle, 2017).

So far, the LRs from both STRMix and TrueAllele have been admitted in numerous courts across the country, in both *Frye* and *Daubert* jurisdictions.¹⁸ In fact, TrueAllele has not been excluded on reliability grounds by any court, although one California trial court—later reversed by a higher court—had deemed the failure to disclose TrueAllele's source code a barrier to its admissibility (People v. Chubbs, 2015). STRMix has been deemed inadmissible in two cases. In the first, the New York Hillary case, the trial judge excluded the evidence under Frye not based on a ruling that STRMix is an inherently unreliable method, but on the lack of internal validation studies by the local laboratory that conducted the testing (Hillary Order, 2016, pp. 9–10). Notably, the inculpatory LR generated by STRMix in Hillary was contradicted by TrueAllele results on the same sample, which indicated that Mr. Hillary was likely not a contributor (Roth, 2017, p. 2019). In the second case, in June 2018, a Texas trial judge excluded under Daubert the STRMix results from male DNA found on the thigh of a female murder victim, after human analysis "came up inconclusive" (Winkle & Goard, 2018). In another recent case, currently pending appeal, a California state judge has conditioned the admissibility of STRMix under *Frye* on the government providing the source code to the defense, which it thus far has refused to do (People v. Dominguez, 2018). While the research institute ESR offers limited access to STRMix's source code to defense experts before trial under a nondisclosure agreement, the company has declined to allow broader access, citing a trade secret privilege. While some legal commentators have suggested that no such trade secret privilege should exist in criminal cases (Wexler, 2018; Chessman, 2017), no appellate court has yet been

18. See, e.g., *People v. Bullard-Daniel*, 54 Misc. 3d 177, 191 (N.Y. Co. Ct. 2016) (holding STRMix results admissible under *Frye*). The Cybergenetics website lists numerous cases in which TrueAllele has been admitted under either *Frye* or *Daubert*. *See* TrueAllele Admissibility, cybgen.com, https://www.cybgen.com/information/admissibility/page. shtml. Likewise, the STRMix website lists numerous cases around the country and globe in which STRMix has been admitted. See https://strmix.esr.cri.nz/#news.

persuaded by such arguments to uphold a trial court's order requiring source code disclosure.

In sum, the results of expert systems TrueAllele and STRMix have thus far been widely held admissible as evidence of both guilt and innocence. Nonetheless, if defense requests for access to source code continue to be granted, and if disclosure of source code is deemed a condition of admissibility, then the proprietors of these programs may have to subject their source code to further scrutiny or face possible exclusion of results in certain cases. Moreover, to the extent these systems continue to be used on complex mixtures beyond the empirically established range of the software—with multiple contributors, extreme peak height differential, or low template DNA—and to the extent different systems continue to generate contradictory results, courts might be more receptive to reliability challenges in the future.

Admissibility of Evidence Related to DNA "Transfer"

Under certain circumstances, DNA can "transfer" from one individual or surface to another (*direct transfer*), or even from that second person/surface to a third person/ surface (secondary transfer) (Butler, 2009, p. 80; 2011, pp. 18–19). The likelihood of transfer occurring is a function of a number of factors, including the type of surface touched and whether the individuals involved are "shedders" or "non-shedders" (Fonneløp et al., 2017). In a given case, the likelihood of transfer might be a critical issue for the factfinder, in terms of what inference to draw from the presence of a person's DNA at a crime scene. For example, in one recent case, a state appellate court ruled that the presence of a defendant's DNA on a handgun found in his house was insufficient evidence to convict him for possession of the gun, because of the high likelihood of transfer (Finley v. State, 2014). And in a high-profile California case, a homeless man, Lukis Anderson, accused of killing a wealthy Silicon Valley investor, was eventually exonerated after the presence of his DNA on the victim's fingernails was explained by DNA transfer; the same EMTs who responded to the murder scene had assisted Anderson earlier in the day and could have transferred traces of Anderson's DNA to the victim (Worth, 2018). While numerous courts have allowed expert testimony as to transfer, several courts have also denied motions for postconviction relief filed by defendants claiming that a DNA transfer expert would have made a difference at trial.¹⁹

^{19.} See, e.g., *Adams v. State*, 161 Idaho 485 (Ct. App. 2016) (holding that the addition of expert testimony on DNA transfer would not have made a difference to the trial outcome); and *Sancier v. Comm'r of Correction*, 139 Conn. App. 644 (2012) (acknowledging that DNA transfer is "theoretically possible" but ruling that transfer evidence would not have affected outcome). *Cf. State v. Freeman*, No. 28150, 2008 WL 142299, at *1 (Mo. Ct. App. Jan. 16, 2008), *rev'd en banc*, 269 S.W.3d 422 (Mo. 2008) (rejecting defendant's claim that the DNA evidence against him was insufficient because of the possibility of transfer).

THE STATUS OF CONSTITUTIONAL ADMISSIBILITY CHALLENGES TO DNA EVIDENCE

This section explores the status of constitutional challenges to DNA evidence under the confrontation clause and Fourth Amendment.

Confrontation Clause Challenges to Reliance on Hearsay DNA Reports of Nontestifying Analysts and to Proprietary Expert Systems

Because of the rule against hearsay and the confrontation clause, the proponent of a forensic DNA report cannot offer *the report itself* into evidence without calling the report's author to the witness stand. However, the proponent of the testimony can circumvent the hearsay rule by having the testifying analyst simply explain to the factfinder that her expert opinion is *based upon* the other analyst's report. Under Federal Rule of Evidence 703 and its state analogs, so long as the hearsay report itself is not offered as evidence, a testifying expert is free to "base an opinion" upon hearsay or other inadmissible evidence (*Williams v. Illinois*; F.R.E. 703).

Although the evidentiary rules allow a testifying DNA analyst to rely on another analyst's hearsay report in rendering an opinion, there is still an open question as to whether such testimony might violate the confrontation clause in a criminal case if offered against the accused. In Williams v. Illinois (2012), the Supreme Court heard a rape case in which the state's DNA analyst testified that the defendant's PCR-STR profile, which was tested and developed at the testifying analyst's state laboratory, "matched" the profile developed from the victim's vaginal swabs, which were tested and analyzed at a different laboratory, Cellmark. The defendant argued that the analyst's testimony violated the confrontation clause because the analyst's expert opinion was based in large part on the analysis and conclusions of Cellmark's analyst, who did not testify. A majority of justices of the Supreme Court concluded that the testimony did not violate the confrontation clause, but no one argument received a full five votes. Four justices concluded that the nontestifying expert's report did not implicate the clause because it was technically offered only to explain the basis of the testifying analyst's opinion, rather than for its "truth." An additional justice concluded that the testimony did not implicate the clause because the hearsay report of the nontestifying analyst was not sufficiently formal or solemn to count as testimonial hearsay, given that the Cellmark analysis was conducted before a suspect had been identified.

Because neither of the theories of admissibility in *Williams* garnered five votes, and because of the changing composition of the Supreme Court, the *Williams* decision leaves unresolved whether future DNA cases with slightly different facts might present a confrontation clause problem. For example, a recent decision by New York's highest state court reversed a burglary conviction on confrontation clause grounds where the testifying DNA analyst, who opined that the defendant's DNA matched the DNA from the crime scene but who had not conducted, witnessed, or supervised the DNA testing in the case, simply read to the jury the hearsay report of another, nontestifying DNA analyst colleague (*People v. Austin*, 2017).

The other potential confrontation clause challenge to DNA evidence relates to the results of proprietary expert systems offered at trial. A reported LR from TrueAllele is not considered "hearsay" under American rules of evidence because it is not an assertion by a human witness; TrueAllele cannot be placed under oath, "cross-examined," or physically confronted. But some commentators have argued that expert systems offering accusatory claims against criminal defendants should perhaps be considered "witnesses against" the defendant for purposes of the confrontation clause (see, e.g., Roth, 2017). While "confrontation" of a proprietary algorithm would not be synonymous with "cross-examination," it might involve disclosure of source code; disclosure of prior statements of the algorithm related to the same subject matter; or a right to some sort of technical transparency report that reveals relevant assumptions of the program, such as the program's estimate of allelic dropout rates, or stutter percentages, at various loci. With the exception of a dissenting California Supreme Court justice, however, no appellate court has yet been persuaded that machinegenerated results might implicate the confrontation clause (People v. Lopez, 2012). Indeed, at least one US Supreme Court justice has intimated that "raw data" from a machine would likely not implicate the confrontation clause (Bullcoming v. New Mexico, 2011, Sotomayor, J., dissenting).

Fourth Amendment Challenges to DNA Database "Cold Hit" Results

Thus far, Fourth Amendment challenges to forcible DNA sampling of those convicted of or arrested for certain crimes, and the uploading of the resulting DNA profiles to CODIS for comparison purposes, have been unsuccessful. Each state, as well as the federal system, maintains a DNA database, authorized by statute, containing the PCR-STR profiles of people convicted of, or arrested for, various crimes (Roth, 2013). These official statutory databases are all interconnected through CODIS, allowing local police anywhere in the country to compare a crime scene DNA profile to the 14+ million profiles in CODIS to look for a match, or "cold hit," to an unsolved case. In 2013 the Supreme Court upheld the constitutionality of Maryland's arrestee database, on grounds that states can reasonably require arrestees to give DNA for identification purposes, just as they are forced to give fingerprints (Maryland v. King, 2013). Most recently, the California Supreme Court held that California's arrestee database was also constitutional under King, a critical decision, given that California's database differs significantly from Maryland's database in that it does not allow for automatic expungement of an arrestee's record and is more expansive in the crimes it covers (People v. Buza, 2018).

To the extent that Fourth Amendment challenges to database "cold hits" might be successful in the future, they will probably relate to more controversial tactics such as familial searching, searching of genealogy websites, or collection of "abandoned" DNA. *Familial searching* entails searching a DNA database not just for a perfect match, but for a partial match, indicating that a person with partially matching might be *related to* the perpetrator (Murphy, 2010; Chapter 4). While familial searching has been banned in a few states, including Maryland, it is explicitly permitted in 12 states, including California (Rainey, 2018). While proponents argue that the practice helps catch elusive criminals (Rainey, 2018), critics argue that it has a significant racially disparate impact and unfairly allows law enforcement to scrutinize people who are not in a criminal or even an arrestee database, in the absence of any suspicion of wrongdoing (Murphy, 2010).

No Fourth Amendment challenge has yet been successful against the collection of "abandoned" DNA, which people inadvertently leave on coffee cups, cigarette butts, and the like. The prevailing logic is that because the DNA has been "abandoned," it is akin to garbage, which is devoid of Fourth Amendment protections because the owner has abandoned it and thus has no "legitimate expectation of privacy" in the contents under existing constitutional doctrine (Joh, 2006). A Fourth Amendment challenge against government searches of commercial genealogy databases, onto which members have voluntarily posted their DNA profiles for comparison with other members, might be precluded on the same grounds. California police recently identified a suspect in the Golden State Killer case based on a search of the opensource genealogy website GEDMatch, conducted without a warrant, without probable cause, and in a way that violated the terms of service (by creating a fake name associated with the crime scene DNA profile they uploaded for comparison purposes) (Zhang, 2018; see chapter 15).

The Supreme Court's recent decision in *Carpenter v. United States* might breathe new life into such challenges, however. In *Carpenter*, the Court held that the government cannot subpoena historical cell phone location records without a warrant, even though the defendant had shared his location with his cell phone company (*Carpenter v. United States*, 2018). In doing so, the Court significantly limited the reach of the "third-party doctrine" that a suspect has no legitimate expectation of privacy in information he shares with others.²⁰ The full implications of *Carpenter* for DNA database search challenges remains to be seen.

CONCLUSION: DNA ADMISSIBILITY ISSUES ON THE HORIZON

The next decade will inevitably bring further DNA admissibility issues as the technology advances. For example, the use of Rapid DNA machines—which can develop a profile from a sample in as little as 90 minutes—on crime scene evidence samples will surely be the subject of *Daubert* and *Frye* reliability challenges. While reference samples developed with Rapid DNA are eligible for upload to CODIS, crime scene

^{20.} See *Carpenter v. United States*, 585 U.S. __ (2018), slip op. at 11 ("Given the unique nature of cell phone location records, the fact that the information is held by a third party does not by itself overcome the user's claim to Fourth Amendment protection.").



Police released images of how an attacker connected to several crimes, including at least a rape and a murder that happened more than 20 years ago in Montgomery County, Md., might have looked at 25 years old, left, and at 45 years old. (Courtesy of Montgomery County Police)

Figure 13.1 Composite sketch of a crime suspect created by Maryland police using DNA phenotyping. *Source:* "Maryland composite suspect sketch created through phenotyping. Courtesy of Montgomery County Police.

(evidence) samples are not (FBI, n.d.). Likewise, the use of DNA *phenotyping* to identify crime suspects may well face admissibility challenges. Phenotyping involves estimating the physical characteristics of a suspect based on a crime scene DNA profile (Southall, 2017). As figure 13.1 shows, the technique is already being used to develop composite sketches of suspects.

Because phenotyping is used only to initially identify a suspect, not to ultimately prove that the suspect matches the DNA from a crime scene, it is unlikely that the practice will trigger reliability challenges at trial. However, the reliability of the technique may well be relevant to Fourth Amendment challenges to searches and seizures based on a suspect's alleged similarity to an estimated phenotype.

In sum, the foundational validity of PCR-STR forensic DNA typing for singlesource robust samples and the use of the RMP to express the statistical significance of two matching single-source profiles are well established as reliable. Nonetheless, several aspects of forensic DNA typing may still continue to raise significant admissibility issues.

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