STATE OF MINNESOTA

COUNTY OF OLMSTED

IN DISTRICT COURT
CRIMINAL DIVISION
THIRD JUDICIAL DISTRICT

State of Minnesota,

Plaintiff,

vs.

Exavier Lloyd Porter,

Defendant,

Court File No. 55-CR-22-7394

SUPPLEMENTAL MEMORANDUM AND ORDER

The above-entitled matter came before the Honorable Pamela A.W. King, Judge of District Court, at the Olmsted County Government Center, Rochester, Minnesota, for an Evidentiary Hearing on February 9, 2024, and March 8, 2024. Assistant Olmsted County Attorneys, Joseph K. Rosholt and Arianna L. Whitney, appeared on behalf of the State of Minnesota. John D. Schmid, Attorney at Law, appeared on behalf of Defendant, Exavier Lloyd Porter, who was also personally present.

The Court heard testimony from the following witnesses: Ms. Cynthia Cale and Dr. Marlijn Hoogendoorn. The Court received Exhibits 1, 5, 101-115, 117, 122-125, 127, 129-143.

The Court issued Findings and an Order on July 10, 2024. This memorandum further explains the Court's Findings and Order.

ORDER

1. The attached Memorandum is incorporated and made part of this Court's July 10, 2024, Order.

BY THE COURT:

King, Pam
2025.02.13
13:33:04 -06'00'

Pamela A.W. King
Judge of District Court

cc: Joseph K. Rosholt & Arianna L. Whitney, Attorneys for Plaintiff
John D. Schmid & James McGeeney, Attorneys for Defendant

MEMORANDUM

Exavier Lloyd Porter has been charged with Attempted First-Degree Murder – With Intent – While Committing a Felony in violation of Minn. Stat. § 609.185(a)(3) and Drive-By Shooting Toward an Occupied Motor Vehicle or Building – Dangerous Weapon in violation of Minn. Stat. § 609.66, subd. 1e(a)(2).

On March 26, 2023, Mr. Porter filed a motion seeking to suppress and exclude the opinions of the Bureau of Criminal Apprehension ("BCA") analyst, Kathryn Roche, concerning her interpretation of two items of evidence. Mr. Porter argues that her opinion lacks foundational reliability under Minn. R. Evid. 702 and should be excluded because the probative value is substantially outweighed by the danger of unfair prejudice under Minn. R. Evid. 403. The Court heard testimony from two expert witnesses, Ms. Cynthia Cale and Dr. Marlijn Hoogendoorn.

FACTS

On October 29, 2022, near Heritage Manor in Rochester, Mr. Porter was seen getting out of a blue car and shooting at the driver of a Mercedes SUV.[1] Mr. Porter was with Diata Dashane Simmons, who shares children in common with both the driver of the SUV and Mr. Porter. After shots were fired, Mr. Porter and Ms. Simmons were seen going into an apartment, returning with a child, and leaving the scene. Mr. Porter and Ms. Simmons were arrested shortly after the shooting. Twelve days later, on November 11, 2022, cleaning staff at the Heritage Manor apartment complex found a pistol inside an apartment where Ms. Simmons and her two children lived prior to the shooting.[2] The pistol was recovered by

[1] These facts are derived from a summary of facts in the prosecution and defense submissions pertaining to this motion and the allegations in the last amended criminal complaint.
[2] Given the information in the complaint, it is reasonable to assume that this was where Mr. Porter was visiting and may have entered the day of the shooting. No other facts regarding whether the gun located in the apartment was tied to or associated with the shooting were submitted. Further, given

Rochester Police ("RPD") Officer Noben.[3] Swabs were taken by RPD from the gun and magazine and sent to the BCA for testing. On April 24, 2023, the BCA generated Report No. 3 from Kathryn Roche with her findings about the DNA from the gun.

Item 1 is a swab from a firearm. 520 picograms of DNA were recovered from the swab. The parties agree that the DNA profile from Item 1 is an indistinguishable mixture. The BCA asserts that five individuals contributed to the DNA mixture obtained from Item 1. Mr. Porter cannot be excluded as a possible contributor. "The probability of observing this DNA profile is greater than 100 billion times more likely if a mixture from Mr. Porter and four, unknown unrelated individuals is the source than if a mixture of five unknown, unrelated, individuals is the source."[4]

Item 2 is a swab from the magazine of a firearm. 180 picograms of DNA were recovered from this swab. The DNA profile developed from Item 2 was interpreted by the BCA as coming from at least two people. Based on the peak heights, a "major male profile" was identified, and Mr. Porter cannot be excluded. The analyst reported that the major male profile matches Mr. Porter, but there is insufficient information on the minor contributors to conduct further analysis. "The probability of observing this DNA profile is greater than 100 billion times more likely if a mixture from Mr. Porter and one, unknown, unrelated individual

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the information in the complaint and submitted by the parties, it is reasonable to assume that there were two children of Ms. Simmons, one who is the child in common with the victim and one who is the child in common with Mr. Porter.

[3] Supplemental Report of Officer Noben, Nov. 15, 2022 (Exhibit 136); Body Worn Camera Footage of Officer Noben (Nov. 11, 2022) (Exhibit 143).

[4] Kathryn Roche, Report on the Examination of Physical Evidence Lab No. S23-03294, Report No. 3 (Apr. 24, 2023) (Exhibit 117); Kathryn Roche, DNA SUMMARY AND INTERPRETATION NOTES S23-03294 (Apr. 17, 2023) (Exhibit 123); Kathryn Roche, DNA EXTRACTION AND QUANTITATION EXP-23-AM4435 (Apr. 3, 2023) (Exhibit 122); Kathryn Roche, Electropherogram QS23-03294-1A (Apr. 10, 2023) (Exhibit 111).

is the source than if a mixture of two unknown, unrelated individuals is the source."[5] It is the result of these tests that the State seeks to introduce to establish that Mr. Porter shot ten rounds at the driver of the SUV. [6]

In support of their assertion that the DNA testing conducted is not foundationally reliable, the defense called Ms. Cynthia Cale. Ms. Cynthia Cale is a forensic DNA expert with DNA Mavens; she has been conducting DNA case reviews, consulting, and testifying as an expert consultant since 2022.[7] Ms. Cale has a Bachelor of Science in Biology from Illinois Wesleyan University, a Master of Science in Human Biology from the University of Indianapolis, and is currently seeking a Doctorate of Philosophy in Forensic Science from the University of Dundee.[8] Both her graduate and doctoral studies have focused on DNA transfer and persistence.[9] Ms. Cale has over 20 years of experience as a laboratory DNA technical leader, DNA analyst, and forensic scientist.[10] Ms. Cale is a member of the American Academy of Forensic Science ("AAFS") and the International Society for Forensic Genetics ("ISFG").[11]

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[5] Kathryn Roche, Report on the Examination of Physical Evidence Lab No. S23-03294, Report No. 3 (Apr. 24, 2023) (Exhibit 117); Kathryn Roche, DNA SUMMARY AND INTERPRETATION NOTES S23-03294 (Apr. 17, 2023) (Exhibit 123); Kathryn Roche, DNA EXTRACTION AND QUANTITATION EXP-23-AM4435 (Apr. 3, 2023) (Exhibit 122); Kathryn Roche, Electropherogram SS23-03294-5A (Apr. 10, 2023) (Exhibit 112).

[6] During the evidentiary hearing, the prosecution asked Ms. Cale, "Are you aware that the case circumstances here indicate the complainant stated that Mr. Porter fired 10 rounds at him and his vehicle…" Transcript Vol. I at 175 (No. 111). The prosecutor followed up by asking, "[m]y question is, is that activity sufficient for Mr. Porter to leave his DNA on Item 1?" The prosecutor went on to ask another hypothetical, "I guess my question is, if I grip a 9-millimeter pistol, and I hold it in my hand, and I fire it for as long as it takes for me to fire 10 rounds, is it possible that my DNA is going to be on that pistol?" Transcript Vol. I at 176-77. The Court listened carefully to the presentation of evidence from both sides and reviewed the nine-page brief filed by the State after the hearing to determine what relevance the State believed this forensic evidence could assist in proving. The only reference to the relevance of this evidence in their nine-page brief was to assert that "[t]he scientific evidence here provides clarity and high probative value." Therefore, the Court must assume the relevance of this evidence to this case from the questions asked by counsel. Namely, this evidence is relevant to establish that Mr. Porter's DNA was left on the gun when Mr. Porter shot a firearm ten times at a vehicle.

[7] Transcript Vol. I at 9; Curriculum Vitae of Cynthia Cale, p. 1 (Exhibit 101).

[8] Transcript Vol. I at 9; Curriculum Vitae of Cynthia Cale, p. 1 (Exhibit 101).

[9] Curriculum Vitae of Cynthia Cale, p. 1 (Exhibit 101).

[10] Curriculum Vitae of Cynthia Cale, pp. 1-2 (Exhibit 101).

[11] Curriculum Vitae of Cynthia Cale, p. 2 (Exhibit 101).

She has published peer-reviewed research in the area of DNA transfer and has presented extensively over the past ten years.[12]

Ms. Cale reviewed the reports pertaining to Items 1 and 2, the BCA case file and underlying data from both items, relevant BCA standard operating procedures ("SOPs"), validation studies and a variety of other quality assurance documents.[13] In addition to her written report, Ms. Cale evaluated the BCA's internal validations studies of STRmix V2.7 using a compliance checklist she generated from Scientific Working Group DNA Analysis Methods ("SWGDAM") guidelines for Validation of Probabilistic Genotyping Systems as well as American National Standards Institute ("ANSI") / Academy Standards Board ("ASB") Standard 018 – Standard for Validation of Probabilistic Genotyping Systems.[14] Based on her examination of these materials, Ms. Cale raised concerns about whether the internal validation studies done by the BCA to validate STRmix were sufficient to support the analysis of the DNA profiled from Item 1.[15] She also raised concerns that the testing used less than the target amounts of DNA and analysis did not take into consideration case facts such as allele sharing by parents and siblings. Considering Ms. Cale's education and experience, her comparison report, her detailed review of pertinent documents provided by the BCA, and the Court's observations of her while testifying, this Court finds Ms. Cale's testimony credible.

In response to the concerns raised by the defense, the State called Dr. Marlijn Hoogendoorn. Dr. Hoogendoorn has been the technical leader for nuclear DNA casework and database testing in the biology section of the BCA laboratory since 2012.[16] She is responsible

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[12] Curriculum Vitae of Cynthia Cale, pp. 3-6 (Exhibit 101).
[13] Cynthia Cale, Forensic Biology/DNA Consultation Summary, p. 1 (Aug. 30, 2023) (providing a complete list of documents reviewed) (Exhibit 102).
[14] DNA Mavens LLC, Internal Validation of Probabilistic Genotyping Systems Compliance Checklist (Exhibit 103).
[15] Details of Ms. Cale's conclusions can be found in her report (Exhibit 102) on page 5, and throughout her testimony.
[16] Transcript Vol. I at 183.

for the technical operations of the DNA section's quality assurance requirements, including training, validation, corrective action, equipment review, and establishment of procedures.[17] Dr. Hoogendoorn has a Master of Science in Biology from the University of Leiden in the Netherlands and a Doctorate in Entomology from the University of Minnesota.[18] Dr. Hoogendoorn is "affiliated" with AAFS and ISFG.[19] She has several peer-reviewed published studies from the early 2000s which appear to be related to her experience in entomology. She has also presented on DNA and STRmix to law enforcement and prosecutors' offices in Minnesota as recently as 2023.[20]

Dr. Hoogendoorn testified that the BCA is an accredited laboratory. She worked on the internal validation of STRmix at the BCA and helped develop the BCA's SOPs for the use of STRmix. She confirmed that STRmix is validated for use on mixtures with five or fewer contributors. She did not do the testing or analysis in this case but reviewed the data and report of the analyst, Ms. Roche. From that data, Dr. Hoogendoorn's opinion is that Ms. Roche is qualified to do the analysis and did so correctly. The Court finds that much of what Dr. Hoogendoorn testified about is credible; however, some of the testimony she offered, although not incorrect, was misleading.

To address the issues raised pertaining to the admissibility of the DNA evidence offered by the State, a separate analysis of each item is required. Given the technical nature of these issues, some background regarding forensic laboratory accreditation, laboratory quality assurance, and forensic DNA testing and analysis is necessary.

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[17] Curriculum Vitae of Dr. Marlijn Hoogendoorn, p. 1 (Exhibit 1); Transcript Vol. I at 184, *see also*, QUALITY ASSURANCE STANDARDS FOR FORENSIC DNA TESTING LABORATORIES pp. 14-16 Standard 5.2 (to take effect July 1, 2020) [hereinafter FBI QAS] (setting forth education and training requirements, as well as the technical lead authority and minimum responsibilities in the forensic laboratory.) (Exhibit 104).
[18] Curriculum Vitae of Dr. Marlijn Hoogendoorn, p. 1 (Exhibit 1); Transcript Vol. I at 184.
[19] Curriculum Vitae of Dr. Marlijn Hoogendoorn, p. 3 (Exhibit 1); Transcript Vol. I at 185.
[20] Curriculum Vitae of Dr. Marlijn Hoogendoorn, (Exhibit 1).

DNA FORENSIC TESTING AND ANALYSIS

A. DNA MIXTURE ANALYSIS GENERALLY.

Forensic DNA testing and analysis have changed dramatically over the past few decades, and the use of forensic DNA technology has brought about "immense benefits to society."[21] This has included the ability to generate DNA profiles from smaller quantities of genetic material and attempts to interpret the results. When nuclear DNA testing first began, large stains of genetic material that could be seen with the naked eye, such as from blood and saliva, were required to generate a DNA profile.[22] Now, the amount of genetic material needed is no longer necessarily visible. In some instances, a profile can be generated from a few cells.[23] The greater sensitivity for detecting DNA and the expansion of the range of sample types submitted for DNA testing has led to more complexity in sample interpretation.[24] To assist in explaining the significance of genetic information, new technology has been developed to perform this interpretive work and provide statistical modeling to aide in understanding the value of the interpretation.[25]

To do this work, forensic laboratories, like the BCA, follow quality assurance measures, which include accreditation, validation studies, and SOPs. These all have a role in making sure that the individual testing done by the laboratory meets minimum requirements to assure repeatable, reproducible, accurate results and that the laboratory understands and

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[21] Butler, et al., DNA MIXTURE INTERPRETATION: A NIST SCIENTIFIC FOUNDATION REVIEW-DRAFT REPORT, p. 1, Executive Summary [hereinafter NIST REPORT] (Exhibit 107).
[22] NIST REPORT, pp. 10-11 ("When forensic DNA analysis was first introduced in the mid-1980s . . . a stain about the size of a quarter was needed to generate a DNA profile.") (Exhibit 107); *see also* NIST REPORT, p. 1, Executive Summary (Exhibit 107).
[23] NIST REPORT, p. 10 ("Today, analysts can extract a DNA profile from the few skin cells that someone might leave behind when handling an object.") (Exhibit 107).
[24] NIST REPORT, p. 30 ("Ambiguity in DNA mixture interpretation arises when [, among other factors,] small quantities of DNA are tested that, when copied, may not fully represent the original sample (i.e., the recovered DNA profile is incomplete and missing information) . . .") (Exhibit 107).
[25] NIST REPORT, p. 39 (Exhibit 107).

conducts their testing within the capability of the instrumentation being used.[26] None, however, are a substitute for admissibility.[27]

As discussed in further detail below, quality assurance measures, minimum requirements, and understanding the limitations of the testing assist in making sure that instruments and systems are working properly. In some ways, they are like standards and regulations in restaurants, which are designed to ensure rules are being followed to keep consumers safe from foodborne illness. However, these standards and regulations have nothing to do with the quality of the meal served to the customer. Both a fast-food burger joint and a high-end steak house follow health and safety rules but produce wildly different hamburgers. Quality assurance measures, minimum requirements, and understanding the limitations of testing are helpful to the legal question of admissibility, but they are only a part of the analysis.

B. ACCREDITATION, VALIDATION, STUDIES, AND STANDARD OPERATING PROCEDURES IN FORENSIC DNA TESTING AND INTERPRETATION.

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[26] *See* AAFS Standards Board, ANSI/ASB STANDARD 020 STANDARD FOR VALIDATION STUDIES OF DNA MIXTURES, AND DEVELOPMENT AND VERIFICATION OF A LABORATORY'S MIXTURE INTERPRETATION PROTOCOL, Annex B, p. 5 (ANSI/ASB 1st ed. 2018) [hereinafter ANSI/ASB STANDARD 020] ("Repeated testing and data analysis are critical to the understanding of variability. While specific requirements for the minimum number of studies and sample sets used for the validation studies and the verification process are not detailed in this standard, the laboratory shall perform sufficient replicate studies to address the variability inherent to the various aspects of DNA testing, data generation and the analysis and interpretation of the data.") (Exhibit 138); AAFS Standards Board, ANSI/ASB STANDARD 040 STANDARD FOR FORENSIC DNA INTERPRETATION AND COMPARISON PROTOCOLS, Annex B p. 5, (ANSI/ASB 1st ed. 2019) [hereinafter ANSI/ASB STANDARD 040] ("Having an adequately detailed protocol tightly connected to internal validation studies that addresses the expected variables of DNA data ensures more consistent and reliable interpretation, comparison, and reporting by all members of the laboratory.") (Exhibit 139); FBI QAS, p. 26, Standard 9.1.1 ("The laboratory shall have and follow a standard operating procedure for each analytical method used by the laboratory including the appropriate analytical controls required for DNA analysis and data interpretation.") (Exhibit 104).

[27] *See e.g.*, President's Council of Advisors on Science and Technology, Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature Comparison Methods, p. 142 (Sept. 2016) [hereinafter PCAST Report] ("The admissibility of expert testimony depends on a threshold test of whether it meets certain legal standards for evidentiary reliability, which are exclusively the province of the judiciary. Yet, in cases involving scientific evidence, these legal standards are to be 'based upon scientific validity.'") (citation omitted) (Exhibit 130).

Accreditation is recognition by an organization that the laboratory meets or exceeds standards required by that organization to perform certain functions.[28] The BCA DNA section is accredited to meet the standards set by ANSI American National Accreditation Board ("ANAB") as well as the FBI Director's Quality Assurance Standards ("FBI QAS").[29] FBI QAS standards cover definitions, laboratory organizational management, personnel requirements, training, evidence control, validation, laboratory documentation, and corrective action procedures, among other quality assurance requirements.[30] These requirements are audited by ANAB to make sure the laboratory is in compliance with FBI QAS and other standards.[31] The accrediting organization's audit process does not ensure the reliability of each test, the appropriateness of any given standard operating procedure or the vigorousness of validation testing done within the laboratory, nor the interpretation conclusions based on validation studies. Instead, it looks to see if the laboratory followed the minimum standards.[32]

In addition to accreditation and FBI QAS standards, other standards have been developed for use in forensic DNA testing and analysis. The Academy Standards Board develops ANSI-accredited standards for forensic DNA,[33] which are on the Organization of Scientific Area Committees for Forensic Science ("OSAC") registry.[34] These documents serve

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[28] FBI QAS, p. 1 (Exhibit 104).
[29] *See generally* Cynthia Cale, Forensic Biology/DNA Consultation Summary, p. 1 (Aug. 30, 2023) (providing a complete list of documents reviewed) (Exhibit 102); FBI QAS, p. 1 (Exhibit 104).
[30] FBI QAS, p. 1 (Exhibit 104).
[31] Transcript Vol. I at 40.
[32] Testimony by Lynn Garcia on Raising the Progress and Future Needs in Forensic Science, United States House of Representatives Committee on Science, Space & Technology (Sept. 10, 2019) [hereinafter Lynn Garcia House Testimony] (Exhibit 140); *see* Transcript Vol. I at 49.
[33] AAFS Standards Board, ANSI/ASB STANDARD 018 STANDARD FOR VALIDATION OF PROBABILISTIC GENOTYPING SYSTEMS p. 1 (ANSI/ASB 1st ed. 2020) [hereinafter ANSI ASB STANDARD 018] (Exhibit 106).
[34] During testimony, Ms. Cale and Dr. Hoogendoorn referenced "OSAC standards," which publish standards for validation testing. Looking at the referenced materials, OSAC has a registry or repository for "selected published and proposed standards for forensic science," some of which are from ANSI/ASB. All ANSI/ASB standards are published, see: https://www.nist.gov/osac/registry?k=DNA

as a guide to understand what a laboratory should be doing in areas of laboratory management, internal validation studies, training, and testing procedures.

Validation studies function to assess the suitability of a method for its intended use.[35] They can assist in gauging optimal ranges at which a particular system will perform and test the limitations of the method or software.[36] Internal validation studies rely on recommendations from SWGDAM and ANSI/ASB standards as well as other recommendations from scientific literature to discern the limitations of the instrumentation, procedures, and interpretations within a specific laboratory.

The laboratory then applies the results to develop its SOPs, used by individual analysts when performing testing and generating reports. They are, in their simplest terms, like a recipe that gives the analyst the steps to follow.

C. GENERATING A DNA PROFILE.

In the context of forensic testing, a DNA profile "is the genetic constitution of an individual at one or more defined locations (also known as loci) in the DNA."[37] "A DNA type [or DNA profile] derived from nuclear DNA typically consists of one or two alleles at several loci."[38] An allele is "a version of a gene."[39] To obtain a DNA profile, a DNA sample must be extracted; the extracted DNA is then quantified, amplified, and then interpreted.[40]

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[35] *See generally* FBI QAS, p. 22, Standard 8 (Exhibit 104).
[36] Transcript Vol. I at 35.
[37] FBI QAS, p. 4 (Exhibit 104); *see also* NIST REPORT, p. x (defining a DNA profile as "a string of values (numbers or letters) compiled from the results of DNA testing at one or more genetic markers (loci); can be single-source or a mixture from multiple contributors.") (Exhibit 107).
[38] FBI QAS, p. 4 (Exhibit 104); NIST REPORT, p. x (defining locus or loci (plural) as "a unique physical location of a gene (or a specific sequence of DNA in the case of STRs) on a chromosome.") (Exhibit 107).
[39] Transcript Vol. II at 211 (No. 112); *see also* NIST REPORT, p. ix (defining an allele as "one of two or more versions of a genetic sequence; humans typically inherit one allele from each parent; however, sometimes three alleles, called tri-allelic patterns, are seen in STR analysis of a single-source DNA sample; genetic sequence at a particular location (a locus) in the genome alleles targeted in STR analysis can vary by sequence in addition to length.") (Exhibit 107).
[40] *See* Transcript Vol. II at 211-17 (explaining at a high level the overarching process of obtaining a DNA profile).

Interpretation is first done on the DNA profile generated from the evidence sample. The analyst will consider what type of profile it is, for example, a single source profile or a mixture, and within a mixture, if there is a "major component" where it appears the majority of the DNA is coming from one or two people.[41] For all mixtures, the analyst must assess the number of contributors. They take into account the number of alleles at different loci, as well as peak height ratios and artifacts that might be a byproduct of the amplification process, like stutter.[42] Once the evidence profile is interpreted, it can be compared to a known DNA profile. Once interpretation is complete, a statistical value may be applied to the result.

D. PROCESS USED AT THE BCA.

When processing DNA evidence, the BCA follows its standard operating procedures. These procedures are used to extract DNA from the item in question and measure the amount of DNA collected.[43] These measurements are done in picograms, which is a trillionth of a gram.[44]

The DNA is then amplified, meaning copies are made.[45] Once the DNA has been amplified and processed, a visual depiction known as an electropherogram[46] is reviewed by an analyst in the interpretation process. An electropherogram has peaks at each locus that

[41] Transcript Vol. II at 214.
[42] Transcript Vol. II at 214-17.
[43] Transcript Vol. II at 213.
[44] NIST REPORT, p. xi (defining picogram or "pg" as "trillionth of a gram (10^{-12} g); there are ≈6 pg of DNA in a single diploid human cell.") (Exhibit 107).
[45] Transcript Vol. II at 213; *see* NIST REPORT, p. ix (defining amplification as "an increase in the number of copies of a specific DNA fragment; in forensic DNA testing laboratories, this refers to the use of the PCR technique to produce many more copies of DNA alleles at specific genetic loci.") (Exhibit 107).
[46] Transcript Vol. II at 213-14; *see* NIST REPORT, p. ix (defining capillary electrophoresis or "CE" as "an electrophoretic technique for separating DNA or other molecules by their size or charge based on migration through a narrow glass tube filled with a liquid polymer.") (Exhibit 107).

correspond with an allele.[47] The number of peaks, as well as the size and shape of these peaks, are used to inform the analyst about the DNA profile found in the item they are testing.[48]

The analyst reviews the DNA profile to determine if it is a single-source profile (i.e., DNA from one individual) or a mixture (i.e., DNA from more than one individual).[49] This involves a number of variables, including considering the number of peaks at each locus, looking at the morphology of the profile, and comparing the size of the peaks for particular alleles to determine if they are within a certain percentage of each other by peak height.[50] The analyst also looks at the peak heights to determine if there are any major or minor contributors.[51] If the analyst can identify "major" or "minor" types in a mixture, this means the genotypes of one contributor can be distinguished from the others and analyzed separately from the mixture, usually as a single source profile. Some mixtures are complex, and a major or minor contributor cannot be identified. These are called "indistinguishable" mixtures.[52]

At this stage of the analysis, the analyst must determine the number of contributors in a mixture.[53] The analyst will look at, among other things, the number of alleles at different

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[47] NIST REPORT, p. x (defining EPG or electropherogram as "a graphic representation of the separation of molecules by electrophoresis in which data appear as 'peaks' along a line.") (Exhibit 107).
[48] NIST REPORT, pp. 25-26 (Exhibit 107).
[49] Transcript Vol. II at 214-15.
[50] NIST REPORT, pp. 25-26 (Exhibit 107).
[51] Transcript Vol. II at 214-15, 219.
[52] Minnesota Bureau of Criminal Apprehension, FSS-P-BI-0708, INTERPRETATION GUIDELINES FOR STR ANALYSIS OF CASEWORK SAMPLES AMPLIFIED WITH GLOBALFILER USING STRMIX p. 6, section III.H. (Nov. 10, 2022) [hereinafter BCA INTERPRETATION SOP] ("Indistinguishable Mixtures: A DNA mixture is said to be indistinguishable when the major or minor contributors cannot be distinguished because of similarity in signal intensities") (Exhibit 110); *see* NIST REPORT, pp. 21, 172 ("If the crime profile is a major/minor mixture, where minor alleles are the same size (height or area) as stutters of major alleles, then stutters and minor alleles are indistinguishable.") (Exhibit 107).
[53] For an evidence sample, the number of contributors is never known. Marlijn Hoogendoorn, et al., MINNESOTA BCA FSSL INTERNAL VALIDATION OF STRMIX V2.7 AND PERFORMANCE CHECK OF STRMIX V2.8 p. 39 (Minnesota Bureau of Criminal Apprehension Forensic Science Laboratory January 2020) (Exhibit 109).

loci to evaluate the number of contributors.[54] They again look at the overall profile and use the factors in their SOPs to determine if what they are seeing is genetic material or a product of the process used such as, "non-allelic peaks/artifacts," "stutter," "degradation," "inhibition," "preferential amplification," "number of contributors," and "concentration of template DNA."[55]

Depending on the analyst's estimate of the number of contributors, the analyst may be able to rely on a computer program called STRmix to "deconvolute" the mixture and assist in understanding how a known sample may relate to the question sample. STRmix was subjected to developmental validation by the manufacturer prior to receipt by the BCA and internal validation for use in casework at the BCA.[56] The BCA began using STRmix for casework in early 2022 on a limited scale. All analysts were trained by early 2023.[57]

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[54] Transcript Vol. II at 215-16; BCA INTERPRETATION SOP, p. 4, section III.D. (Exhibit 110).
[55] BCA INTERPRETATION SOP, p. 2-5, sections III.A.-F. (Exhibit 110); *see also* Transcript Vol. II at 218-19; NIST REPORT, p. ix (defining artifact as "any non-allelic product of the amplification process (e.g., a stutter product), an anomaly of the detection process, such as spectral pull-up, or a dye blob, which is by-product of primer synthesis, that may be observed in an electropherogram; may complicate interpretation of a DNA profile when they cannot be distinguished from actual allele(s) data.") (Exhibit 107).
[56] Transcript Vol. I at 200; FBI QAS, p. 12 (defining validation as "a process by which a method is evaluated to determine its efficacy and reliability for forensic casework analysis and includes the following: 1) Developmental validation, which is the acquisition of test data and determination of conditions and limitations of a new or novel DNA method for use on forensic samples. 2) Internal validation, which is an accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory.") (Exhibit 104); ANSI ASB STANDARD 018, p. 1 (defining developmental validation as "The accumulation of test data to demonstrate that established parameters, software settings, formulae, algorithms and mathematical functions perform as expected. Developmental validation should also demonstrate any known limitations of the system. Developmental validation may be conducted outside the laboratory planning to use it (i.e., by the manufacturer, developer, or other testing laboratory) and will precede any internal validations.") (Exhibit 106); ANSI ASB STANDARD 018, p. 2 (defining internal validation as "[t]he acquisition of test data within the laboratory to verify the functionality of the system, the accuracy of statistical parameters, the appropriateness of analytical and statistical parameters, and the determination of limitations of the system.") (Exhibit 106).
[57] Transcript Vol. I at 201-02, 231.

According to the BCA's SOPs, if there are more than five contributors, the analyst cannot use STRmix.[58] If there are five or less contributors, then STRmix may be used. The analyst must tell STRmix how many contributors are in the mixture to perform the analysis. The BCA uses a manual approach for counting the number of contributors, meaning the analyst is responsible for looking at the profile and determining the number of contributors.[59]

STRmix is a commercially available software program that leverages computing power to assist in the analysis of mixtures.[60] This kind of analysis is called probabilistic genotyping. It has been adopted by the BCA and is widely used to generate likelihood ratios for understanding mixtures.[61] Likelihood ratios have been the preferred method versus combined probability of inclusion ("CPI") or combined probability of exclusion ("CPE") of mixture analysis for many years and were, in recent years, adopted by the BCA with the use of STRmix.[62] Mr. Porter does not challenge the use of or admissibility of probabilistic genotyping or STRmix generally.

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[58] BCA INTERPRETATION SOP, p. 6, section IV.A. (Exhibit 110); *see* FBI QAS, p. 27, Standard 9.6 ("The laboratory shall have and follow written guidelines for the interpretation of data that are based on and supported by internal validation studies.") (Exhibit 104).
[59] Transcript Vol. II at 216-17.
[60] *See* Transcript Vol. I at 19; Transcript Vol. II at 215.
[61] *See* Transcript Vol. II at 232-33; ANSI/ASB STANDARD 018, p. 3, section 3.7 (defining probabilistic genotyping as "[t]he use of biological modeling (i.e., statistical modeling informed by biological data), statistical theory, computer algorithms, and/or probability distributions to infer genotypes and/or calculate likelihood ratios.") (Exhibit 106).
[62] NIST REPORT, pp. 32-36 (Exhibit 107); Scientific Working Group on DNA Analysis Methods ("SWGDAM"), GUIDELINES FOR THE VALIDATION OF PROBABILISTIC GENOTYPING SYSTEMS, p. 3 (June 15, 2025) [hereinafter SWGDAM GUIDELINES] ("The use of a likelihood ratio as a reporting statistic for probabilistic genotyping differs substantially from binary statistics such as the combined probability of exclusion.") (Exhibit 105); PCAST Report, p. 76 ("Initial approaches to the interpretation of complex mixtures relied on subjective judgment by examiners, together with the use of simplified statistical methods such as the 'Combined Probability of Inclusion' (CPI). These approaches are problematic because subjective choices made by examiners, such as about which alleles to include in the calculation, can dramatically alter the result and lead to inaccurate answers.") (Exhibit 130).

STRmix ascertains the possible genotype sets that could be the source of the mixture.[63] In other words, STRmix puts the alleles together in all the possible combinations and considers how different combinations might explain the information in the sample. To accomplish this, the analyst tells the computer the number of contributors and adds the raw data into STRmix to obtain the results of deconvolution.[64]

The BCA can then compare evidence profiles with profiles from a person of interest. ("POI")[65] The result of this comparison is expressed in a likelihood ratio. A likelihood ratio ("LR") is a statistic, based on the ratio between two conditional probabilities that are mutually exclusive.[66] Typically, the first hypothesis includes the person of interest POI and unknown individuals equaling the total remaining estimated number of contributors.[67] The second hypothesis is typically a set of unknown individuals equal to the total estimated number of contributors.[68] An LR of zero means that the POI can be excluded as a contributor.[69] An LR of one means that the evidence supports both hypotheses equally.[70] An LR greater than one means more support for the first hypothesis; an LR less than one but

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[63] Transcript Vol. II at 221; *see* NIST REPORT, p. x (defining deconvolution as "separation of component DNA genotypes of contributors to a mixed DNA profile based on quantitative peak height information and any underlying assumptions (e.g., the number of contributors to the mixture, mixture ratios, or known contributors).") (Exhibit 107). The fact that a genotype set "could" be in a mixture does not mean that this set is actually in the mixture, only that is one of multiple combinations that could be part of the mixture.

[64] Transcript Vol. II at 221, 227-28; FBI QAS, p. 3 (defining casework reference samples as "biological material (e.g., buccal swab, finger prick, or blood draw) obtained directly from a known individual and used for purposes of comparison to forensic samples.") (Exhibit 104).

[65] Transcript Vol. II at 214.

[66] Transcript Vol. I at 16; Transcript Vol. II at 228-29; NIST REPORT, p. x (defining likelihood ratio or "LR" as "the probability of the evidence under one proposition divided by the probability of the evidence under an alternative, mutually exclusive proposition; the magnitude of its value is commonly used to express a strength of the evidence based on the propositions proposed.") (Exhibit 107).

[67] Transcript Vol. I at 17; Transcript Vol. II at 229.

[68] Transcript Vol. I at 17-18; Transcript Vol. II at 229. The BCA uses unknown, unrelated individuals as their default hypothesis.

[69] Transcript Vol. I at 16-17.

[70] Transcript Vol. I at 17.

greater than zero means more support for the second hypothesis.[71] LR is not a frequency calculation or an explanation of the likelihood of one proposition over the other (i.e., a transposed conditional).[72] The BCA uses a verbal scale from SWGDAM's recommendations to explain the support or lack of support for the first hypothesis compared to the second hypothesis.[73]

If the BCA is made aware of other facts in a case, such as the possibility of relatives as possible contributors, they can seek a known sample from that other individual or individuals and factor that information into the interpretation of the mixture due to allele sharing between relatives.[74] This additional sample is known as a "conditioning profile."[75] With this additional information, the first hypothesis is altered to the POI, one known individual, and unknown individuals equaling the total remaining estimated number of contributors.[76] The second hypothesis is changed to one known individual and unknown individuals equal to the total estimated number of contributors.[77] Even without a known sample, the possible presence of a relative can be factored into the subsequent LR.

LEGAL ANALYSIS

Items 1 and 2 present different legal issues. Therefore, each will be addressed in turn.

I. ADMISSIBILITY OF ITEM 1.

When it comes to scientific evidence, Minnesota Rule of Evidence 702 requires the proponent to show "that the testimony passes a four-part test: (1) [t]he witness must qualify

[71] Transcript Vol. I at 17.
[72] Transcript Vol. I at 149-50.
[73] Transcript Vol. II at 229-30.
[74] Transcript Vol. II at 237-38.
[75] Transcript Vol. I at 54-55, 118.
[76] Transcript Vol. I at 117; Transcript Vol. II at 229.
[77] Transcript Vol. I at 117-18; Transcript Vol. II at 229. The BCA uses unknown, unrelated individuals as their default hypothesis.

as an expert; (2) the expert's opinion must have foundational reliability; (3) the expert testimony must be helpful to the trier of fact; and (4) if the testimony involves a novel scientific theory, it must satisfy the *Frye-Mack* standard."[78]

The DNA profile from Item 1 is a complex mixture. As it pertains to this Item, Mr. Porter's challenge primarily focuses on parts one and two of this test. First, he asserts that Ms. Roche is not qualified to interpret this complex mixture. Second, he argues her opinion that the DNA profile from Item 1 is a mixture of DNA from five people and lacks foundational reliability. Therefore, STRmix should not have been used to interpret this profile. Additionally, he argues that even if the profile was appropriate for interpretation, the propositions used by Ms. Roche to calculate a likelihood ratio do not adequately reflect the case-specific facts, and therefore, the LR being offered is misleading and unhelpful to the trier of fact.

To counter these arguments and establish admissibility, the State relies on the fact that the BCA is accredited and followed procedures, and any other questions about the validity of the testing go to weight and not admissibility. As this Court noted above, accreditation alone does not equate to admissibility, nor does an assertion that standard operating procedures were followed. Accreditation and the use of SOPs assist in this analysis, but they do not alone meet the State's burden. Each factor found in Minn. R. Evid. 702 must be considered.

As a preliminary matter, the State did not call Ms. Roche to testify or offer evidence about her qualifications as an expert other than Dr. Hoogendoorn's assertion that Ms. Roche received proper training to do the analysis and did the work correctly. Without more, there is insufficient evidence to determine Ms. Roche's qualifications to interpret this complex

[78] *Doe v. Archdiocese of St. Paul*, 817 N.W.2d 150, 164 (Minn. 2012) (citing *States v. Obeta*, 796 N.W.2d 282, 289 (Minn. 2011)).

mixture. The State has not met its burden of establishing that Ms. Roche qualifies as an expert. This alone could be sufficient to preclude admission. However, because the second factor, namely the foundational reliability of the analysis, is not satisfactory in supporting the admissibility of this sample, the first factor alone is not the entire basis for this Court's decision.

As for the objections raised by Mr. Porter regarding potential prejudice from testimony on the likelihood ratio based on the proposition, which includes only unrelated individuals, this issue will not be addressed in depth. The report provided by the BCA includes a qualifying statement, "[t]he propositions used to determine the likelihood ratio(s) that were/was calculated for this report were from the information available at that time. Should any additional information become available, it may be necessary to reconsider other propositions."[79] Since the BCA acknowledges the limitation of their conclusion, either party could run the data with different propositions or point out those propositions during direct and/or cross-examination, this issue goes to weight, not admissibility, and will not be analyzed further.

A. The Conclusion That the DNA Profile From Item 1 Is Suitable For Analysis Lacks Foundational Reliability.

Testing, analysis, and interpretation used in each individual case must have "foundational reliability."[80] "Reliability is particularly important in a criminal proceeding because a suspect may face the loss of liberty due to a DNA identification."[81] The State correctly points out the Minnesota Supreme Court has stated, "specific DNA tests results are only as reliable and accurate as the testing procedures used by the particular laboratory."[82]

[79] Kathryn Roche, Report on the Examination of Physical Evidence Lab No. S23-03294, Report No. 3 (Apr. 24, 2023) (Exhibit 117).
[80] *State v. Roman Nose*, 649 N.W.2d 815, 818 (Minn. 2000).
[81] *State v. Schwartz*, 447 N.W.422, 426 (Minn. 1989).
[82] *Schwartz*, 447 N.W.2d at 426.

This is as true today as it was in 1989 when the Minnesota Supreme Court decided *Schwartz*. This is why it is crucial to ensure that the laboratory is following SOPs supported by their validation studies. This was highlighted in *Schwartz,* which specifically referenced the Technical Working Group on DNA Analysis Methods (TWGDAM), the predecessor to SWGDAM. This organization makes guidelines upon which the BCA now relies. It is the alleged failure of the BCA to establish that in this case, as it pertains to the five-person mixture analysis done on the DNA profile from Item 1, the appropriate procedures were followed, and limitations were recognized to assure the accuracy and reproducibility of the result.

In assessing the foundational reliability of the expert's opinion, the Court is guided by three considerations: (1) "the purpose for which [the testimony] is being offered;" (2) "the underlying reliability, consistency, and accuracy of the subject about which the expert is testifying;" and (3) the reliability of the evidence in the specific case.[83]

Mr. Porter argues that Ms. Roche's opinion on the number of contributors to the profile from Item 1 lacks foundational reliability because (1) the method used by the BCA cannot reliably, consistently, or accurately determine the number of contributors given the complexity of the mixture; and (2) the State has failed to show that Ms. Roche correctly applied the BCA's methods given the limited notes and that she was not called to testify. The State argues that because Mr. Porter was a major contributor, underestimating the number of contributors would have a minimal effect. Furthermore, the State contends that the analysis by Ms. Roche was reaffirmed during the technical review process, the administrative review process, and Dr. Hoogendoorn's review. The Court will take each issue in turn.

[83] *Doe*, 817 N.W.2d at 167 (citing *Jacobson v. $55,900 in U.S. Currency*, 728 N.W.2d 510, 529 (Minn. 2007)).

1. *Research Studies Addressing the Challenges of Accurately Identifying the Number of Contributors to Complex Mixtures.*

Before turning to Ms. Roche's opinion that the profile from Item 1 is from five people, it is helpful to consider the challenges those in the forensic DNA community have faced in trying to estimate the number of contributors in a mixture and how these studies inform the challenges faced by the BCA.

Studies have shown that the more complex a mixture is, the more difficult it is to interpret including determining how many individuals contributed to the mixture.[84] For example, in a study where laboratories used their own SOPs to review three-, four-, five-, and six-person mixtures, the study revealed that no laboratory accurately interpreted a six-person mixture; 69% of laboratories believed it was a four-person mixture, 28% of laboratories believed it was a five-person mixture, and 3% of laboratories believed it was a three-person mixture.[85] This led the study's authors to conclude, "[o]ur findings show that as mixture complexity increases, the ability of an analyst to designate the known number of contributor is reduced."[86] In another study using GlobalFiler, where only total alleles were considered and peak height information and drop-out were ignored, the study found that six-person mixtures were underestimated as five-person mixtures with the following major U.S. subpopulations and at the following frequency: African American: 93.84%; Caucasian: 85.99%; Hispanic: 90.74%; and Asian: 92.78%.[87] As the authors noted in the second study,

[84] *See* NIST REPORT, p. 4 ("DNA mixtures vary in complexity, and the more complex the sample, the greater the uncertainty surrounding interpretation.") (Exhibit 107).
[85] Bright, et al., *Internal validation of STRmix – A multi laboratory response to PCAST*, 34 Forens. Sci. Int'l: Genetics 11, 21 (2018) [hereinafter *Bright study*] (Exhibit 115).
[86] *Bright study*, p. 22 (Exhibit 115).
[87] Coble, et al., *Uncertainty in the number of contributors in the proposed new CODIS set*, 19 Forens. Sci. Int'l: Genetics 207, 208-10, Tables 2-5 (2015) [hereinafter *Coble study*] (Exhibit 114).

"[t]he probability of a higher order mixture appearing as having originated from one fewer individuals is high."[88]

A third study asked 134 participants from 67 different laboratories, as part of a larger study called *DNAmix 2021*, to evaluate DNA mixtures using their SOPs and determine if the mixture was suitable for interpretation and, if so, the number of contributors.[89] In evaluating two five-person mixtures and one six-person mixture, a supermajority of the laboratories indicated that the mixtures were not suitable for comparison or statistical analysis.[90] The authors also found that "[f]or the five- and six-person mixtures in this study, we conclude that assessing [an estimated number of contributors] precisely is not a reasonable expectation."[91]

The scientific literature on five- and six-person mixtures reveals three points: (1) six-person mixtures are frequently misinterpreted as four- or five-person mixtures;[92] (2) a supermajority of laboratories indicated that in five- or six-person mixtures, they were not suitable for comparison or statistical analysis;[93] and (3) for five- and six-person mixtures, assessing the number of contributors precisely "is not a reasonable expectation."[94]

Dr. Hoogendoorn, as well as the authors of the second study, note the limitations of using only total alleles and not considering peak heights, which the authors of the study expected would lower the statistics noted above.[95] However when taken in conjunction with the scientific literature on the difficulties in assessing the number of contributors in complex

[88] *Coble study*, p. 209 (Exhibit 114).
[89] Hicklin, et al., *Variation in assessment of suitability and number of contributors for DNA mixtures*, 65 Forens. Sci. Int'l: Genetics 102892, at *1 (2023) [hereinafter *DNAmix 21*] (Exhibit 113).
[90] *DNAmix 21*, pp. *6-7 (Exhibit 113).
[91] *DNAmix 21*, p. *13 (Exhibit 113).
[92] *Coble study*, Tables 2-5 (Exhibit 114); *Bright study*, p. 21 (Exhibit 115).
[93] *DNAmix 21*, p. *6 (Exhibit 113).
[94] *DNAmix 21*, p. *13 (Exhibit 113).
[95] Transcript Vol. II at 254.

mixtures, it does not significantly reduce the concern these high probabilities present as to the ability of laboratories to accurately estimate five-person or more mixtures. Dr. Hoogendoorn and the authors do not suggest that the statistics would drop precipitously from 85%-93% based solely on accounting for other factors such as peak heights; rather, they suggest some reduction of those percentages but do not provide how much. When determining the "underlying reliability, consistency, and accuracy of the subject about which the expert is testifying," these exceedingly high statistics raise serious concerns about the practical ability of BCA analysts to assess the correct number of contributors.

A second limitation of these studies is that they do not provide the SOPs that each laboratory used and how those procedures compare to the BCA's SOPs. While there is some merit to that critique, the State has not provided evidence that the BCA's SOPs are somehow unique or novel in a way that would allay the concerns raised by the studies. Furthermore, there is evidence in some of the studies to suggest that the laboratories in the study and the BCA use similar approaches and techniques in determining the number of contributors. In the *DNAmix 2021* study, 83/86 laboratories manually assessed the number of contributors, with 81/86 using maximum allele count per locus, 80/86 using "relative peak heights (peak height ratios and possible shared/stacked alleles)," 79/86 using "peak heights (RFU)," and 69/86 using expected stutter ratios, among many other factors.[96]

Dr. Hoogendoorn explained, "The whole purpose of the testing is that we do test unknown items of evidence, and then using procedures, validation studies, both developmental validation and our internal validation and published articles, we try as best we can to interpret that profile based on the information that we do have from known samples

[96] *DNAmix 21*, p. *5 (Exhibit 113); *see* BCA INTERPRETATION SOP, p. 4, section III.D. (providing that BCA analysts should consider factors like maximum alleles, peak heights, and the possibility of stacking alleles, among others, when interpreting mixtures) (Exhibit 110).

that were tested in the process of validation."[97] It is these tools that drive whether the number of contributors can be reliably, consistently, or accurately assessed. Yet, in studies where ground truth is known and analysts try their best to reliably, consistently, and accurately determine the number of contributors, the accuracy of determining the correct number of contributors is alarmingly low regardless of the standard procedures utilized. This does not mean that the BCA can never do so, but before doing so, they must establish that the method for doing so, in this case, is foundationally reliable.

2. *The Method Used by BCA Cannot Reliably, Consistently, or Accurately Determine the Number of Contributors, Given the Complexity of the DNA Mixture generated from Item 1.*

Ms. Roche is offering her opinion that the DNA profile from Item 1 is a mixture of DNA from five people, which makes it suitable for interpretation using STRmix.[98] The parties agree that the BCA has not validated STRmix to interpret mixtures with more than five contributors. Therefore, if a BCA analyst can reliably, consistently, and accurately estimate the number of contributors at five people in a mixture as complex as the profile from Item 1, results can be interpreted; if they cannot, then the BCA should not have interpreted this mixture.

The BCA's SOPs and guidelines for analysts state the following:

> "***The number of contributors to a mixed sample can generally be determined based on peak height ratios across the profile and on the locus that exhibits the greatest number of alleles at the MDT.*** For example, based on the number of alleles, a mixture with at most five alleles detected per locus is consistent with coming from at least three individuals. If a mixture includes a locus with 4 alleles that based on the PHR[99] cannot be explained by two heterozygous contributors, this would also indicate that the mixture contains DNA from at least three contributors. ***For more complex mixtures it may not be possible to use PHR to aid in the determination of the minimum number of contributors.*** For profiles with a major mixture

[97] *See* Transcript Vol. II at 310.
[98] *Doe*, 817 N.W.2d at 167-68 (citing *Jacobson*, 728 N.W.2d at 529) (requiring consideration of the purpose for which the testimony is being offered).
[99] "Peak Height Ratio."

> component within the overall mixture, the total number of contributors may be derived from the number of assumed contributors in the major mixture plus the minimum number of minor contributors." (emphasis added).[100]

It also states,

> When evaluating the profile for STRmix deconvolutions and LR calculations, the profile should be evaluated for the possibility of both allelic peaks masked by stutter and also stutter peaks above the stutter filter thresholds. This is especially important when determining the number of contributors to a mixture."[101]

"Peaks in stutter positions detected just above the stutter filter cut-off may be either stutter or a minor contributor, and both possibilities must be considered when determining the assumed number of contributors to a mixture."[102]

> "The more contributors that are present in a mixture, the more difficult it may be to distinguish a major contributor due to allele sharing. ***Also, with the increasing complexity of the mixture, the minimum number of contributors, as determined by the greatest number of alleles at a locus, is more likely to underestimate the actual number of contributors due to allele sharing***. The potential for stacking must be taken into consideration when considering the number of contributors in a DNA mixture."[103]

The SOPs acknowledge that the more complex a mixture is, the greater the danger of incorrectly identifying the number of contributors. This statement is supported by several peer-reviewed published studies discussed above, which also raise doubts about the accuracy, reliability, and consistency of laboratories to interpret five- and six-person mixtures.

"Deciding whether a DNA mixture is suitable for comparison and statistical analysis requires expert judgment coupled with defined policies and validated procedures set by the laboratory."[104] Multiple studies suggest that for complex mixtures of five or six contributors: (1) laboratories and analysts are determining by significant margins that they are unfit for

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[100] BCA INTERPRETATION SOP, p. 4, section III.D.2 (Exhibit 110).
[101] BCA INTERPRETATION SOP, p. 4, section III.D.1. (Exhibit 110).
[102] BCA INTERPRETATION SOP, p. 4, section III.D.3. (Exhibit 110).
[103] BCA INTERPRETATION SOP, p. 5, section III.F.4. (emphasis added) (Exhibit 110).
[104] *DNAmix 21*, p. *2 (Exhibit 113).

statistical analysis, undercutting the reliability of testing and analysis that are done; (2) analysts are underestimating the number of contributors, leading to inaccuracies; and (3) analysts are not uniform in their agreement as to the number of contributors leading to inconsistencies across laboratories.

Dr. Hoogendoorn testified at length about how, in her opinion, the laboratory studies that have been done are deficient and do not reflect the BCA's ability to accurately discern when the number of contributors in a complex mixture is five versus six people. She does not explain how the SOPs, other than a warning to the analysts, protect against incorrectly determining the number of contributors to a mixture as complex as that found in Item 1.

Dr. Hoogendoorn also relies on the validation studies conducted at the BCA to support the analysis of this complex mixture and, by implication, resolve the challenges seen in research. How the validation studies were designed and whether they supported the interpretation of the mixture in this case was also an issue of contention.

3. *The Role of Validation Studies in Supporting the Use of the BCA's Method for Assessing the Number of Contributors.*

Validation studies can assist in gauging optimal ranges at which a particular system will perform and test the limitations of the method or software.[105] They are also used to develop laboratory SOPs. Mr. Porter raises concerns regarding the robustness of the BCA's validation studies. He argues that the BCA did not use samples similar to those seen in casework in its validation studies. Therefore, the validation studies do not support assigning the number of contributors as five to the complex mixture developed from Item 1.

The BCA's accrediting body, ANAB, evaluates the BCA according to their standards and requirements every four years.[106] ANAB also conducts a biannual audit of the BCA's

[105] Transcript Vol. I at 35.
[106] Transcript Vol. I at 187-88.

DNA laboratory to comport with the FBI QAS.[107] The biology section has a section-specific supplemental quality assurance manual that comports with both the ANAB requirements and those set forth in the FBI QAS.[108] Additionally, the BCA's DNA section also follows the International Standards Organization ("ISO") standards and SWGDAM's practice guidelines.[109] The BCA also maintains laboratory wide and section-specific SOPs.[110] As part of these accreditation requirements, the BCA has had two external quality assurance standard audits since they began using STRmix.[111] The first audit, among other things, reviewed the validation of STRmix to ensure it complied with the requirements of the FBI QAS.[112] The second audit reviewed procedures and a sampling of casework where STRmix was used, which may have included five-person mixtures.[113] The BCA's validation of STRmix met the requirements of the FBI QAS.[114] While accreditation and audits serve important roles, these systems set a minimum baseline for quality assurance of the BCA's processes and methods. Accreditation and audits provide some information in establishing a particular

[107] Transcript Vol. I at 187-88; *see* FBI QAS, p. 37, Standard 15.1 & Standard 15.2 ("The laboratory shall be audited annually in accordance with these standards . . . At least once every two years, an external audit shall be conducted by one or more auditor(s) from a second agency(ies).") (Exhibit 104).
[108] Transcript Vol. I at 190-91
[109] Transcript Vol. I at 195-96, 199.
[110] Transcript Vol. I at 191.
[111] Transcript Vol. II at 241.
[112] Transcript Vol. II at 241-42.
[113] Transcript Vol. II at 242. When Dr. Hoogendoorn was asked, "When it comes to casework, were complex mixtures of five contributors' part of that audit process? Her response was, "[y]eah, we typically just provide – we are typically just asked to provide a random sampling of cases from – usually we're asked to provide at least five cases per caseworking scientist to the audit team, so those case are pulled by – usually they call it the assurance group, and then when the auditors are on-site and when they have a chance to review that paperwork, if they feel they haven't had a representative sample of casework, they can ask for additional cases to review…" Dr. Hoogendoorn's response starts with what appears to be her knowledge of what was actually provided, but her explanation only describes the general process. Given her response, the Court is not convinced that Dr. Hoogendoorn has any personal knowledge about whether, in this second audit, the auditor was provided five-person mixtures.
[114] Transcript Vol. II at 243.

validation was done but do not establish that the internal validation and the methods developed or testing in an individual case developed from them are reliable.

Validation provides the laboratory with an understanding of the bounds of the testing that can be performed. It demonstrates limitations on the instruments or testing so a user can be sure not to test beyond those limitations. While accreditation and audits serve important roles, these systems set a minimum baseline for quality assurance of the BCA's processes and methods. Accreditation and audits are necessary for establishing a particular test or process that is reliable but are not themselves sufficient to do so.

FBI QAS, ANSI/ASB Standards, SWGDAM Guidelines, and scientific literature all say that "[m]ixture interpretation validation studies shall include samples with a range of number of contributors, template amounts, and mixture ratios expected to be encountered in casework."[115] Ms. Cale pointed out that the BCA's validation studies did not include samples with multiple people of interest as co-contributors to a sample; did not test the system's ability to model extreme stutter; failed to include a broad range of template amounts of DNA; did not explore the complexity of allele sharing particularly with close relatives; and had too few low template amounts of DNA, all of which come from SWGDAM guidelines. Because of these deficiencies, she believes the BCA has not sufficiently tested the limitations of STRmix to reliably deconvolute complex mixtures.[116] Although there may be some merit to these

[115] FBI QAS, p. 22, STANDARD 8.2.1 (Exhibit 104); ANSI/ASB STANDARD 018, p. 3, section 4.1.6 ("For internal validation, the laboratory shall evaluate both the appropriate sample types (i.e., number of contributors, mixture ratios, and template quantities) and the number of samples within each type to demonstrate the potential limitations and reliability of the software. The laboratory shall base this evaluation on the intended application of the software.") (Exhibit 106); ANSI/ASB STANDARD 020, p. 1, section 1.1 ("This standard includes a requirement that the laboratory verify and document that the mixture interpretation protocols developed from the completed validation studies generate reliable and consistent interpretations and conclusions for the types of mixed DNA samples typically encountered by the laboratory.") (Exhibit 138).

[116] Cynthia Cale, Forensic Biology/DNA Consultation Summary, p. 5 (Aug. 30, 2023) (providing a complete list of documents reviewed) (Exhibit 102).

criticisms, this Court is only being asked to determine whether the BCA was capable of deconvoluting the DNA mixture from Item 1, not whether their validation studies are robust enough for them to engage in the deconvolution of all complex mixtures. Therefore, only those issues raised that are relevant to Item 1 will be considered.

To establish that the DNA mixture developed from Item 1 can be called a five-person mixture such that it can be evaluated using STRmix, the BCA must establish that their validation studies were done using the kinds of mixtures found in the casework. Ms. Cale made several observations about the BCA's Internal validation of STRmix v2.8 ("MN BCA FSSL") to support Mr. Porter's argument that the validation studies are not sufficient to support the method used to deconvolute DNA mixture from Item 1.[117] The BCA did not include related individuals, six-person mixtures, or multiple persons of interest as co-contributors in its validation study. Mr. Porter argues these situations must be tested to determine what profiles are suitable for interpretation using STRmix and the effect of allele sharing in those specific situations.[118]

i. The Absence of Related Individuals in the BCA's Validation Studies.

Ms. Cale pointed out that including closely related individuals in validation studies assists in addressing "that extreme scenario" where there will be "extensive allele sharing between contributors."[119] This would have allowed the BCA to assess the limitations of these scenarios to determine "what profiles are going to be suitable for interpretation using STRmix.[120] This, as she explained, would also allow the BCA to account for allele sharing in

[117] Cynthia Cale, Forensic Biology/DNA Consultation Summary, p. 5 (Aug. 30, 2023) (providing a complete list of documents reviewed) (Exhibit 102).
[118] Transcript Vol. I at, 62, 69.
[119] Transcript Vol. I at 62.
[120] Transcript Vol. I at 62.

these situations. She pointed to National Institute of Standards and Technology ("NIST") as well as the ERS[121] that recommend doing validation studies with related individuals.[122]

As to this concern, Dr. Hoogendoorn testified that there is no consensus in the field on the necessity of using related individuals in validation studies.[123] Dr. Hoogendoorn further stated that she believes that relatives are not used in validation studies because allele sharing between relatives is predictable by simple genetics, and so one knows what amount of sharing one expects to see based on the relationship.[124] Without more, Mr. Porter has not shown that the failure to include related individuals in the BCA's validation studies significantly impacted the method used by the BCA in mixture deconvolution. However, given the fact that Item 1 comes from an apartment where it is very likely that the sample could include close relatives, this leads to some concern about how the method was used in Ms. Roche's interpretation of this mixture.[125]

Part of this concern is, as Ms. Cale pointed out, about the role of validation studies. She testified that if the limitations of the software are not adequately tested, "you're kind of

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[121] "ESR" is the Institute of Environmental Research and Science Research based in New Zealand. It is the developer of STRmix. Transcript Vol. I, 65; *see also* Coble, et al., *DNA Commission of the International Society of Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications*, 25 Forens. Sci. Int'l: Genetics 191, 191 (2016) (Exhibit 141).

[122] Transcript Vol. I at 62.

[123] Transcript Vol. II at 312.

[124] Transcript Vol. II at 272, 313.

[125] Although this Court concludes that there is insufficient evidence to establish the need for related individuals to be used in the BCA's validation studies, it is worth noting a particular concern regarding Dr. Hoogendoorn's testimony. When defending the BCA validation study design and opining about the reason relatives were not used in validation studies, she pointed out that one of the developers of STRmix, Dr. John Buckleton, supported her assertion that using samples from relatives in validation studies was not useful. Transcript Vol. II at 319. She asserted he may have expressed these opinions on a DNA forum she follows. Transcript Vol. II at 319. However, Dr. Buckleton is a signatory on the ISFG Recommendations, which include using relative samples in their validation studies. *See* Lynn Garcia House Testimony (Exhibit 140). It may be that Dr. Buckleton has revised his opinion since this publication or that Dr. Hoogendoorn was referring to specific situations when these do not need to be used. This was not explained. Without further explanation, her assertion is misleading.

doing a disservice for your analyst because they're not going to understand at what point that software is not going to perform appropriately."[126] She explained that failing to properly test for complexity due to allele sharing can impact the SOPs because they will not include information on how to deal with mixtures that may involve individuals who are closely related.[127] As noted above, the only direction given in the SOP is that, "the minimum number of contributors, as determined by the greatest number of alleles at a locus, is more likely to underestimate the actual number of contributors due to allele sharing. The potential for stacking must be taken into consideration when considering the number of contributors in a DNA mixture."[128]

ii. The Absence of Multiple Persons of Interest as Possible Co-Contributors in the BCA's Validation Studies.

Another criticism raised about the BCA's validation studies was that the BCA did not include multiple persons of interest as co-contributors in its validation study. Therefore, the BCA does not have sufficient information to know how this impacts mixture deconvolution when used in this manner. This appears to be a general criticism of the sufficiency of the validation studies. Although this may impact situations that involve co-contributors, Mr. Porter has not shown that the lack of testing in the BCA's validation studies on multiple persons of interest as co-contributors has specific relevance to the testing done in this case.

iii. The Absence of Six-Person Mixtures in the BCA's Validation Studies.

Mr. Porter further argues that the BCA's methods to interpret the profile from Item 1 cannot be reliable because the BCA did not include six-person mixtures in its validation studies. The BCA ran samples during its validation studies, including single-source samples

[126] Transcript Vol. I at 36.
[127] Transcript Vol. I at 69-70.
[128] BCA INTERPRETATION SOP, p. 5, section III.F.4. (emphasis added) (Exhibit 110).

as well as two-, three-, four-, and five-person mixtures.[129] It did not include any six-person mixtures.[130] Including known six-person mixtures in their validation study is part of an approach called "bracketing."[131] This means that you include known samples with DNA from six-people and then interpret those as five-person mixtures.[132] This helps the lab test the limits of their method. As Ms. Cale pointed out, this is recommended by SWGDAM.[133] Yet, six-person mixtures run as five-person mixtures were not part of the equation. Mr. Porter argues that the BCA has not assessed the impact of underestimating the number of contributors in a mixture that is misinterpreted as a five-person mixture. He also points out that there are recommendations in the scientific literature to engage in a bracketing approach of testing bounds above five-person mixtures to include six-person mixtures to understand extremes and suitability of interpreting profiles.[134] Mr. Porter has not provided sufficient information to establish that six-person mixtures must be part of the BCA's validation study for the BCA to test what it believes is five-person mixtures. However, it does suggest that there is limited information to fully understand the complexity of the DNA mixture from Item 1.

Additionally, in the BCA's validation studies, the secondary diagnostics indicated that "[a]ll of the five-person mixtures and two of the four-person mixtures were better explained as originating from N-1 contributors," or one less than the actual number of contributors.[135]

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[129] Transcript Vol. II at 235.
[130] Transcript Vol. II at 276, 284. Earlier in her testimony, Dr. Hoogendoorn stated, "When we were doing our internal validation of STRmix, I tried to do deconvolution on some six-person mixtures, but it wouldn't complete because it runs out of memory." Although Dr. Hoogendoorn may have attempted analysis of some six-person mixtures, it is unclear in what context.
[131] Transcript Vol. I at 71.
[132] Transcript Vol. I at 71.
[133] Transcript Vol. I at 72; *see also* SWGDAM GUIDELINES, p. 9, section 4.1.6.4 (Exhibit 105).
[134] Transcript Vol. I at 71-72.
[135] Marlijn Hoogendoorn, et al., MINNESOTA BCA FSSL INTERNAL VALIDATION OF STRMIX V2.7 AND PERFORMANCE CHECK OF STRMIX V2.8 p. 44 (Minnesota Bureau of Criminal Apprehension Forensic Science Laboratory January 2020) (Exhibit 109); Transcript Vol. II at 284.

Given that this is the case, it also seems logical that a six-person mixture could be better explained as originating from N-1 contributors, meaning it too could look like five people. Why this is not the case was not explained.

iv. The Absence of Mixtures as Complex as the Current Mixture Derived from Item 1 in the BCA's Validation Studies.

Mr. Porter's last challenge is that the BCA did not run samples in its validation studies as complex as the profile from Item 1. The BCA's validation study included three different five-person mixtures with some allele sharing at every locus in each mixture. The maximum allele count in those studies was either eight or nine alleles, while the profile from Item 1 presents a single locus with ten different alleles. The profile from Item 1 differs from any of the five-person mixtures within the BCA's validation study and is more complex than what was tested in the study.

Validation studies set the bounds for reliable and accurate testing. Yet the mixture from Item 1 has factors such as a higher number of alleles that have not been adequately tested by the BCA for consistency and reliability. The mixture from Item 1 is a more complex mixture than any of the five-person mixtures tested by the BCA. This could be due to the lack of six-person mixtures in the validation studies design or potential allele sharing among related individuals, as noted above. This appears to be an unanswered question. No matter the reason, the BCA's validation studies do not reflect a single mixture with this number of alleles at one locus, nor do they explore how that might occur. As for the method developed from the validation studies, as noted, the SOP has little guidance other than to use extreme caution with complex mixtures. The State has not provided sufficient evidence to support a finding that the BCA's testing methods for determining the number of contributors as it pertains to a mixture with this level of complexity are consistent, accurate, and reliable.

To some degree, the State and Dr. Hoogendoorn seem to concede the difficulty in accurately determining the number of contributors to this evidentiary sample. When faced with this challenge, the State argues that Mr. Porter was a major contributor to the mixture and, as a result, underestimating the number of contributors would have a minimal effect on the analysis and ultimate likelihood ratio generated for the analysis of the mixture from Item 1.[136] Specifically, the State suggests that underestimating the number of contributors may lead to false exclusion of low-level contributors but typically would not affect higher level contributors.[137] Therefore, they conclude that the likelihood ratio for a major contributor if the number of contributors is underestimated would be very similar to the likelihood ratio if the number of contributors were accurately estimated.[138] Again, as noted above, the issue is not whether under-inclusion modifies the likelihood ratio in a way that produces a less favorable LR for Mr. Porter; it is whether the BCA was able to perform this analysis at all.

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[136] The State mischaracterizes the mixture generated from Item 1. This mixture is indistinguishable. Ms. Roche did not identify a major profile or a major mixture component as part of her analysis. *See* BCA INTERPRETATION SOP, p. 4, section III.G. (Exhibit 110). No "major contributor" was identified. However, this mischaracterization comes directly from Dr. Hoogendoorn's testimony when she attempted to support her position that the number of contributors was called correctly. Dr. Hoogendoorn testified that Mr. Porter's contribution to this mixture was that of a "higher level contributor." Transcript Vol. II at 261. She pointed to a feature of STRmix called an "interpretation report." Transcript Vol. II at 263, *see also* S232394 DNA Packet (Exhibit 5). This report gives a summary of contributors and attempts to quantify the percentage of DNA that would have come from genotypes considered in the probabilistic modeling. *See* Transcript Vol. II at 261, 263-66, 330-31. She explained that according to STRmix, contributor one provided 58.31% of the genetic material, and the second contributor provided 28.90%. *Id.* She used this to support her independent assessment of the electropherogram, which was that "the majority of the DNA in this mixture is from two or three individuals, then there is additional minor contributors present." Transcript Vol. II at 246, 263-66. She was careful not to call it a "major profile" or "major mixture" component. Still, she testified in a way that was misleading, at least to the prosecution, about what this number represented. This led to the assumption by the State that Mr. Porter contributed over 50% of the DNA found in Item 1.

[137] Transcript Vol. II at 252-53; 260-61. This Court also discounts any assertion that an error in calculating the number of contributors, if calculated at six versus five contributors, has only a minimal effect on the analysis. The effect is that the sample would not have been suitable for analysis. *See* Transcript Vol. II at 276 ("We did not validate six-person mixtures, and we don't interpret six-person mixtures.").

[138] Transcript Vol. II at 253.

Without further validation of the BCA's methods, which reflect the level of complexity found in the mixture from Item 1, the State has failed to show the foundational reliability of the expert's opinion regarding the number of contributors.

B. Even if the BCA's Method is Reliable, the State Has Failed to Show Ms. Roche Reliably Applied the Method.

Mr. Porter argues that even if the BCA's method of determining a five-person mixture is reliable, Ms. Roche did not properly apply the method; therefore, the third element of the foundational reliability test is not met.

Ms. Roche did not testify. In Ms. Roche's interpretation notes for Item 1, she noted the DNA profile was a "mix of 5" with "high stutter" and "ELP [Exavier Lloyd Porter] not exc [excluded]."[139] The notes do not provide information on how Ms. Roche interpreted the data, whether or how she considered peak height ratios, whether or how she accounted for allele stacking or sharing, where she believed the high stutter occurred on the electropherogram or her approach to concluding that it is a five-person mixture.

Dr. Hoogendoorn stated that from her review of Ms. Roche's work, "it appears that [Ms. Roche] followed all of our procedures correctly" and that she used the BCA's SOPs when estimating the number of contributors.[140] Dr. Hoogendoorn also expressed confidence that Ms. Roche followed procedures because she was trained to use peak height ratios, numbers of alleles, and other factors in determining the number of contributors.[141] Dr. Hoogendoorn further stated that she was not concerned that Ms. Roche may have been underestimating the number of contributors from Item 1's DNA profile. The only testimony offered by Dr.

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[139] Kathryn Roche, DNA SUMMARY AND INTERPRETATION NOTES S23-03294 (Apr. 17, 2023) (Exhibit 123).
[140] Transcript Vol. II at 244, 279.
[141] Transcript Vol. II at 329-30. The State did not offer a CV for Ms. Roche or any other information about her training. All that was offered was a general overview by Dr. Hoogendoorn as to the kind of training analysts at the BCA receive.

Hoogendoorn, which was specifically related to Ms. Roche's interpretation, is that there could be stutter present in the mixture, which Ms. Roche may have used to assist her in concluding this was a mixture of only five people.[142] Whether that was how Ms. Roche reached her conclusion is unknown.

Instead of explaining how Ms. Roche arrived at her opinion, Dr. Hoogendoorn offered her own assessment of the profile to bolster Ms. Roche's decision to call this profile a mixture of five individuals. She explained that it appeared that the mixture was consistent with five individuals, but the majority of the DNA is from two or three individuals, and then additional minor contributors.[143] Dr. Hoogendoorn also believed that the profile was consistent with Mr. Porter being one of the higher-level contributors.[144] Dr. Hoogendoorn noted that beyond the two loci where nine or ten alleles were present, all others had no more than six alleles present.[145] As noted, there is no evidence that Ms. Roche relied on the same factors as Dr. Hoogendoorn to reach her conclusion. Dr. Hoogendoorn lands on the same number, but it does not explain how Ms. Roche arrived at her conclusion.

"[I]n determining the foundational reliability of a laboratory's DNA testing methodology . . ., this Court looks at 'whether the laboratory conducting the tests in the individual case complied with appropriate standards and controls.'"[146] Based on the interpretation notes and expert report, the Court cannot conclude that Ms. Roche properly

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[142] Transcript Vol. II at 246.
[143] Transcript Vol. II at 245-46. The BCA's SOP says that if there is a profile with a "major mixture," it must be documented. Ms. Roche did not document any such observation, and it is unclear if what Dr. Hoogendoorn was referencing in her own assessment would require such documentation.
[144] Transcript Vol. II at 261.
[145] Transcript Vol. II at 245.
[146] *State v. Traylor*, 656 N.W.2d 885, 893-94 (Minn. 2003) (citing *Roman Nose*, 649 N.W.2d at 820). Though *Traylor* was decided prior to the modification of Minn. R. Evid. 702 in 2006, the foundational reliability standard of the *Frye-Mack* test addressed in *Traylor* was explicitly added to Minn. R. Evid. 702 in 2006. Therefore, *Traylor*'s discussion of foundational reliability is pertinent to the issues in this case.

and reliably applied the BCA's methods for determining numbers of contributors given the lack of information within the record. While the Court has Ms. Roche's conclusion that it is a mixture of five contributors that involved high stutter, the evidence presented does not show how that determination of high stutter impacted Ms. Roche's assessment of the number of contributors or if Ms. Roche considered peak height ratios or other considerations raised in the BCA's SOPs.[147]

While Dr. Hoogendoorn may independently agree with Ms. Roche's interpretation and find support in the electropherograms and STRmix data for a determination of five contributors with two or three majors and the remainder of minor contributors, that does not provide the Court information as to Ms. Roche's actual analysis. This Court is asked to extrapolate the reliability of Ms. Roche's opinion by accepting Dr. Hoogendoorn's testimony, which does not explain how Roche arrived at her opinion.[148] Without more, the State has not shown that Ms. Roche reliably applied the BCA's methods in determining the number of contributors in the mixture developed from Item 1.

The broader problem is the SOPs do not give a lot of guidance about what factors to consider or how those should be looked at when one is looking at a sample as complex as that derived from Item 1. As Ms. Cale points out, the DNA from Item 1 is just barely over 500 pg. Yet there is no explanation about why the BCA's SOP recommendation to "increase the DNA input per contributor because the number of contributors is more likely to be underestimated" was not followed...[149] The DNA profile from Item 1 has more alleles at one locus than is seen

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[147] *See* FBI QAS, p. 31, STANDARD 11.1 ("The laboratory shall retain, in written, printed, or electronic format, sufficient documentation for each technical analysis to support the report conclusions such that another qualified individual can evaluate what was done and interpret the data.") (Exhibit 104).
[148] Transcript Vol. II at 261.
[149] BCA INTERPRETATION SOP, p. 5, section III.F.5. (Recommended minimum input is 100pg per contributor, and for complex mixtures, it is advisable to increase the DNA input per contributor because the number of contributors is more likely to be underestimated) (Exhibit 110).

in any of the validation studies. The BCA's SOPs state, "With increasing complexity of the mixture, the minimum number of contributors, as determined by the greatest number of alleles at a locus, is more likely to underestimate the actual number of contributors due to allele sharing."[150] This sample also came from an apartment where allele sharing among relatives is quite likely. This, too, supports overestimating the number of contributors.[151] The guidance provided by the BCA's SOPs, the validation studies, and peer-reviewed research is that there is a significant risk of underestimating the number of contributors. The State has failed to provide sufficient evidence to explain why this profile was determined to be a five-person mix and ally these concerns.

II. THE PROBATIVE VALUE OF THE RESULTS FROM TESTING ON ITEM 2 IS SUBSTANTIALLY OUTWEIGHED BY THE DANGER OF UNFAIR PREJUDICE.

Although Mr. Porter puts forth several arguments for precluding this evidence, there is no need to reach all the issues raised. The issues that are the most persuasive and dispositive are how the sample size and statistical analysis impact the balance between the probative value and any unfair prejudice.[152]

"'Relevant evidence' means evidence having any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence."[153] Here, the fact that can be established from the results of DNA analysis on Item 2 is that there may be some of Mr. Porter's DNA present on the magazine of a firearm. Thus, for purposes of establishing the source of DNA found on the magazine, this evidence is relevant.

[150] BCA INTERPRETATION SOP, p. 5, section III.F.4. (Exhibit 110).
[151] BCA INTERPRETATION SOP, p. 5, section III.F.4. (Exhibit 110).
[152] Minn. R. Evid. 403.
[153] Minn. R. Evid. 401.

Evidence is inadmissible, however, when the "probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury . . ."[154] "The term 'prejudice' in Rule 403 'does not mean the damage to the opponent's case that results from the legitimate probative force of the evidence; rather, it refers to the unfair advantage that results from the capacity of the evidence to persuade by illegitimate means.'"[155] "Expert testimony can be both powerful and quite misleading because of the difficulty in evaluating it."[156] In reviewing evidence for its probative and prejudicial effect district courts must "exercise more control over experts than over lay witnesses."[157] This is particularly true in assessing DNA evidence and the expectations among jurors about what it can tell them.[158]

In considering the probative value, the State asserts that "[t]he conclusions of BCA Report #3 are relevant and admissible at trial . . . The scientific evidence here provides clarity and high probative value. While it is complicated, this evidence is by no means misleading." Unfortunately, the State's brief does not explain why it has high probative value. What fact of consequence the State is seeking this evidence to establish that would make it so valuable can only be gleaned from the record.

As previously noted, it appears the State believes the relevance of this evidence, and thus, its probative value is to establish that Mr. Porter shot this firearm during a drive-by

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[154] Minn. R. Evid. 403.
[155] *State v. Mosley*, 853 N.W.2d 789, 797 (Minn. 2014).
[156] *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 595 (1993).
[157] *Daubert*, 509 U.S. at 595.
[158] NIST REPORT, p. 8, section 5.2 ("When assessing evidence that involves very small quantities of DNA, it is especially important to consider relevance.") (Exhibit 107); *McDaniel v. Brown*, 558 U.S. 120, 136 (2010); *see also State v. Phillips*, 844 S.E.2d 651, 658 (S.C. 2020).

shooting. Put another way, Ms. Roche's opinion depends on her ability to demonstrate that Mr. Porter handled the firearm's magazine at or near the time of the crime. [159]

Ms. Roche's ability to do this is limited at best. The most basic understanding of the probative value of Ms. Roche's testimony is that, if believed, it can show that Mr. Porter's DNA came in contact with the firearm and magazine in some way. Ms. Roche cannot provide the fact finder any information on when or how DNA got onto the magazine or any statement regarding the likelihood of transfer beyond speculating as to infinite possibilities.

A. The Sample Size and the Role of Transfer Decreases the Evidence's Probative Value.

The profile derived from Item 2 is not a complex mixture. The amount of DNA analyzed from Item 2 was 180 picograms or approximately 26 cells.[160] This small amount, referred to as a "low-level sample,"[161] has its own unique challenges.

To understand how to balance the probative value of the results from Item 2 with the potential for unfair prejudice first requires an understanding of the uniqueness of low-level samples and the role of transfer.

As previously noted, "[t]he field of forensic DNA analysis is constantly advancing. Technology has allowed scientists to detect and analyze very small quantities of DNA. During the early decades of forensic DNA analysis, an evidence sample containing thousands of cells, such as a visible blood or semen stain, was needed to produce a DNA profile. When first introduced in the mid-1980s, the amount of DNA needed to generate a DNA profile was a

[159] When arguing about the relevance of the DNA in this case, the State does not distinguish between the DNA found on the pistol, which is Item 1, and that found on the magazine, which is Item 2. Because the Court has already determined the results from the DNA analysis of Item 1 are not admissible on other grounds, the analysis here is focusing on Item 2.
[160] Kathryn Roche, DNA EXTRACTION AND QUANTITATION EXP-23-AM4435 (Apr. 3, 2023) (Exhibit 122); Transcript Vol. II at 140-41.
[161] Kathryn Roche, DNA SUMMARY AND INTERPRETATION NOTES S23-03294 (Apr. 17, 2023) (Exhibit 123)

"stain of about the size of a quarter."[162] It was not until the late 1990s that the sensitivity of the method was sufficient to recover DNA from "touched" objects.[163] Meaning, today, analysts can extract a DNA profile from a few skin cells left behind.[164] The term "touch" DNA is associated with this kind of sample.[165] This has expanded DNA's usefulness beyond samples of bodily fluid into property crimes or, as in this case, firearms. It also creates new challenges. The persistence of DNA and its ability to move from one place to another when it is not visible to the human eye has created a multitude of new crime-solving opportunities while adding layers of complexity. When there was a visible stain from bodily fluid, where the DNA likely originated from, questions about how the DNA may have gotten on an item were not as complicated as they are today, and the danger of significant prejudicial value was lessened.

To give some perspective to how much 180 picograms are and how sensitive the analysis has become, it is also helpful to understand the number of cells in any environment that could yield DNA profiles by considering the number of cells a person sheds on any given day. "Humans shed between 2×10^8 and 10×10^8 (two hundred million to one billion) cells every day."[166] If one thinks about how many cells might be in an area such as a home when considering this number, it gives a better understanding of why there is a huge challenge in answering questions beyond the identity of the contributor to a DNA sample. All sorts of possibilities come into play when considering the significance of the presence of DNA. Here, there are about 28 cells belonging to two people. Even assuming Mr. Porter's DNA

[162] NIST REPORT, p. 11 (Exhibit 107).
[163] NIST REPORT, p. 7 (Exhibit 107).
[164] NIST REPORT, p. 10 (citations omitted) (Exhibit 107).
[165] Even the term "touch" is misleading, especially with the ability of laboratories to generate samples from only a few skin cells. The word "touch" suggests a mechanism for the DNA to reach the item tested, which is not supported by the scientific evidence presented in this case.
[166] Puliatti, et al., *The level of DNA an individual transfers to untouched items in their immediate surroundings*, 54 Forens. Sci. Int'l: Genetics 102561, at *1 (2021) [hereinafter *Puliatti study*] (Exhibit 124).

contributed the most genetic material, this is still a tiny number, which leads to a variety of concerns and considerations.

The relevance of a found DNA profile has traditionally been in how genetic and biological information is used to answer questions about the identity of the person whose DNA is found in a sample, also known as "sub-source" questions, as well as the biological material it may have come from, "source questions." [167]

In some cases, like here, the question of how the DNA got onto a surface is really the focus of the inquiry. This is where questions about transfer may come into play. "The fact that DNA can be transferred between surfaces upon contact is a foundational principle of forensic DNA analysis."[168] Transfer may, in some cases, provide very useful information. There are times when it may be appropriate to admit a sub-source proposition in a case as part of the evidence for a jury to consider in determining what led to the DNA being found in a particular place. Consider, for example, a sexual assault case where the source is semen, and the sub-source is a defendant's DNA. In those cases, the DNA is a large enough sample size that by examination, it can be seen on an object (like underwear), the cell type (sperm), and what activity (ejaculation) caused it to be deposited could be fairly easily inferred. The farther afield the analysis gets from being an amount of DNA that can be seen from a biological sample such as blood, saliva, or semen, the more challenging it is to make

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[167] NIST REPORT, pp. 134-36, section 5.4.2.5 (Exhibit 107). The NIST Report outlines the hierarchy of propositions in evidentiary evaluations. Sub-source level propositions ask whether the DNA profile found on an item of evidence is from a person of interest. Source-level propositions ask whether the DNA is from a particular biological source such as blood, semen, or skin cells. In this case, the sub-source question is whether Mr. Porter's DNA contributed to the DNA mixture. The source-level proposition would be what kind of biological material this DNA came from. This question was not explored in this case. Beyond source propositions are activity propositions that address questions of how the DNA came to be present in the sample. A possible activity level proposition here, as the State appears to suggest, is that Mr. Porter's DNA was deposited on the magazine because he transferred it during touch contact. Finally, offense-level propositions address questions of guilt or innocence. A possible offense-level proposition here is that Mr. Porter's DNA was deposited on the magazine because he transferred it during touch contact when he fired the gun at the victim.

[168] NIST REPORT, p. 7 (Exhibit 107).

connections as to the method of transfer and the more speculative the information becomes.[169] This impacts the balance of the information's probative value and the danger for unfair prejudice.

How DNA can be transferred can also create issues. "The question of relevance arises because DNA can be transferred between surfaces, potentially more than once. Because DNA can be transferred before, during, and after a crime event and transferred multiple times, "DNA found at a crime scene may be irrelevant to the crime."[170]

The ways in which DNA found at a crime scene can cause challenges and potentially mislead investigations are noted in the following principles found in literature review:

- "It is possible to handle an item without transferring any detectable DNA to it."
- "Genetic material may have been deposited before or after the crime and therefore may not be relevant to it."
- "Detected DNA might be present due to indirect (secondary or tertiary) transfer, whether by a person or an object."[171]

As noted by the authors of the NIST Report:

> The "three points apply to any low-level profile and therefore also apply to profiles containing mixtures. While the traditional view is to focus on the major contributor to a mixture based on the assumption that the profile belongs to the last person to handle the item, some studies have shown this is not always the case"[172]

In this case, Mr. Porter is identified as the source of the "predominate" profile, which lends support to his contribution of more DNA to the sample than the other contributors. However, the total amount is still only about 26 cells. This minuscule amount of DNA leads to a significant concern about the multitude of completely irrelevant reasons for the presence of the DNA. In addition to the small amount, the facts in this case are that the shooting

[169] NIST REPORT, p. 97 (Exhibit 107).
[170] NIST REPORT, p. 98 (Exhibit 107).
[171] NIST REPORT, pp. 129-30 (Exhibit 107).
[172] NIST REPORT, p. 130 (Exhibit 107).

occurred almost two weeks before this firearm was found. There are no facts that establish that this firearm, recovered almost two weeks after the shooting, was the same firearm that was used in the shooting.[173] Yet the jury would be allowed to speculate that Mr. Porter shot at the victim using this gun two weeks earlier. The NIST Report warned about the use of low-level samples, saying, "[h]ighly sensitive methods increase the likelihood of detecting irrelevant DNA. When assessing evidence that involves very small quantities of DNA, it is especially important to consider relevance."[174] Given the State's presentation of evidence and the scope of Ms. Roche's testimony, while her testimony is relevant, its probative value is minimal. Allowing her to speculate about how the DNA got there from her findings with no scientific support for any of those hypotheses is prejudicial.

B. <u>The Likelihood Ratio is Misleading.</u>

Mr. Porter raised concerns regarding the application of the appropriate likelihood ratio to DNA found on both items 1 and 2. Because this Court found Item 1 inadmissible on other grounds, the challenges with LR were not discussed, nor does this Court decide it now. However, with Item 2, the lack of alternative propositions in calculating a likelihood ratio is different and requires further analysis.

The defense's first concern, in an oversimplified version, is that because the BCA did not use case-specific facts, such as the presence of relatives at the place where the gun was collected into their likelihood ratio, the number is, at best, misleading, and at worst, incorrect. This, as previously discussed, has to do with the competing hypotheses on which a

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[173] *See State v. Smith*, 825 N.W.2d 131, 137-38 (Minn. Ct. App. 2012) (finding a district court abused its discretion in admitting a box cutter where there was no evidence that the box cutter was used in the incident); *but see State v. Daniels*, 361 N.W.2d 819, 827-28 (Minn. 1985) (concluding that a gun is admissible and relevant by being sufficiently connected to the defendant where the gun was found in a car the night of the shooting, the car was found near the scene of the crime with the three co-defendants, that witnesses identified seeing the car flee the scene, and a witness saw the defendant with a handgun at the scene).

[174] NIST REPORT, p. 8, Key Takeaway 5.2 (emphasis added) (Exhibit 107).

likelihood ratio is calculated. The literature submitted supports using alternative propositions when calculating this statistic, which was not done here.

A co-developer of STRmix, among others, has suggested that a conditioning profile should be incorporated when there is a "reasonable prior probability" that the individual's DNA is present in the mixture and their inclusion is supported by the profile."[175] Scientific literature has further emphasized that "[t]he primary motivating factor is that the use of a conditioning profile . . . greatly improves the ability to discriminate between true and false donors."[176] A study of LRs generated with or without first-order relatives further suggested there is an increased risk of heightened support for the person of interest when relatives of the person of interest are true donors to the mixture.[177] Given the small amount of DNA found, and that the conclusion is that Mr. Porter is the "predominate profile," not including in the hypothesis for the LR the possibility of relatives, there is significant and heightened concern by this Court that the statistic being presented is misleading.

Additionally, concerns raised by the scientific community about the potential for sub-source LRs to mislead or confuse the jury are present here. First, the tendency to incorrectly believe that an LR represents the probability of an assigned proposition versus a comparison of two competing propositions; second, a tendency to use sub-source LRs to draw inferences about how the DNA got to the place it was found.

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[175] Buckleton, et al., *When evaluating DNA evidence within a likelihood ratio framework, should the propositions be exhaustive?* 50 Forens. Sci. Int'l: Genetics 102406, at *1 (2021) (Exhibit 142); *see* Buckleton, et al., *Guiding proposition setting in forensic DNA interpretation*, 62 Sci. & Justice 540 (2022) (Exhibit 131); Buckleton, et al., *Helping formulate propositions in forensic DNA analysis*, 54 Sci. & Justice 258 (2014) (Exhibit 132); Gill, et al., *DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence – Guidelines highlighting the importance of propositions Part I: evaluation of DNA profiling comparisons given (sub-) source propositions*, 36 Forens. Sci. Int'l: Genetics 189 (2018) (Exhibit 133).

[176] Buckleton, et al., *Guiding proposition setting in forensic DNA interpretation*, 62 Sci. & Justice 540 (2022) (Exhibit 131).

[177] Kalafut, et al., *Investigation into the effect on mixtures comprising related people on non-donor likelihood ratios and potential practices to mitigate providing misleading opinions*, 59 Forens. Sci. Int'l: Genetics 102691 (2022) (Exhibit 127).

As it pertains to Item 2, the State seeks to offer this statement, "[t]he probability of observing this DNA profile is greater than 100 billion times more likely if a mixture from Mr. Porter and one, unknown, unrelated individual is the source than if a mixture of two unknown, unrelated individuals is the source."[178] This does not mean that either proposition is correct and more importantly, it only comments on the value of the sub-source DNA found on Item 2. It does not provide a likelihood ratio about how the DNA got onto Item 2, which is the activity level conclusion the State hopes the jury will make.[179] The fact that the BCA uses a verbal scale would mean the jury would be told that there is "very strong support" for this proposition does not lessen the concerns. The Minnesota Supreme Court has previously expressed concerns about how statistical calculations used in DNA cases could confuse the jury.[180] The *Bloom* court talked about the chain of inferences needed to get from the starting point to the conclusion that the defendant is the perpetrator.[181] It also considered concerns about a "prosecutor's fallacy," where the probability of, in that case, a "random match" is wrongly interpreted as "the probability that the defendant is the perpetrator of the crime."[182] In that case, the court determined that ultimately, the statistic was admissible.

These concerns are even greater in this case than they were in *Bloom*. The risk that the jury will misunderstand what the likelihood ratio is conveying is high. But even more importantly, the chain of inferences here, to reach the conclusion that Mr. Porter shot this particular gun during this crime, given the small amount of DNA, the length of time between

[178] Kathryn Roche, Report on the Examination of Physical Evidence Lab No. S23-03294, Report No. 3 (Apr. 24, 2023) (Exhibit 117); Kathryn Roche, DNA SUMMARY AND INTERPRETATION NOTES S23-03294 (Apr. 17, 2023) (Exhibit 123); Kathryn Roche, DNA EXTRACTION AND QUANTITATION EXP-23-AM4435 (Apr. 3, 2023) (Exhibit 122); Kathryn Roche, Electropherogram SS23-03294-5A (Apr. 10, 2023) (Exhibit 112).
[179] NIST REPORT, p. 8, Key Takeaway 5.2 (Exhibit 107).
[180] *State v. Bloom*, 516 N.W.2d 159, 162 (Minn. 1994).
[181] *Bloom*, 516 N.W.2d at 162.
[182] *Bloom*, 516 N.W.2d at 162-63.

the crime and recovery of the evidence, and the possibility for the DNA to have gotten on this gun through indirect transfer, render the relevance of this particular piece of evidence too remote to have any significant probative value.

While typically "alleged deficiencies in [an expert's] factual basis go more to the weight of the expert's opinion than to its admissibility," the ultimate conclusion by Ms. Roche is a statistic used to assist the jury in understanding whether Mr. Porter's DNA was on the firearm or not.[183] The State wants to use this evidence to establish Mr. Porter's DNA was transferred to the gun while he was shooting it. The danger, as noted, is that the jury will be confused and/or misled. The testimony will lead to unfair prejudice, given the significant assumptions required to pair the DNA on the gun with the crime. Even the State struggled to understand the meaning of the evidence when mistakenly arguing that Mr. Porter was a major contributor to the DNA profile from Item 1. DNA is complicated and can still be extremely helpful in many cases, but that is not the case here.

CONCLUSION

Forensic DNA testing and analysis is a powerful and important tool that helps our justice system solve crimes and, therefore, keeps our communities safer. The advances that have been made and continue to be made in forensic DNA analysis and interpretation play an integral role in this work. This Court appreciates how important these tools are. It is equally important that when this information is being used as evidence in a criminal case, it must meet the requirements of admissibility and relevance and not be misleading to the fact finder. This requires that the laboratory resists the temptation to go outside of the limitations of their validation studies and SOPs, that analysts take great care in not testifying in ways that are misleading to the finder of fact, and that the person offering the evidence have a

[183] *Kedrowski v Lycoming Engines*, 933 N.W.2d 45, 60 (Minn. 2019) (citing *Bohach v. Thompson*, 239 N.W.2d 764, 767 (Minn. 1976)).

clear understanding of the value of the information provided by the laboratory, how it relates to their case, and be able to assist in explaining this to the finder of fact.

Here, after careful consideration of the evidence in this case and how it relates to the Minnesota Rules of Evidence, Items 1A and 2 do not meet the requirements necessary for admissibility. This Court has given careful thought to other options, such as limiting the terminology used by the experts and counsel, not allowing testimony referring to the DNA as "touch DNA," requiring the BCA analyst to testify extensively about DNA transfer, or even offering a jury instruction as to what the DNA testimony can be considered to establish. However, none of these options adequately address the concerns raised in this case.

P.A.W.K.

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