7.21 DNA Evidence[1]

(1) <u>Definitions.</u>

(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 to provide raw data for the preparation of DNA profile(s).

(2) <u>Admissibility; in general.</u>

(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) <u>The admissibility of types of DNA evidence</u>

(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) <u>Application of principles of hearsay and confrontation.</u>

(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, the constitutional restriction on the introduction of testimonial hearsay:

(i) does not apply to evidence about DNA testing through the electrophoresis process, as that work is ancillary to the generation of data by a machine, absent circumstances indicating that this preliminary work was skewed to implicate a particular individual;

(ii) does apply to evidence about laboratory DNA analysis following electrophoresis, including analysis of the raw data produced by electrophoresis; and

(iii) does apply to evidence about the extent to which DNA profiles match an individual or one another.

(c) When the admission of forensic DNA evidence is governed by the Confrontation Clause, a competent witness is a person who either

participated in or directly supervised the "final" step that generates the DNA profile, or conducted an independent analysis of the data used to do so in a manner that enables replication of the determinations made at that stage in order to verify the profile. The witness must either detail the witness's level of participation or supervision in the analysis, or, if the witness did not participate or supervise in the analysis, the witness must demonstrate that the witness conducted an independent analysis on the raw data and was not merely functioning as a conduit for the conclusions of others.

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 University 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*, 2023 WL 4479325, *2-3, 2023 US App LEXIS 17617, *5-9 [2d Cir, July 12, 2023, 22-238-pr].)

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 raw data can allow

an expert to construct the contributor's reveal 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). Subsequently, after an evidentiary hearing,

the court in *People v Burrus* (81 Misc 3d 550, 659 [Sup Ct, Kings County 2023]) held that "the People met the burden of showing that the offered evidence, the LCN testing and FST, met the *Frye* standard of acceptability within the relevant scientific community."

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*, 2023 WL 4479325, *2-3, 2023 US App LEXIS 17617, *5-9 [2d Cir, July 12, 2023, 22-238-pr].) 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) and (c) 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]). (*See generally* Guide to NY Evid rule 8.02, Admissibility Limited by Confrontation Clause [*Crawford*] [rev June 2022].)

Crawford held that: "A 'testimonial statement' of a person who does not testify at trial is not admissible against a defendant for the truth of the statement, unless the witness is unavailable to testify and the defendant had a prior opportunity for cross-examination, or the defendant engaged or acquiesced in wrongdoing that was intended to and did procure the unavailability of the witness" (Guide to NY Evid rule 8.02 [1]).

Subdivision (4) (b) delineates when a stage of DNA testing and a conclusion drawn therefrom are subject to the dictates of *Crawford*, and paragraph (c) states the necessary requirement for the admissibility of DNA evidence subject to the dictates of *Crawford.*

In brief, subdivision (4) (b) (i) specifies the only stage of DNA analysis to which *Crawford* does not apply, namely (absent the stated exception), the "preliminary" testing of the DNA evidence through the electrophoresis stage (*People v Jordan*, 40 NY3d 396, 401 [2023]; *People v John*, 27 NY3d 294, 313-315 [2016]). Other than that "preliminary" stage, the remaining stages of DNA analysis and any conclusion drawn therefrom are, as specified in subdivision 4 (b) (ii) and (iii), subject to the dictates of *Crawford* (*Jordan* at 401-402; *People v Rawlins*, 10 NY3d 136, 157, 160 [2008]). The admissibility of that evidence requires, as specified in subdivision (4) (c), a witness who "either participated in or directly supervised this 'final' step that generates the DNA profile, or [conducted]

an ‘independent analysis’ of the data used to do so in a manner that enables replication of the determinations made at that stage in order to verify the profile” (*Jordan* at 402; *see People v Ortega*, 40 NY3d 463, 476 [2023] [holding that an autopsy report constituted testimonial evidence and similarly required a witness who “performed, supervised, or observed the autopsy or used their independent analysis on the primary data”]).

With respect to the “preliminary stage” of DNA testing (i.e. portions of a laboratory DNA report describing what occurred before and during electrophoresis, about which a witness, with or without personal knowledge, may give explanatory testimony), the Court of Appeals reasoned that those steps prior to the analysis of the raw electrophoresis data involve “ ‘essentially ministerial tasks’ ” in which the analyst “simply prepare[s] the DNA samples for testing” and during which “the analyst’s role is to facilitate the operation of a machine” (*Jordan* at 400-401; *see John* at 313 [“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”]). Thus, “[i]nstead of imposing a rule that required production of every person who comes into contact with the evidence at these preliminary stages of testing,” the Court of Appeals determined that the key “witness is one directly involved in the critical final stage of testing, when an analyst must exercise judgment to cull the data and generate the DNA profile” (*Jordan* at 401).

Thus, with respect to post-electrophoresis analysis, *Jordan* holds that the prosecution may present testimony about post-electrophoresis analysis only from witnesses with personal knowledge of the facts. An expert witness testifying about a DNA test has such knowledge only if that witness performed the test or witnessed or supervised its performance, or personally undertook an independent analysis of the data (*Jordan* at 401).

The import of *Jordan* and *Ortega* is that the need for a defendant to cross-examine the testimony of a witness about post-electrophoresis analysis, as well as to examine the credibility of that witness, is compelling even if the defendant became a suspect only after the analysis; indeed, confrontation about how DNA profiles were created from the raw electrophoresis data can be critical to the reliability of the result (*see Jordan* at 401, 403; *Ortega*, 40 NY3d at 475-476).

A conclusory description of the involvement of the witness in the analytical process does not constitute an adequate showing of the witness’s personal knowledge. In *Jordan*, an expert’s statements that for one DNA sample he

"received reports and reviewed them" and conducted an "independent interpretation of the testing data" was too vague to show that the witness could testify about a profile (*Jordan* at 403). As to a second DNA sample, the witness's testimony that he received the raw electrophoresis data and drew his "own interpretations based on that data," coupled with his statement that he reviewed another analyst's work, likewise were too conclusory (*id*.). These statements did not allow the Court to discern the expert's level of involvement at this "crucial" stage in the generation of the DNA profiles and to dismiss the possibility that he was simply a "conduit for the conclusions of others" (*Jordan* at 403, quoting *John* at 315).

It should be noted that before *Jordan*, the Court of Appeals had recognized a broader exception to *Crawford*'s holding that it finds no longer viable. The Court had concluded that the Confrontation Clause was inapplicable not only to testimony about procedures before electrophoresis but also the procedures after if the "primary purpose" of the analysis was to create evidence against an unknown criminal (*People v John*, 27 NY3d 294, 315 [2016]). In *Ortega*, however, the Court held that an autopsy report constituted testimonial evidence and in doing so recognized that intervening decisions of the United States Supreme Court rendered this "primary purpose" rationale untenable (*see* 40 NY3d at 473-474).

Jordan concluded with a word of caution: "We note that our holding today is made absent clear guidance from the U.S. Supreme Court. The Supreme Court may revisit the issues . . . in a manner that affects today's holding. Technology may also develop in a way that affects confrontation rights and our holding is limited to the process for forensic DNA analysis as currently conducted" (*Jordan* at 404 [citations omitted]).

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[1] In February 2024, the rule and Note to subdivision (4) were updated primarily to account for the holdings and import of two Court of Appeals cases: *People v Jordan* (40 NY3d 396, 401 [2023]) and *People v Ortega* (40 NY3d 463 [2023]).