STATE OF NEBRASKA, APPELLEE, V. CHARLES M. SIMMER, APPELLANT.

___ N.W.2d ___

Filed November 1, 2019. No. S-18-500.

1. **Expert Witnesses: Appeal and Error.** The standard for reviewing the admissibility of expert testimony is abuse of discretion.
2. **Judgments: Expert Witnesses: Words and Phrases.** An abuse of discretion in the trial court's determination under *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993), and *Schafersman v. Agland Coop*, 262 Neb. 215, 631 N.W.2d 862 (2001), occurs when a trial court's decision is based upon reasons that are untenable or unreasonable or if its action is clearly against justice or conscience, reason, and evidence.
3. **Courts: Expert Witnesses.** Under the *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993), and *Schafersman v. Agland Coop*, 262 Neb. 215, 631 N.W.2d 862 (2001), framework, the trial court acts as a gatekeeper to ensure the evidentiary relevance and reliability of an expert's opinion.
4. **Trial: Expert Witnesses: Intent.** The purpose of the gatekeeping function is to ensure that the courtroom door remains closed to "junk science" that might unduly influence the jury, while admitting reliable expert testimony that will assist the trier of fact.
5. **Trial: Expert Witnesses.** A trial court can consider several nonexclusive factors in determining the reliability of an expert's opinion: (1) whether a theory or technique can be (and has been) tested; (2) whether it has been subjected to peer review and publication; (3) whether, in respect to a particular technique, there is a high known or potential rate of error; (4) whether there are standards controlling the technique's operation; and (5) whether the theory or technique enjoys general acceptance within a relevant scientific community.
6. ____: ____. Once the reasoning or methodology of an expert opinion has been found to be reliable, the court must determine whether the

expert's reasoning or methodology can be properly applied to the facts in issue.

Appeal from the District Court for Douglas County: Thomas A. Otepka, Judge. Affirmed.

Thomas C. Riley, Douglas County Public Defender, for appellant.

Douglas J. Peterson, Attorney General, and Melissa R. Vincent for appellee.

Heavican, C.J., Miller-Lerman, Cassel, Stacy, Funke, Papik, and Freudenberg, JJ.

Papik, J.

Charles M. Simmer appeals his conviction for first degree murder. DNA evidence presented at Simmer's jury trial linked him to the crime. The sole issue presented by this appeal is whether the district court erred in admitting DNA analysis conducted by using TrueAllele probabilistic genotyping software, over Simmer's *Daubert/Schafersman* challenges. Finding no abuse of discretion, we affirm.

I. BACKGROUND

1. Overview

On November 3, 2007, Simmer's aunt, Joy Blanchard, was murdered in her home. She was discovered lying face down on the floor with two knives protruding from her neck. Close by was a spindle broken from the nearby bannister. An autopsy revealed the cause of death to be blunt force trauma and stab wounds to the head and neck.

When law enforcement processed the crime scene, they swabbed several items for DNA, including the spindle, the handles on both knives, and the interior doorknob on the front door of the residence. DNA testing and analysis conducted in 2015 and 2016 indicated the presence of Simmer's DNA on one of the knife handles and the interior doorknob.

On June 7, 2016, Simmer was charged by information in Douglas County District Court with one count of first degree murder, a Class IA felony. Prior to trial, Simmer filed a motion in limine asserting a challenge to DNA analysis performed by Cybergenetics, Inc., which challenge was pursuant to *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993), and *Schafersman v. Agland Coop*, 262 Neb. 215, 631 N.W.2d 862 (2001) (*Daubert*/*Schafersman*). He sought to preclude the State from introducing at trial "any and all testimony concerning DNA testing and the results of said testing," including "identification" and "comparison" of DNA testing. Simmer alleged that the reliability of the theories, techniques, and procedures used by the State's experts had not been established and that the proposed testimony was "based on insufficient facts and data." Hearings were held on the motion, and the district court overruled it.

At the subsequent jury trial, Simmer preserved the *Daubert*/*Schafersman* challenges raised in his pretrial motion. He lodged a continuing objection when Dr. Mark Perlin, the chief scientist and executive officer at Cybergenetics, was called to testify about TrueAllele probabilistic genotyping and its application in this case. The district court overruled the objection. The jury heard DNA evidence and other circumstantial evidence connecting Simmer to Blanchard's murder, and Simmer was convicted of the crime charged and sentenced to life imprisonment.

The sections below summarize the *Daubert*/*Schafersman* proceedings and the relevant evidence at trial.

2. *DAUBERT*/*SCHAFERSMAN* PROCEEDINGS

At pretrial proceedings on Simmer's motion in limine, the district court received exhibits and heard expert testimony about DNA evidence from three witnesses. Generally, Mellissa Helligso's testimony provided context for Perlin's testimony about Cybergenetics' TrueAllele probabilistic genotyping program. Simmer elicited testimony from Nathaniel Adams to challenge TrueAllele's methodology.

(a) Testimony of Helligso

Helligso, a forensic DNA analyst employed by the University of Nebraska Medical Center (UNMC), testified about the DNA tests that she performed in this case. Helligso explained the process by which an autosomal DNA profile is obtained and analyzed. Upon receiving evidence containing biological material, she extracts the DNA, quantifies and amplifies it, and ultimately runs it through a genetic analyzer. The genetic analyzer generates a DNA profile that can then be compared to DNA from known individuals. Typically, the analysis is limited to specific locations in the DNA and does not include a full profile. If she identifies consistencies between the evidence profile and the known individual's profile, she will "generate a statistic to show the likelihood of that match happening."

Helligso also explained the difference between autosomal DNA and Y-STR DNA. Humans have 23 pairs of chromosomes with each pair consisting of one each from the father and mother. The term "allele" describes the varying forms of a gene that can be specific to an individual but found for everyone at the same place in the same chromosome. Differences in alleles at predetermined chromosome locations, referred to as "loci," define a person's DNA profile and can be used for comparison with evidence samples.

Helligso explained that autosomal DNA is composed of DNA inherited from both parents. Y-STR DNA, on the other hand, involves only the Y chromosome, which is found only in males and is passed from father to son. Because all males in the same family have the same Y-STR DNA, it cannot identify a particular male within that family and is less discriminating than autosomal DNA. In Y-STR DNA testing, a DNA extract is amplified with a particular "kit" that only looks at the Y-STR locations found on the Y chromosome.

In this case, among the items that Helligso received in 2007 were swabs obtained from one of the knife handles and the spindle. Y-STR DNA testing of both items disclosed the presence of two Y chromosomes, indicating a mixture of two males. Simmer could not be excluded as the major male contributor in either sample, but neither could his brother, since they share the same Y chromosome. The probability of a match was stronger on the knife handle than on the spindle.

In November 2015, Helligso received several additional items for testing, including a swab from the interior doorknob on the front door to Blanchard's residence. Helligso determined the sample contained autosomal DNA from at least two individuals. Neither Blanchard nor Simmer could be excluded as full contributors on the doorknob, and "[t]he probability of a random individual matching a DNA profile within the mixture, given that . . . Simmer expresses such a profile, [was] 1 in 357 million . . . for Caucasians, 1 in 844 million . . . for African Americans, and 1 in 2.37 billion . . . for American Hispanics."

Helligso suggested sending her work to Perlin at Cybergenetics for additional analysis. To provide the background for that decision, Helligso explained the process by which a DNA profile is obtained and analyzed and the significance of data "thresholds." She stated that for any type of testing done by UNMC, the laboratory must go through a validation process:

> [O]ne of the things that you have to establish is your threshold, which is the height at which, in your laboratory, you can determine the difference between what would be considered a real peak or real allele and background noise of the instrumentation, because every instrument has background noise just by the technology in which it works. And so every laboratory, for their own instrumentation, has to determine where that cutoff lies within the data.
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> . . . In our laboratory, the threshold for autosomal, and I believe for Y-STR in this case as well, was set at 50

> [relative fluorescence units (RFU)]. So any peak that is below 50 RFU does not get labeled by the software program that we have, so then we, in general, do not look at those peaks. They can be considered if you're trying to determine if you have a mixture, but, in general, no, we don't look at those peaks then.

Helligso explained that at UNMC, none of the data below the threshold is used in her statistical calculations.

Helligso testified that Cybergenetics had developed a software program that is not bound by data thresholds. Using a series of mathematical calculations, the software analyzes every peak to determine whether it is "an artifact [or] a real allele." Helligso also testified that Perlin does not retest the evidence; rather, his software simply uses all the data compiled by the laboratory during its analysis. Helligso testified that the human brain could perform the same calculations as the software, but it would require "an extreme amount of time." She stated that it makes sense to use software that performs the necessary calculations quickly and accurately.

Helligso testified that probabilistic genotyping has "definitely been a hot topic for a couple of years now." When Helligso was asked whether there was some dispute about the general acceptance of Perlin's approach in the broader scientific community, Helligso replied, "[I]f you [had] asked me that question six or seven years ago, I would have agreed, but I would say now within the last five years that, in general, the community is — is agreeing that these types of software programs are necessary." The number of people who do not agree are "becoming fewer and fewer." She pointed out that TrueAllele addresses a need in the DNA analysis community by facilitating the use of all of the DNA data to calculate a "good statistic." Helligso noted that the accuracy of TrueAllele software had been tested over at least 10 years with thousands of known profiles with an "extremely high success rate." She also noted that a similar program, "STRmix," is "being highly touted by the FBI and the national government" and "has kind of taken off to where lots of laboratories have those."

(b) Testimony of Perlin

As noted above, Perlin is the chief scientist and executive officer at Cybergenetics, a bioinformation company. He testified about his company's software, TrueAllele, and its application in Simmer's case.

Perlin explained that TrueAllele is designed to separate the various contributors to DNA samples processed by crime laboratories and assess the likelihood that a contributor matches a known sample. Like Helligso, Perlin testified that TrueAllele's method of analysis differs from traditional DNA analysis performed by humans in that TrueAllele does not utilize thresholds, which exclude or discard data that falls below a predetermined level. Instead, it analyzes all of the data, taking into account peak heights and other patterns. According to Perlin, TrueAllele yields more accurate results, that is, it can produce a stronger "match statistic" or, alternatively, exclude an individual who may have otherwise been included.

Crime scene samples can consist of very small amounts of DNA, incomplete DNA, and DNA from more than one contributor. Using a series of complex probability equations and statistical sampling, TrueAllele tries out thousands of possible explanations, or possible genotypes, for the crime scene data, and calculates the probability of each explanation. Those that explain the data well generate higher probability, while those that explain the data not as well, or not at all, generate lower probability. This process suggests genotypes and their probabilities at every genetic location for each contributor to the crime scene sample.

Perlin testified that TrueAllele ultimately infers a genotype, or DNA barcode, for each contributor to the crime scene evidence, which is a probability distribution over possible allele pairs, and then calculates the probability that an inferred genotype matches (1) the suspect and (2) a random person in the population. The program then divides the former by the latter to generate a likelihood ratio or “match statistic.” The match statistic answers the question: “How much more does the suspect match the evidence at this location than a random person?”

Perlin explained that TrueAllele is more objective than the traditional method, because the computer analyzes the data without comparing it to a known sample from a suspect or “anybody’s preferred answer.” A suspect’s genotype is not given to the computer until it calculates the match statistic.

Perlin recounted the development of TrueAllele. Perlin, who has a bachelor’s degree in chemistry, is a doctor of medicine, and has Ph.D.’s in mathematics and computer science, began using computers to interpret genetic information in the early 1990’s while working on the Human Genome Project. At that time, he became involved in the development of software that would enable a computer to understand and eliminate artifacts in DNA data. He continued that work after founding Cybergenetics in 1994 and published his first article on the subject in 1995. Over the course of 15 years, Perlin developed TrueAllele. TrueAllele is based on “Bayesian” probability modeling and “Markov chain Monte Carlo” statistical sampling, both widely accepted in the relevant communities for decades. Perlin testified that TrueAllele uses mathematics and algorithms developed 20 years prior to trial, with the “core math of calculating genotypes [remaining] the same since 2008.”

Perlin testified that TrueAllele is widely used. He stated that he and his company have been extensively involved in educating and training laboratory analysts to use TrueAllele. Perlin testified that at least 10 laboratories around the country have used TrueAllele, 7 of them regularly, and have done their own internal validations of the software. TrueAllele had conducted analyses in at least 500 cases in 37 states, though not all of the analyses were used in court. Further, TrueAllele had been used to analyze small quantities of damaged DNA from thousands of human remains to help identify victims of the September 11, 2001, terrorist attack on the World Trade Center. Perlin also testified that TrueAllele had been used by the DNA group at the National Institute of Standards and Technology, a part of the U.S. Department of Commerce that "create[s] resources for the forensic community in the U.S. and the world that are standards." He stated that the national institute had used TrueAllele to create standards for a DNA mixture against which laboratories could check their equipment and methods.

Perlin testified that TrueAllele had been used in court proceedings. He stated that he had testified in at least 10 admissibility hearings and that no court had found his testimony to be inadmissible. The district court received nine trial court admissibility rulings from other jurisdictions in the United States allowing TrueAllele evidence, five of them applying a *Daubert* standard. Perlin testified that Cybergenetics does work for both the prosecution and the defense. He noted that TrueAllele had been used in more than 10 cases by the Innocence Project, a group that seeks to exonerate the wrongly convicted. Perlin testified that Cybergenetics screens DNA from any group at no cost and only charges for additional services, such as a written report or testimony. He also stated that TrueAllele provides the opportunity for any group to run its software for free to independently confirm results and that results could also be confirmed through competing software.

Perlin also testified concerning approval of TrueAllele by the Scientific Working Group on DNA Analysis Methods (SWGDAM). SWGDAM is composed of highly respected individuals in the DNA analysis community who author guidelines for DNA analysis that are often adopted by accrediting agencies. SWGDAM approved the use of probabilistic genotyping software in 2010, as long as it had been validated and documented. And in 2015, SWGDAM issued guidelines for validating probabilistic genotyping programs, centering on laboratory validation, sensitivity, specificity, and reproducibility.

Sensitivity reflects the extent to which interpretation identifies the correct person, specificity reflects the extent to which interpretation does not identify the wrong person, and reproducibility reflects the extent to which interpretation consistently gives the same answer to the same question. According to Perlin's testimony and documentary evidence generated by Cybergenetics, TrueAllele complies with those guidelines.

The district court received numerous validation studies of TrueAllele. Perlin described validation studies as "tests that are done where known data is put into a method, like a computer program for calculating match statistics, and the results are assessed on 10 to 100 samples, depending on the study, and its performance is measured, along with error rates." According to Perlin, 34 studies conducted by the TrueAllele laboratory and other crime laboratories and groups had shown that TrueAllele produces accurate and reliable results with "no surprises."

Perlin stated that typically in the field of science, a method like TrueAllele would be featured in only one peer-reviewed publication. However, of the 34 validation studies in evidence, 7 studies had been published in peer-reviewed journals and 6 of the 7 studies in evidence identified Perlin as a coauthor.

Perlin testified that TrueAllele's error rates had been tested multiple times in two ways, which Perlin described in detail. First, error rates had been tested through validation studies of large ensembles of "real," "less pristine" samples from casework to demonstrate how the system works in practice. And second, error rates were tested by the application of information theory to determine the expected distribution of match statistics from one evidence genotype of known composition to "provide information about a sample in a case and what the error rate would be for a particular match statistic." Of the seven peer-reviewed validation studies, four used laboratory samples of known composition and three drew from less pristine crime scene data.

In this case, Perlin used TrueAllele to analyze the data from UNMC and calculated likelihood ratios for Simmer on both the knife handle and the doorknob. According to Perlin's analysis, the match between the knife handle and Simmer was 3.71 thousand times more probable than a coincidental match to an unrelated person, while the match between the doorknob and Simmer was 4.22 quintillion times more probable than a coincidental match to an unrelated person. Perlin also calculated likelihood ratios for Simmer's brother as to both items; however, his ratios were exclusionary.

Other portions of Perlin's testimony are mentioned, as relevant, in the analysis section below.

(c) Testimony of Adams

Adams has a bachelor's degree in computer science and is employed by a company that "consult[s] with lawyers to help them understand what kind of [DNA] testing was conducted, whether there are any issues with that testing with the analysis or interpretation of the data." The company reviews "standard operating procedures, validation studies of the testing laboratories, [and] relevant literature in the forensic DNA field." Adams' duties involve the review of electronic data generated during the course of forensic DNA testing and case files from criminal investigations involving DNA testing.

Adams' testimony and written report expressed concerns about the validity of TrueAllele's probabilistic genotyping program from a software engineering perspective. Adams' primary objection to the software was that it had not been confirmed that the software does what Perlin says it does. He testified, "This is one of the major topics of verification and validation . . . in the field of software engineering. We need to demonstrate, not just assume or expect, that a program is operating as described . . . ."

Adams testified that the problem with probabilistic genotyping programs like TrueAllele is that "[t]he field of forensic DNA does not have any standards specific to it that software must adhere to before it's utilized in casework." He stated that TrueAllele encompassed computing statistics and biology and that minimum quality assurance standards required a multidisciplinary, multiparty approach. Adams' report acknowledged that the International Society of Forensic Genetics and SWGDAM had published guidance documents addressing validation of probabilistic genotyping software, but the field of forensic DNA analysis still lacked formal standards specific to its development and validation. His report observed that while there were no common software development standards for probabilistic genotyping, general software engineering industry standards and principles could be used to ensure correctness of the systems. However, this had not been done. As a result, he contended that defects may exist in the software and that their significance to its operation would persist undetected.

Adams noted that a program's source code, the programming language instructing the computer what to do, can be inspected to determine whether the software program has been appropriately constructed. However, according to Adams, the TrueAllele source code had never been independently reviewed to determine whether the program operates as described by Perlin. The district court received evidence that Cybergenetics had recently decided to allow defense experts access to the TrueAllele source code, with limitations. In Adams' view, reviewing the source code in the context of a particular case was prohibitive under the time and financial constraints of litigation, especially if certain software development materials were not involved in the review. In Adams' opinion, review of the source code ought to occur over a long period prior to use in a criminal case.

Adams acknowledged that one way to determine whether a program works as intended is to use it, but that it was not the only way under software engineering general practices for quality assurance. He considered it "dangerous to allocate our only software defect detection efforts to the actual use of that software" because of the significant impact latent defects could have. Adams testified that TrueAllele had achieved only the "illusion of validation" because it had not been validated in the domain of software engineering. And while he also acknowledged that TrueAllele had been developed over a period of several years before it was ever used in a criminal case, he stated that he still had concerns about it since he "[didn't] know what defect prevention or mitigation strategies were employed during that time."

In addition, Adams' report questioned validation studies of the quantitative likelihood ratios generated by probabilistic genotyping "because no knowable correct output exists for any given input, against which the system's behaviors could be tested." Adams explained that "we can't know exactly what likelihood ratio should be developed, even if we know the inputs to the systems, the genotypes of the true contributors."

Adams also expressed concern about the accuracy of likelihood ratios in general, even with known contributors, and stated that while he also has concerns about the accuracy of traditional DNA analysis, he prefers it to computer programs because it is more transparent and its calculations "can be replicated by anybody with a pocket calculator or an Excel spreadsheet."

(d) Motion in Limine Overruled

Following the hearing, the district court overruled Simmer's motion in limine. It found Perlin to be an expert in the field of probabilistic genotyping. The district court further found that the TrueAllele evidence was relevant and that it would be helpful to the finder of fact in this case. The district court applied the *Daubert/Schafersman* analytical framework and determined the methodology of TrueAllele probabilistic genotyping was reliable, noting that the *Daubert* test was flexible and that not every factor need be considered. We summarize the district court's ruling in detail in the analysis section below.

3. RELEVANT EVIDENCE AT TRIAL

At trial, the State presented DNA evidence connecting Simmer to the crime scene. Helligso and Perlin both gave testimony consistent with their testimony at the hearing on Simmer's motion in limine. Helligso testified that her analysis showed that neither Simmer nor his brother could be excluded as the major male contributor to DNA on the spindle and the knife handle. As for the DNA on the interior doorknob, Helligso's analysis determined that the sample contained a mixture of at least two individuals and that neither Blanchard nor Simmer could be excluded as full contributors. She stated that the probability of a random individual matching a DNA profile within the mixture on the interior doorknob, given that Simmer expresses such a profile, was 1 in 357 million. Regarding the TrueAllele analysis of the evidence in this case, Perlin testified that the match between the knife handle and Simmer was 3.71 thousand times more probable than a coincidental match to an unrelated person, while the match between the doorknob and Simmer was 4.22 quintillion times more probable than a coincidental match to an unrelated person. As he did at the hearing on Simmer's motion in limine, Perlin also described at trial how TrueAllele works.

In addition to DNA evidence, the State introduced other evidence linking Simmer to Blanchard's murder. Although there was no direct evidence that Simmer had been at Blanchard's residence on the night of the murder, from early on, he was a suspect in the police investigation. The State presented evidence at trial that Simmer had not been to Blanchard's residence during the 2½ years prior to Blanchard's murder; that Simmer had misinformed police about his whereabouts during the timeframe of Blanchard's murder; that 2 days after the murder, Simmer tried to conceal injuries to his hands from police; that he physically resisted providing a court-ordered DNA sample; and that about 3 months after the murder, he had confided in a friend about stabbing someone to death.

II. ASSIGNMENTS OF ERROR

Simmer assigns that the district court committed reversible error in rejecting his *Daubert/Schafersman* challenge and in allowing the State to present Perlin's expert opinion testimony and evidence concerning Perlin's conclusions on DNA evidence connecting Simmer to the crime scene.

III. STANDARD OF REVIEW

[1,2] The standard for reviewing the admissibility of expert testimony is abuse of discretion. *State v. Tucker*, 301 Neb. 856, 920 N.W.2d 680 (2018). An abuse of discretion in the trial court's *Daubert/Schafersman* determination occurs when a trial court's decision is based upon reasons that are untenable or unreasonable or if its action is clearly against justice or conscience, reason, and evidence. *State v. Hill*, 288 Neb. 767, 851 N.W.2d 670 (2014).

IV. ANALYSIS

Simmer's sole assignment of error challenges the admission of TrueAllele probabilistic genotyping evidence linking him to the crime scene. While Simmer's appeal focuses exclusively on the admission of this evidence, his arguments fall into two different categories within the *Daubert/Schafersman* analysis. Simmer makes a number of arguments aimed at the general reliability of TrueAllele. Other arguments focus on whether TrueAllele, even if generally reliable, was properly applied to the facts in this case. After briefly reviewing the basic governing legal principles, we will proceed to analyze Simmer's arguments in turn.

1. *DAUBERT/SCHAFERSMAN* STANDARDS

The Nebraska Evidence Rules provide: "If scientific, technical, or other specialized knowledge will assist the trier of fact to understand the evidence or to determine a fact in issue, a witness qualified as an expert by knowledge, skill, experience, training, or education, may testify thereto in the form of an opinion or otherwise." Neb. Evid. R. 702, Neb. Rev.

Stat. § 27-702 (Reissue 2016). Perlin's qualifications are not at issue in this appeal. Rather, Simmer argues that the State failed to demonstrate that the TrueAllele evidence was admissible under the *Daubert/Schafersman* framework and that the district court therefore abused its discretion in allowing it in evidence. See *State v. Casillas*, 279 Neb. 820, 782 N.W.2d 882 (2010) (burden is on proponent of evidence to establish admissibility under *Daubert/Schafersman*).

[3,4] Under the *Daubert/Schafersman* framework, the trial court acts as a gatekeeper to ensure the evidentiary relevance and reliability of an expert's opinion. *Hemsley v. Langdon*, 299 Neb. 464, 909 N.W.2d 59 (2018). The purpose of this gatekeeping function is to ensure that the courtroom door remains closed to "junk science" that might unduly influence the jury, while admitting reliable expert testimony that will assist the trier of fact. *State v. Herrera*, 289 Neb. 575, 856 N.W.2d 310 (2014). The *Daubert/Schafersman* standards require proof of the scientific validity of principles and methodology utilized by an expert in arriving at an opinion. See *Hemsley v. Langdon, supra.*

[5] A trial court can consider several nonexclusive factors in determining the reliability of an expert's opinion: (1) whether a theory or technique can be (and has been) tested; (2) whether it has been subjected to peer review and publication; (3) whether, in respect to a particular technique, there is a high known or potential rate of error; (4) whether there are standards controlling the technique's operation; and (5) whether the theory or technique enjoys general acceptance within a relevant scientific community. *State v. Braesch,* 292 Neb. 930, 874 N.W.2d 874 (2016). A trial court may consider one or more of these factors when doing so will help determine that testimony's reliability, but the test of reliability is "'flexible'" and the list of specific factors neither necessarily nor exclusively applies to all experts or in every case. See *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 141, 119 S. Ct. 1167, 143 L. Ed. 2d 238 (1999), quoting *Daubert v. Merrell Dow*

Pharmaceuticals, Inc., 509 U.S. 579, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993).

[6] Once the reasoning or methodology of an expert opinion has been found to be reliable, the trial court must determine whether the expert's reasoning or methodology can be properly applied to the facts in issue. *See State v. Edwards*, 278 Neb. 55, 767 N.W.2d 784 (2009).

2. GENERAL RELIABILITY OF TRUEALLELE EVIDENCE

Simmer contends that the State failed to show the evidence generated by TrueAllele was sufficiently reliable under the *Daubert*/*Schafersman* framework. The district court concluded otherwise. In its order denying Simmer's motion in limine, the district court first observed that TrueAllele had been tested by 34 validation studies and that it conforms to the SWGDAM guidelines for validating probabilistic genotyping systems. The district court next stated that TrueAllele had, on multiple occasions, been peer reviewed and subject to publication in an "unusually large number" of validation studies and that no significant scientific evidence suggested the reliability of TrueAllele had been refuted. Regarding TrueAllele's error rate, the district court cited evidence that it had been assessed through validation studies and information theory comparing one evidence genotype to the expected distribution of match statistics. Finally, the district court determined that TrueAllele had been generally accepted in the relevant scientific community because it had been used in over two-thirds of the states in the United States, it had been used to identify mass casualty victims of the 2001 terrorist attack on the World Trade Center, it was used in over 10 cases by the Innocence Project, and 7 crime laboratories were using the software regularly.

Simmer does not contest many of the facts underlying the district court's analysis summarized above. Rather, he contends that the district court ignored other factors that call into question the reliability of TrueAllele.

Simmer, for example, does not and cannot dispute the significant number of validation studies in the record concerning TrueAllele. Instead, he suggests that the validation studies must be discounted because Perlin is a coauthor of some of the publications and, as the owner of the company that owns TrueAllele, has a financial interest in seeing it found reliable. In other words, Simmer is contending that there are reasons to question Perlin's credibility. Even assuming that is true, an attack on the credibility of an expert witness is not aimed at the expert's reasoning or methodology and is thus not the proper basis for a *Daubert/Schafersman* challenge. See *Smith v. Colorado Organ Recovery Sys.*, 269 Neb. 578, 694 N.W.2d 610 (2005) (stating that challenge to expert witnesses' credibility is not *Daubert/Schafersman* claim).

In any event, Perlin's part in the validation studies was not as pervasive or unchecked as Simmer suggests. Perlin was not involved in 10 validation studies in the record. In addition, six of the studies in which he was listed as an author were published in peer-reviewed publications. As this court has previously recognized, "The reason that peer-reviewed publication is valuable is that it places research in the public domain and permits evaluation and criticism." *State v. Daly*, 278 Neb. 903, 914, 775 N.W.2d 47, 60 (2009). See, also, *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 593, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993) ("submission to the scrutiny of the scientific community is a component of 'good science,' in part because it increases the likelihood that substantive flaws in methodology will be detected"). Furthermore, Perlin was not the lone author on any of the published, peer-reviewed validation studies. That is, other members of the scientific community also staked their reputations on the reliability of TrueAllele. We see no basis to say that the district court abused its discretion by relying on the validation studies.

Simmer also argues that, apart from Perlin's involvement in some of the validation studies, the studies themselves do not demonstrate TrueAllele's reliability. Here, Simmer relies heavily on the testimony of his expert, Adams. Adams acknowledged the studies in the record validating TrueAllele, but claimed that there is a difference between the "forensic DNA definition of validation and the software engineering definition of validation." Adams emphasized that TrueAllele had not been tested from a software engineering perspective. In particular, Adams expressed concerns that the TrueAllele software source code had not been subjected to independent testing. He testified that without such a review, confirmation was lacking as to whether the TrueAllele software actually performs as described by Perlin.

We do not believe that the district court was required to find that TrueAllele had been validated "from a software engineering perspective" to find it reliable. In the *Daubert/Schafersman* context, a trial court has discretion to decide what factors are reasonable measures of reliability in each case. See *Zimmerman v. Powell*, 268 Neb. 422, 684 N.W.2d 1 (2004), citing *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 119 S. Ct. 1167, 143 L. Ed. 2d 238 (1999) (Scalia, J., concurring). While a review of the TrueAllele source code might also have confirmed the reliability of TrueAllele, we cannot say that the district court abused its discretion by relying on the numerous validation studies confirming the reliability of TrueAllele by other means. See *Com. v. Foley*, 38 A.3d 882 (Pa. Super. 2012) (noting in *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), analysis of TrueAllele that scientists can validate reliability of computerized process even if source code underlying process is unavailable to public). See, also, Edward J. Imwinkelried, *Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques*, 66 DePaul L. Rev. 97 (2016).

Neither are we persuaded by Simmer's argument that the validation studies are inadequate because the likelihood ratios generated by TrueAllele cannot be confirmed as accurate. Here again, Simmer relies heavily on Adams' assertions. Adams conceded that by running the TrueAllele software on known DNA profiles, one can determine whether TrueAllele accurately includes or excludes potential contributors. But Adams asserted that these same studies cannot confirm whether the specific likelihood ratios are accurate because there is no "knowable correct output."

Perlin, however, testified that TrueAllele's match statistics can be verified by comparing a broad range of match statistics to an expected distribution based on probability theory. At least one of the peer-reviewed validation studies did so and concluded that there was no significant difference between TrueAllele's match statistics and a uniform distribution. The study concluded that this provided statistical support for the system's accuracy. This method of testing may not have demonstrated to an absolute certainty that match statistics generated by TrueAllele are accurate, but a court performing a *Daubert*/*Schafersman* inquiry should not require absolute certainty. See, e.g., *State v. Herrera*, 289 Neb. 575, 856 N.W.2d 310 (2014).

Finally, Simmer argues that the district court failed to acknowledge the existence of a California study which, Simmer contends, reported "significant errors" by TrueAllele. Brief for appellant at 21. This study, however, is not in the record in this case. Perlin referred to it in his testimony, but he also testified that it was a "procurement study," which was never published, and that the laboratory conducting the study changed the parameters of TrueAllele so it did not work properly. We do not see how the district court could have abused its discretion by declining to rely on a study that was not in the record and was undermined by Perlin's unrefuted testimony.

For the reasons we have explained, we disagree with Simmer's argument that the district court ignored information it was required to consider in determining whether the TrueAllele evidence was reliable. Neither do we believe the district court's ultimate conclusion that the State proved the reliability of TrueAllele amounted to an abuse of discretion.

The State adduced significant evidence that TrueAllele is reliable. The State presented Perlin's testimony and copious documentary evidence describing TrueAllele's methodology, which is based on established mathematical principles. SWGDAM has approved the use of validated and documented probabilistic genotyping software and provided guidelines for its validation. TrueAllele has complied with those guidelines: TrueAllele's methodology has been repeatedly tested and validated in peer-reviewed studies.

Even if TrueAllele has not garnered universal acceptance in the relevant scientific community, that does not automatically disqualify it for admission. See *Epp v. Lauby*, 271 Neb. 640, 715 N.W.2d 501 (2006). The wide use of TrueAllele by government crime laboratories and other groups nationwide, Perlin's participation in multiple lectures and conferences, and Helligso's testimony that the scientific community had agreed in recent years that programs like TrueAllele are necessary, all tend to show that TrueAllele has been generally accepted in the relevant scientific community. Moreover, at least one appellate court opinion and several trial court orders in our record have found, based on similar evidence, that TrueAllele has gained such acceptance. See, e.g., *Com. v. Foley*, 38 A.3d 882 (Pa. Super. 2012) (rejecting challenge to TrueAllele, under *Frye v. United States*, 293 F. 1013 (D.C. Cir. 1923), standard, which requires general acceptance in relevant scientific community). See, also, e.g., *State v. Wakefield*, 47 Misc. 3d 850, 9 N.Y.S.3d 540 (2015) (same).

3. Application of TrueAllele in This Case

As mentioned above, some of Simmer's arguments on appeal are not directed to the TrueAllele methodology in a general sense, but instead attack the application of the methodology in this particular case. Specifically, Simmer contends that two reports, a 2015 validation study conducted by the Virginia Department of Forensic Science and a 2016 report by the President's Council of Advisors on Science and Technology (PCAST), suggest that TrueAllele could not be reliably applied to the particular facts in this case.

While Simmer criticizes the district court for not addressing his arguments based on these reports, we note that it is not clear that Simmer adequately raised these arguments in the district court. Simmer's pretrial motion in limine challenged the reliability of TrueAllele evidence, but it did not specifically raise any concern about whether TrueAllele could properly be applied to the particular facts of this case. A challenge to the admissibility of evidence under *Daubert/Schafersman* should take the form of a concise pretrial motion. *State v. Herrera*, 289 Neb. 575, 856 N.W.2d 310 (2014). It should identify, in terms of the *Daubert/Schafersman* factors, what is believed to be lacking with respect to the validity and reliability of the evidence and any challenge to the relevance of the evidence to the issues of the case, along with all other bases for challenging its admissibility. See *id.* See, also, *State v. Ellis*, 281 Neb. 571, 799 N.W.2d 267 (2011). The closest Simmer's motion in limine came to raising a challenge to the application of TrueAllele in this case was its allegation that the proposed testimony was "based on insufficient facts and data." It is far from clear this was specific enough to signal a challenge to the application of TrueAllele to the facts of this case. See *id.*

Even assuming Simmer properly preserved the issue, however, we see no basis to find that a conclusion that TrueAllele could be reliably applied to the facts of this case would amount to an abuse of discretion. To begin, we do not believe the Virginia validation study demonstrates that TrueAllele could not be reliably applied in this case. Simmer contends a portion of that study casts doubt on the conclusions reached in this case. One section of that study did, based on testing, conclude that TrueAllele produced a "[p]oor" analysis when the standard deviation in the mixture weight was less than .03. And, as Simmer points out, Perlin acknowledged that runs of the

TrueAllele software yielded a standard deviation below .03 for the knife handle.

Perlin did not, however, agree with the Virginia study to the extent it concluded that TrueAllele could not produce a reliable analysis when the standard deviation on mixture weights fell below a certain threshold. He testified that the Virginia study's results were "a reflection of the data" the authors analyzed and that they inappropriately tried to apply "hard and fast thresholds on statistical parameters" rather than "actually looking at concordance in the genotypes in their probability distributions." Perlin described concordance as similar results with acceptably small variations across multiple runs of the software. Perlin's trial testimony also suggests that the Virginia laboratory that performed the study eventually came to hold his view regarding the reliability of TrueAllele even with a low standard deviation in mixture weights: Perlin testified that the laboratory now uses TrueAllele "for all their reported mixtures."

Even setting aside Perlin's testimony disagreeing with the Virginia study's conclusion as to TrueAllele's analysis of mixture weights with a standard deviation below .03, the Virginia study reached that conclusion in the context of testing performed on *three-person mixtures*. There is no dispute that the sample from the knife handle in this case is a two-person mixture. The record does not show that the Virginia study's conclusion regarding standard deviation applies to the facts in this case, much less demonstrates that TrueAllele's analysis was unreliable here. Perlin testified that even a 1-percent standard deviation for the two-person mixture on the knife handle did not pose a problem for the reliability of the TrueAllele results.

Simmer's argument based on the PCAST report fares no better. Simmer contends that this report found that TrueAllele was reliable when the minor contributor to a two-person DNA mixture contributes at least 10 percent of the mixture. Simmer asserts that because the minor contribution on the knife handle in this case was only 2 percent, the PCAST report casts doubt on the reliability of the TrueAllele analysis in this case. As we will explain, however, the record before us is murky as to what the PCAST report concluded, the basis for those conclusions, and the weight those conclusions deserve.

The PCAST report is not in our record. Unable to cite directly to the report, Simmer directs us to a Washington trial court order containing a description of the report. That order does note that the report concluded that TrueAllele and a similar software program "appear to be reliable for . . . two person mixtures where the minor contributor constitutes at least 10% of the mixture." The same order, however, summarized several experts' criticism of the PCAST report, including its statements regarding mixture weights. It also observed that the PCAST report did not cite to any study that supported mixture weight limitations, a point Perlin also emphasized when he was asked about the report on cross-examination. The Washington trial court ultimately denied the defendant's motion to exclude TrueAllele evidence despite the fact that the minor contributor fell below the limitations purportedly expressed in the PCAST report. With no scientific evidence in the record indicating that TrueAllele could not generate reliable results under the circumstances here, we cannot say that a conclusion that TrueAllele could reliably be applied to the facts of this case would amount to an abuse of discretion.

In addition, other evidence in the record did address the effect that low mixture weights can have on the TrueAllele analysis, but it did not suggest that TrueAllele's analysis of low mixture weights was unreliable. Perlin and the Virginia study explained that mixture weights are reflected in the match statistic generated by TrueAllele: the lower the mixture weight, the lower the probability given by the match statistic. Therefore, the low mixture weight of minor contributor DNA found on the knife handle was reflected by the finding that the match between the knife handle and Simmer was 3.71 thousand times more probable than a coincidental match to an unrelated person, a probability much lower than the match between the doorknob and Simmer (4.22 quintillion times more probable than a coincidental match to an unrelated person).

The fact that a lower mixture weight makes a match statistic less certain is not a basis for exclusion of the evidence. We have previously recognized that DNA analysis is not subject to exclusion simply because the probability of a match falls below a certain threshold. See, *State v. Tucker*, 301 Neb. 856, 920 N.W.2d 680 (2018); *State v. Ellis*, 281 Neb. 571, 799 N.W.2d 267 (2011). Instead, we have emphasized the need for DNA analysis to "be accompanied by evidence of the statistical significance of the findings," and we have rejected arguments that jurors are not capable of assigning appropriate weight to those statistics. *Tucker*, 301 Neb. at 866, 920 N.W.2d at 688. Here, the evidence furnished the jury with the statistical context to carry out its duty. To the extent the disparity between the major and minor contributor on the knife handle reduced the certainty of a noncoincidental match, that was an issue of weight for the jury to consider and not a bar to admissibility.

We see no basis to conclude that the district court could not, consistent with our abuse of discretion standard of review, conclude that TrueAllele could be reliably applied to the particular facts of this case.

4. Limitations of Our Decision

We conclude by cautioning that this opinion should not be understood as mandating the admission of TrueAllele evidence in all future cases. "*Daubert* . . . does not require that courts reinvent the wheel each time that evidence is adduced, but it does permit the re-examination of certain types of evidence where recent developments raise doubts about the validity of previously relied-upon theories or techniques." *Schafersman v. Agland Coop*, 262 Neb. 215, 228, 631 N.W.2d 862, 874 (2001). And our *Daubert* framework "permits re-examination of the issue if the validity of the prior determination can be appropriately questioned." *Schafersman v. Agland Coop, supra*. See, also, *State v. Casillas*, 279 Neb. 820, 782 N.W.2d 882 (2010). As the instant case demonstrates, "[s]cientific conclusions are subject to perpetual revision" and "hypotheses . . . that are incorrect will eventually be shown to be so." *Daubert v. Merrell Dow Pharmaceuticals, Inc.*, 509 U.S. 579, 597, 113 S. Ct. 2786, 125 L. Ed. 2d 469 (1993). Based on the record before us in this case, however, we cannot say that the district court abused its discretion in allowing admission of the TrueAllele evidence.

V. CONCLUSION

For the foregoing reasons, we determine that the district court did not abuse its discretion in admitting DNA analysis conducted by using TrueAllele, over Simmer's *Daubert/Schafersman* challenges. Therefore, we affirm.

Affirmed.