

7.21 DNA Evidence

(1) Definitions.

(a) DNA is:

(i) the biological substance known as autosomal DNA which is present in the nucleus of human cells and comprises the human genome, exclusive of the similar substance on the sex chromosomes;

(ii) the biological substance known as mitochondrial DNA (“mtDNA”) which is present in the mitochondria in a human cell and contains the genetic contributions of an individual’s mother; and

(iii) the biological substance known as Y-STR DNA which is present on a male’s Y chromosome and contains the genetic contributions of that male’s father.

(b) DNA evidence is evidence about the recovery and analysis of DNA, including an expert appraisal of the likelihood that DNA obtained from a person or place came from a particular individual.

(c) DNA evidence is “deconvoluted” when the profile of at least one contributor to a DNA mixture can be isolated from the profile(s) of the remaining contributor(s).

(d) Simple DNA is:

(i) autosomal DNA apparently from one individual and

(ii) autosomal DNA apparently from one individual whose contribution to a mixture of individuals’ DNA was deconvoluted.

(e) Complex DNA is a mixture of individuals' autosomal DNA, or a portion of such a mixture, which cannot be deconvoluted.

(f) A likelihood ratio is a mathematical statement of the probability that a DNA sample contains DNA from one or more known individuals rather than solely from one or more other individuals.

(g) Electrophoresis is the stage of DNA analysis at which a machine measures distinguishing markers in a DNA sample at key locations of the genome.

(2) Admissibility; in general.

(a) Subject to the foundational requirements of paragraph (b), expert testimony about the analysis of DNA evidence is admissible when the theories and procedures of analysis are generally accepted as reliable by the relevant scientific community.

(b) The admission of DNA evidence is subject to the foundational requirements identified in Guide to New York Evidence rules 4.01 (Relevant Evidence) and 7.01 (Opinion of Expert Witness [rev June 2022]) and article 8 (Hearsay). In addition, a foundation for the admissibility of DNA evidence should include testimony that the appropriate steps were taken in analyzing the evidence. The required foundation should not include a determination by the court whether the evidence is accurate; that determination remains with the jury.

(3) The admissibility of types of DNA evidence

(a) At present, widely used theories and procedures for analyzing autosomal DNA in simple DNA samples, mtDNA, and Y-STR DNA have been found reliable by general consensus of the relevant

scientific community. Some but not all proposed theories and procedures for analyzing complex DNA have been found reliable by general consensus of the relevant scientific community. Evidence of analysis performed through the accepted theories and procedures is admissible, subject to subdivision two and absent a showing that the theories and procedures are no longer generally accepted as reliable by consensus of the relevant scientific community.

(b) When a party offers simple DNA evidence as proof that the DNA did or did not come from a particular individual, the evidence need not include the expression of a likelihood ratio unless the court in its discretion rules otherwise.

(c) An expert testifying about a sample containing complex DNA may not state that a particular individual contributed to the sample. An expert may testify to a likelihood ratio and should inform the finder of fact about the significance of the likelihood ratio or of other statistics derived from DNA analysis.

(4) Application of principles of hearsay and confrontation.

(a) The rules applicable to hearsay apply to DNA evidence in civil and criminal cases. See Guide to New York Evidence article 8 and in particular rule 8.02 (Admissibility [of Hearsay] Limited by Confrontation Clause [*Crawford*] [rev June 2022]).

(b) In a criminal case, constitutional restrictions on the introduction of testimonial hearsay:

(i) do not apply to evidence about laboratory DNA work through the electrophoresis stage, absent circumstances indicating that this

preliminary work was skewed to implicate a particular individual;

(ii) do apply to evidence about laboratory DNA analysis that follows electrophoresis, including analysis of the electrophoresis data, if the primary purpose of the analysis was to assess whether DNA came from a particular person of interest to law enforcement. Evidence about analysis that follows electrophoresis therefore must be presented by one or more expert witnesses who personally performed, witnessed, or supervised the analysis, or who can independently opine whether the analysis is correct.

Note

Subdivision (1)

Subdivision (1) (a) (i) addresses autosomal DNA. Autosomal DNA, a string of biological substances contributed equally by each individual's father and mother, comprises most of the human genome. Autosomal DNA is located in the nucleus of most human cells but does not include the similar substances on the sex chromosomes in the nucleus. It is unique for every individual (except for identical twins). Autosomal DNA can therefore identify, for example, which human left physical evidence at a crime scene or is the parent of a child. (*See People v Wesley*, 83 NY2d 417, 421 [1994]; *People v Wakefield*, 38 NY3d 367 [2022] [description of the theories and procedures of DNA analysis]; *People v Williams*, 35 NY3d 24 [2020] [same]; Roth, *Chapter 13: Admissibility of DNA Evidence in Court*, *Silent Witness: Forensic DNA Analysis in Criminal Investigations and Humanitarian Disasters* at 295-297 [Oxford Univ Press 2020].) Identification evidence based on a single individual's autosomal DNA has long been accepted as scientifically sound. (*Wesley* at 424-425; Roth at 295.)

Subdivision (1) (a) (ii) and (iii) addresses two less familiar types of DNA. Mitochondrial DNA ("mtDNA") is present in a cell's mitochondria, structures outside the cell's nucleus. The genome in mitochondria differs from that in the cell's nucleus, but its components are examined with the same procedures employed for autosomal DNA. MtDNA almost always comes only from a person's

mother. Absent a mutation, a mother's mtDNA will be passed on from generation to generation to her male and female descendants. (See *People v Klinger*, 185 Misc 2d 574 [Nassau County Ct 2000]; Roth at 298; Court, *Mitochondrial DNA in forensic use*, 5 Emerging Topics Life Scis [Issue 3] 415 [Portland Press 2021]; Budowle et al., *Forensics and Mitochondrial DNA: Applications, Debates, and Foundations*, 4 Ann Rev Genomics & Hum Genetics 119, 121-122 [2003].) The descendants of a woman with a particular mtDNA genome can be recognized—but mtDNA cannot distinguish the woman's descendants from one another. Nonetheless, when an autosomal DNA sample is too small for analysis or is degraded, mtDNA can provide information that may exonerate individuals of interest or substantially narrow the universe of possible DNA contributors.

Like autosomal DNA evidence, evidence about mtDNA has been held scientifically sound. (See *People v Ko*, 304 AD2d 451, 452 [1st Dept 2003] [“The court correctly determined that mitochondrial DNA analysis has been found reliable by the relevant scientific community, and that issues regarding contamination go to the weight to be given such evidence”], *judgment vacated on other grounds* 542 US 901 [2004], *on remand judgment affd* 15 AD3d 173 [1st Dept 2005]; *Klinger*, 185 Misc 2d 574.)

The third form of DNA is Y-STR DNA. Y-STR DNA is in a cell's nucleus, on the Y chromosome. It is pertinent only to the identification of males, as only they have a Y chromosome. Y-STR DNA profiles are subject to mutations, but otherwise are passed down over generations from father to son. (See *People v Wright*, 115 AD3d 1257, 1259-1260 [4th Dept 2014, Fahey & Carni, JJ., dissenting], *revd* 25 NY3d 769 [2015]; Kayser, *Forensic use of Y-chromosome DNA: a general overview*, 136 Hum Genetics 621 [2017].) Y-STR DNA analysis cannot distinguish one male in a paternal line from another. It simply allows a conclusion about whether an individual of interest is included in that paternal line and, if so, an estimate of the odds that a random person would be included. But like mtDNA it can exonerate the innocent or substantially narrow the universe of possible DNA contributors. See *Harrell v Miller*, 22-238-PR, 2023 WL 4479325, at 2-3 [2d Cir, 2023].

Y-STR DNA has apparently not been subjected to a *Frye* hearing in New York. The admission of Y-STR DNA evidence by the New York trial courts, however, has been noted without negative comment by the appellate courts. (See *e.g. People v Wright*, 25 NY3d 769 [2015]; *People v Longo*, 212 AD3d 471 [1st Dept 2023].) The theories and procedures underlying Y-STR DNA analysis are,

through the electrophoresis stage, the same as those that apply to autosomal DNA and mtDNA analysis. Beyond that, the acceptability of Y-STR DNA evidence is assumed in the state regulations on forensic DNA methodology (9 NYCRR 6192.3 [e]) and such evidence has been admitted in trials in many states (*see* LaRue, *The Science of Change: Familial Searches And Y-STR DNA*, 17 Ohio State J Crim L 241, 256-259 [2019] [collecting cases]).

Subdivision (1) (b) recognizes that DNA evidence includes evidence about the recovery of DNA samples. Contamination or degradation of a DNA sample may affect the probative value of DNA evidence. And “touch” DNA from an innocent person can be passed on to another individual and then left where it may incriminate that innocent person. The circumstances of the recovery of DNA may be relevant to an assessment of those and similar possibilities. (*See* Roth at 303; *and see* Williamson, *Touch DNA: Forensic Collection and Application to Investigations*, 18 J Assn Crime Scene Reconstr 1, 3-4 [2012].)

Subdivision (1) (c) defines “deconvoluted” as utilized in the analysis of simple and complex DNA, as specified in subdivision (1) (d) and (e). (*See e.g.* Butler et al., *DNA Mixture Interpretation: A NIST Scientific Foundation Review*, National Institute of Standards & Tech Internal Rep 8351-DRAFT at x [June 2021], available at <https://nvlpubs.nist.gov/nistpubs/ir/2021/NIST.IR.8351-draft.pdf>.)

Subdivision (1) (d) defines “simple” DNA. The first type is autosomal DNA that apparently came from one individual. Analysis of a substantial quantity of such DNA to determine whether it matches a DNA profile from a separate sample is now routine. (Roth at 295; *DNA Mixture Interpretation* at 12; Jobling & Gill, *Encoded Evidence: DNA in Forensic Analysis*, 5 Nature Revs Genetics 739, 739 [2004].) The second type of simple DNA comes from a mixture of individuals’ autosomal DNA that can be fully or partially “deconvoluted” or “resolved”—that is, from which the DNA of at least one contributor can be isolated. One individual’s DNA may be present in a much larger or smaller amount than that of other contributors. That difference can make it possible to create a DNA profile of the larger or smaller contributor. (*See People v Griffin*, 122 AD3d 1068 [3d Dept 2014] [major contributor provided 90% of the DNA].) In addition, the identity of one or more contributors may be known. A known donor’s DNA profile can simplify analysis of the mixture, helping to expose the DNA profile of another contributor (*see People v Powell*, 165 AD3d 842 [2d Dept 2018] [the likelihood that two suspected donors contributed to a three-person mixture]). In sex crime cases, scientists have for years been able to recognize which DNA comes from sperm cells and can create a profile from those cells alone. (*See People v Rawlins*, 10 NY3d

136, 158-159 [2008]; Williamson et al., *Enhanced DNA mixture deconvolution of sexual offense samples using the DEPArray system*, 34 *Forensic Sci Intl: Genetics* 265 [2018]; Gill et al., *DNA Profiling in Forensic Science*, *Encyclopedia of Life Sciences* [2001], available at <https://doi.org/10.1038/npg.els.0001001>.)

Subdivision (1) (e) addresses complex DNA, that is, DNA mixtures that cannot be deconvoluted. In the past, experts who analyzed a complex mixture could opine only that an individual of interest could be excluded as a contributor, that he could not be excluded, or that testing results were inconclusive. (See e.g. *People v Wright*, 25 NY3d 769, 771, 775-777 [2015] [the defendant could not be excluded as a contributor to a mixture]; *People v Watley*, 245 AD2d 323 [2d Dept 1997] [same].) Experts have now developed “probabilistic genotyping” software that permits the creation of the more informative likelihood ratios. (See *People v Williams*, 35 NY3d 24, 47-49 [2020]; *People v Foster-Bey*, 35 NY3d 959 [2020].)

Subdivision (1) (f) explains a likelihood ratio; for example, in analyzing a two-person mixture, an analyst might hypothesize that a known individual and an unknown random individual were the contributors and calculate the probability (likelihood ratio) that the known individual was a contributor as 100,000 times greater than the probability that the contributors instead were two unknown random individuals. (*DNA Mixture Interpretation* at 37.) Decisional law cites testimony about likelihood ratios with apparent approval of their use. (See e.g. *Wakefield*, 38 NY3d at 371-380.)

It is important that the probative value of a likelihood ratio be understood. When a two-person mixture cannot be deconvoluted, an analyst deals with a stew of about four or more DNA markers from each of about two dozen locations on the genome. Analysis of mixtures from more contributors is still more complicated. There is no way to determine which markers combine to create the profiles of the individual contributors. Thus, in the example above the expert cannot say that the odds are 100,000 to one that the known individual’s DNA is in a mixture. Nor can the expert say that only one individual in 100,000 could have been a contributor. The expert is expressing how much more likely it is that the known individual and one other are contributors than two random individuals on the street. The expert will have no idea whether an individual with a higher likelihood ratio might be living next door to the known individual. (See *DNA Mixture Interpretation* at 37-38, 90-91.)

Subdivision (1) (g) introduces the concept of electrophoresis. At identified locations on the genome, an individual’s DNA markers will differ in length from

those of most other people. The electrophoresis machine measures the length of the DNA markers at those locations. For a simple DNA sample this data can reveal the individual's profile. For a complex sample, an expert can graph all the markers and use the data to create a likelihood ratio for a known person of interest. The electrophoresis stage marks a significant border for Confrontation Clause purposes. (*See* subd 4, *infra*.)

Subdivision (2)

Subdivision (2) (a) addresses the admissibility of DNA evidence created through scientific theories and procedures that are challenged by a party. If that party makes a prima facie showing in support of the challenge, the proponent of the evidence must demonstrate that the theories and procedures underlying the DNA analysis are generally accepted in the scientific community. (*See Wesley*, 83 NY2d at 422-423 [applying *Frye v United States* (293 F 1013 [DC Cir 1923]) to DNA evidence]; *People v Williams*, 35 NY3d 24, 37-38 [2020]; Guide to NY Evid rule 7.01 (2), Opinion of Expert Witness [rev June 2022]; *see also* Report of the President's Council of Advisors on Science and Technology, *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods* [2016] [PCAST report].)

Subdivision (2) (b) is a reminder that a proper foundation for DNA evidence must be provided and specifies that the foundation must include proof that approved procedures were utilized and explained (*Wesley* at 425). In addition, a ruling on admissibility does not turn on any assessment by the court of whether the proffered evidence is correct (*id.*).

Subdivision (3)

Subdivision (3) (a) addresses the status of DNA procedures under the *Frye* rule. DNA testimony purporting to show the identity of an individual who left a simple DNA sample has been found admissible under *Frye*. (*Wesley*, 83 NY2d at 420.) However, some methods for interpreting complex DNA evidence with probabilistic genotyping software are not authoritatively endorsed at this time. (*See People v Foster-Bey*, 35 NY3d 959, 961 [2020] [(I)t was an abuse of discretion as a matter of law to admit . . . (forensic statistical tool) evidence without first holding a *Frye* hearing given defendant's showing that there was uncertainty regarding whether such proof was generally accepted in the relevant scientific community at the time of the subject motion"]; *see People v Williams*, 35 NY3d 24 [2020] [same].) *Williams*, however, made it clear that, among the unsettled questions is

whether software adequately analyzes complex samples containing very small quantities of DNA—“low copy number” or “LCN” DNA (*see Williams* at 30, 39-40; *DNA Mixture Interpretation* at 31).

Today’s *Frye* challenges to mixture analysis software include attacks on the use of “continuous” probabilistic software in place of “semi-continuous” probabilistic software like that discussed in *Williams*. (*See DNA Mixture Interpretation* at 31.) The PCAST report stated that, as of 2016, probabilistic genotyping software in general was a “promising” method for mixture analysis (PCAST report at 82, 148). The report added that, according to published reports, two brands of continuous software, TrueAllele and STRmix, are reliable for two- and three-person mixtures under certain conditions (PCAST report at 80, 82). New York appellate courts have since gone farther. In particular, *People v Wakefield* (38 NY3d 367 [2022]) found that TrueAllele software passed the *Frye* test even for LCN mixture samples. (*See also People v Bullard-Daniel*, 203 AD3d 1630 [4th Dept 2022] [STRmix result was admissible]; *People v Wilson*, 192 AD3d 1379 [3d Dept 2021] [TrueAllele result was admissible].)

Subdivision (3) (b) recognizes that expert witnesses frequently testify about the likelihood that a particular individual is the source of a simple DNA sample and it notes that such testimony need not come in the form of a likelihood ratio. Witnesses have, for example, testified without controversy that the odds that someone other than the defendant provided a DNA sample were “1 in greater than 1 trillion people” (*People v John*, 27 NY3d 294, 298 [2016]). In an earlier case the chances of another profile matching the defendant’s profile were said to be 500 million to one (*People v Rush*, 242 AD2d 108 [2d Dept 1998]). And in *People v Dearmas* (48 AD3d 1226 [4th Dept 2008]), an expert opined that the odds that someone other than the defendant left the DNA sample were one in 12.2 trillion.

Subdivision 3 (c) recognizes that practice is different for testimony about complex DNA samples. In the past experts could offer only vague testimony about the possibility that a particular individual contributed to a DNA mixture. As noted, DNA experts now use software to create the more helpful likelihood ratios. It appears that no court has required that reports about mixture contributions be delivered in the form of a likelihood ratio, but the employment of likelihood ratios seems now to be universal.

Jurors, and indeed counsel, may find testimony about likelihood ratios difficult to understand and subdivision 3 (c) also addresses that circumstance. The court should ensure that the parties correctly state the significance of a likelihood

ratio. To date, appellate disapproval of trial comments has centered on prosecutors' overstatements about the meaning of ratios. (See e.g. *People v Wright*, 25 NY3d 769, 778-782 [2015]; *People v Powell*, 165 AD3d 842 [2d Dept 2018]; cf. *Harrell v Miller*, 22-238-PR, 2023 WL 4479325, at 2-3 [2d Cir, 2023]). The principle would seem to apply to expert testimony as well.

Subdivision (4)

Subdivision (4) (a) is a reminder that New York's hearsay rules apply to DNA evidence, and subdivision (4) (b) details those principles as applied in a criminal proceeding.

Subdivision (4) (b) addresses the application of the Sixth Amendment right of confrontation to DNA evidence in criminal cases in light of *Crawford v Washington* (541 US 36 [2004]). That case and its progeny determine when evidence of DNA laboratory reports is admissible. (See generally Guide to NY Evid rule 8.02, Admissibility Limited by Confrontation Clause [*Crawford*] [rev June 2022].)

Crawford held that the right to confrontation dictates that "testimonial hearsay" proffered by the prosecution, no matter how reliable, is inadmissible even if the declarant is unavailable if "the defendant had [no] prior opportunity for cross-examination," so long as the witness's unavailability is not due to actions of the defendant. (*Id.* at 53-60, 62.) If a DNA laboratory report is testimonial hearsay under that rule, it is inadmissible unless introduced through the testimony of the declarant or another witness with first-hand knowledge of the laboratory analysis.

Subdivision (4) (b) sets forth the current answer to when a laboratory report of DNA evidence is testimonial and is derived principally from *People v John* (27 NY3d 294 [2016]).

John held that the introduction of "DNA reports into evidence, asserting that defendant's DNA profile was found on the gun that was the subject of the charged possessory weapon offense, without producing a single witness who conducted, witnessed or supervised the laboratory's generation of the DNA profile from the gun or defendant's exemplar" violated the defendant's right to confrontation. (*Id.* at 297.)

John explained that "we have deemed the primary purpose test essential to determining whether particular evidence is testimonial hearsay requiring the

declarant to be a live witness at trial. . . . We have considered two factors of particular importance in deciding whether a statement is testimonial—first, whether the statement was prepared in a manner resembling *ex parte* examination and second, whether the statement accuses defendant of criminal wrongdoing. Furthermore, the purpose of making or generating the statement, and the declarant’s motive for doing so, also inform these two interrelated touchstones.” (*Id.* at 307 [internal quotation marks and citations omitted].)

The “primary purpose” in *John* “of the laboratory examination on the gun swabs [to identify the defendant as the possessor of the gun] could not have been lost on the . . . analysts, as the laboratory reports contain the police request for examination of the gun swabs on the basis that the ‘perp’ handled the gun and repeatedly identify the samples as ‘gun swabs.’ ” (*John* at 308.) Thus, to the extent that the primary purpose of the DNA reports in *John* was to accuse the defendant of the crime, they constituted testimonial hearsay and were inadmissible absent the requisite witness (subd [4] [b] [ii]).

John noted, however, that even if the primary purpose of a DNA laboratory report were to create evidence against a known individual, portions of the report describing what took place before the “raw data” from electrophoresis was forwarded for expert analysis were not testimonial hearsay (subd [4] [b] [i]). Those preliminary steps are so routine that they are not considered accusatory, even if the suspect is known. (*Id.* at 313 [in the *John* case “any hypothetical missteps of the analysts in the multiple stages preliminary to the DNA typing at the electrophoresis stage would result in either no DNA profile or an incomplete DNA profile, or one readily inconsistent with a single source 16 loci profile”].)

Following *John*’s “primary purpose” rationale, if the primary purpose of a DNA report is not to accuse a person of an offense, the DNA report would not be testimonial. Thus, for example, in *People v Meekins* (10 NY3d 136 [2008]), decided before *John*, a rape kit DNA sample was analyzed before any individual was a suspect. A report of the result, including a profile later found to match defendant’s, was not testimonial, as the testing was not conducted to provide a result accusing a known individual. (*See Meekins* at 158-161; *see generally People v Pealer*, 20 NY3d 447 [2013] [primary purpose of calibration and maintenance of breathalyzer machine was not to incriminate any particular individual or prove an element of a crime]; *People v Brown*, 13 NY3d 332 [2009] [expert witness drew her conclusions from raw DNA data developed before the defendant was a suspect].)

Parenthetically, it should be noted that in *Williams v Illinois* (567 US 50 [2012]), which was decided by a plurality of four judges, the remaining five justices refused to subscribe to the “primary purpose” test.