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A New Black Box: How Proprietary DNA Testing Programs are Harming Criminal Defendants

Sean Lorthioir

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The increasing capability of artificial intelligence (AI) has revolutionized the world we live in and will continue to change almost all facets of society. While computer scientists are still working on self-driving cars and other advancements, AI has already reached the forefront of forensic DNA testing. Forensic DNA testing to determine matches of a suspect's DNA at a crime scene can now be done by AI. After the sample from the scene and the suspect's DNA are placed in the program, it calculates the probability that the two samples matched by more than mere coincidence. The programs also have enhanced capabilities to analyze contaminated or damaged samples, a process that used to be impossible with traditional DNA analysis. This new capability is a major boost to DNA testing. Suspects can now be exonerated or incriminated by analyzing samples that could not analyzed before.

While this new technology shows promise, there have been questions about how quickly it has been adopted. Many defendants have raised concerns about the few validation studies done to prove the program's reliability. Additionally, courts must find a way to address the boundaries of admissibility and make a determination when the program is reliable and when it cannot make a determination in the task at hand. Defendants also face new challenges at trial. Some programs like TrueAllele are proprietary. This means that the defense cannot have access to the code to learn how the program makes certain determinations and challenge them effectively. Since defendants, or any other outside party cannot access the code, it has created a new black box where courts and juries are forced to trust that the program does not contain any errors or flawed assumptions. This is effectively removing any debate from DNA analysis and is inhibiting defendants from being able to challenge evidence brought against them. Courts must compel

TrueAllele to turn over the source code of the program to Defendants who request it in order to ensure fair trials.

I. Background on Forensic DNA Testing

Deoxyribonucleic acid (DNA) analysis is an intricate science that most jurors, lawyers, and judges do not completely understand. Yet, it developed into one of the most impactful forms of evidence in criminal cases. Before discussing the evolving realm of DNA interpretation, one must understand the foundational knowledge of DNA and testing. DNA is a coding structure present in each cell of the body and is shaped like a "twisted ladder."[1] The "rungs" of the ladder are known as basses and are formed of sequences of bases linked together.[2] This forms the DNA sequence that is analyzed.[3] While many parts of the sequence are the same, or similar for many organisms of the same species, but certain sections are polymorphic and differ for each person.[4] This differing sequences produce certain genetic alleles, such as the different blood types for humans.[5]

The most compelling and useful part about DNA is that each person, due to the polymorphic nature of certain sequences, has unique DNA. No two individuals, except for identical twins have the same sequences.[6] It is also consistent throughout each type of cell in a person's body, and remains the same throughout a person's life. "The DNA found in a man's hair follicles at birth is identical (apart from occasional slight changes called "mutations") to the

[1] William C. Thompson & Simon Ford, *DNA Typing: Acceptance and Weight of the New Genetic Identification Tests*, 75 Va. L. Rev. 45, 62 (1989).
[2] *Id.*
[3] *Id.*
[4] *Id.*
[5] *Id.*
[6] *Id.*

DNA found in his blood at age seventy."[7] This means that any sample (be it hair, saliva, blood etc.) from a person from any point in their life should match with any other sample taken from them. This allows for specimens to be preserved and they can be tested years after they were collected, if stored properly.

The testing process begins with the collection of a sample. The sample is genetic material (blood, hair, semen, etc.) left behind on a surface. The DNA is then extracted from the sample and isolated. Once the sample is isolated, technicians can perform Restriction Fragment Length Polymorphism (RFLP) or Polymerase Chain Reaction (PCR) analysis.[8] These are two methods to highlight the polymorphic sequences that will be compared with the known sample provided.[9] Both methods can be used for analysis, but PCR requires less material because the process allows the technician to amplify the sample.[10] However, this makes PCR more vulnerable to contamination or inaccurate results if the incorrect part of the sample is amplified.[11]

After the sample is processed it is ready for statistical interpretation. Traditionally, this was done manually by a technician or scientist. Analysis involves three steps. First, analysis of a known sample (e.g., a sample from a crime scene) and an unknown sample (e.g., a sample from a crime suspect) to determine if there is a match.[12] Second, the statistical significance of the match is calculated. This is the likelihood that a random person would match the same bands as those matched between the crime scene and the crime suspect.[13] Third, they determine the frequency of

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[7] *Id* at 61-62.
[8] *See The admission of DNA evidence in state and federal courts*, 65 Fordham L. Rev. 2465, 2468-2471
[9] *Id.*
[10] *Id.*
[11] *Id.*
[12] *Id*.
[13] *Id*.

the occurrence of each matched band in the general population.[14]When a match is declared this does not necessarily mean that both samples came from the same person because the part of the sequence that matched may occur frequently in the larger human population.[15] Therefore, this is why calculating the frequency of the matched sequence of the population (the third step in analysis) is important. However, these calculations rely on existing populations databases, which can be a limiting factor if they do not provide a sufficient survey of the general population.[16] This traditional DNA analysis has been widely recognized in practically all jurisdictions as scientifically reliable expert testimony so long as proper laboratory standards are followed. It is recognized under the *Frye* and *Daubert* standards. The first criminal convictions using DNA evidence in the United States was obtained in 1987, and upheld after appeal in 1988.[17]

II. Using AI to Conduct DNA Analysis

The limiting factor on traditional DNA analysis has been the quality of the sample. If a sample is contaminated, or contains DNA from multiple people, it can become too intricate for traditional isolation and analysis of a particular strand of DNA. The best samples are bodily fluids, since they contain more DNA that can be analyzed.[18] However, real world crime scene samples are rarely this kind of perfect uncontaminated and excellent sample.

An example of this problem is a 2009 case where a woman was found murdered in Pennsylvania. A DNA sample was found underneath the victim's fingernails. The small amount

[14] *Id* at 2472.
[15] *Id*.
[16] *Id*. At 2478
[17] *See Andrews v. State*, 533 So. 2d 841 (Fla. Dist. Ct. App. 1988).
[18] *No Longer the Gold Standard: Probabilistic Genotyping is Changing the Nature of DNA Evidence in Criminal Trials*, 24 Berkeley J. Crim. L. 110, 114-115.

of DNA collected was 90 percent the victim's and 10 percent belonging to another party.[19] Technicians conducted Traditional DNA analysis and declared a match to the defendant, Kevin Foley. When traditional DNA probability was calculated, it was found that the probability that someone else had a similar DNA coding was 1 in 13,000.[20] Another expert using traditional analysis found that the probability was 1 in 23 million.[21] While these sound like good odds, they did not provide conclusive evidence that prosecutors wanted because it was still reasonably possible that the DNA could belong to others.[22]

In order to strengthen their DNA evidence, the prosecution turned to Mark Perlin, the founder of Cybergenetics Inc. The company developed a new program called TrueAllele that produced more accurate probability calculations, especially in cases with mixed, contaminated, or damaged DNA samples. TrueAllele calculated probabilities for the same sample and Dr. Perlin testified in court that the probability of another person sharing the same DNA sequence was 1 in 189 billion. This stronger confirmation that it was Foley's DNA under the victim's fingernails, along with other evidence, led to Foley's conviction.[23] This was the first time that TrueAllele had been used to secure a criminal conviction.

How was TrueAllele able to make a much narrower determination than the human analysts? TrueAllele is able to make more advanced determinations using the entire sample, rather than relying on the more traditional methods of only analyzing in-tact "peaks" of DNA

[19] *Commonwealth v. Foley*, 38 A.3d 882, 887 (Pa. Super. Ct., 2012)
[20] *Id.*
[21] *Id.*
[22] Given that there are over 300 million people living in the United States, there are other Americans who could share that profile under either of the traditionally calculated probabilities.
[23] *Id*.

over a certain threshold determined by the analyzer.[24] The program then factors uncertainty of certain points of the sample into its calculations, giving less weight to more unclear sections, and more weight to undamaged or uncontaminated sections.[25] The program then calculates the likelihood that the suspect's DNA is in the sample and the likelihood that it is not in the sample.[26] The two numbers are then compared in a likelihood ratio, as seen in the *Foley* case.

Mark Perlin, the creator of TrueAllele, and his company, Cybergenetics, have been outspoken advocated for new computer-calculated probabilities and analysis in forensic science. TrueAllele can process and analyze samples much quicker than traditional analysis. In one demonstration, TrueAllele was able to accurately analyze a complex two-person sample in 30 minutes.[27] Its more detailed analysis can also handle more complex samples that have multiple contributors, contain minute amounts of DNA, or contain damaged DNA. Before being used in the criminal context, the program was used to identify the remains of World Trade Center victims. Cybergenetics also touts the objectivity of the program, which it purports does not show the same bias of a human analyst towards seeking a match.[28] The program also "learns" from previous data and requires no calibration.[29] These factors have led to the increasing popularity of TrueAllele and similar programs such as STRmix.

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[24] Mark Perlin, *Explaining the likelihood ratio in DNA mixture interpretation*, 9-10 (2010).
[25] *Id*.
[26] *Id* at 1.
[27] *Id*.
[28] The TrueAllele Difference, https://www.cybgen.com/products/casework.shtml (last visited May 3, 20202).
[29] *Id*.

III. Admissibility in Court

The verdict in the *Foley* case was reached in 2009 and marked the first admission of TrueAllele in a criminal case. However, admissibility was not unchallenged in this case and cases in other jurisdictions where TrueAllele was introduced. This took the form of two major points of contention with admissibility. First, the evidence generated by the program was allowed into evidence without a *Frye* or *Daubert* hearing in some jurisdictions. This was primarily an argument whether the program constituted "novel" science and if its results could be properly replicated by other scientists. Second, there were also issues with defining the boundaries of admissibility. Once the program was admitted for analysis as a proven scientific expert, courts still had to determine when the program could be used, and what determinations were beyond its approved limits.

A. Frye and Daubert Considerations

Foley appealed in 2012 and argued, *inter alia*, that Perlin's testimony about TrueAllele was inadmissible because the program was "novel science" and had not met the standards of the *Frye* test.[3031] In Pennsylvania, "novel scientific evidence is admissible if the methodology that underlies the evidence has general acceptance in the relevant scientific community."[32] This acceptance is required before a type of expert testimony is permitted in a trial. Foley argued that the technology was novel, and there was still a genuine material dispute as to the acceptance of TrueAllele's methods in the forensic community.[33] If this was the case, a *Frye* hearing would have been necessary to determine the validity of TrueAllele. The prosecution argued that there

[30] *Commonwealth v. Foley*, 38 A.3d at 888.
[31] *See Frye v. United States*, 293 F. 1013, 1014 (D.C. Cir. 1923).
[32] *Grady v. Frito-Lay, Inc*., 839 A.2d 1038, 1044 (Penn. Supreme Ct., 2003).
[33] *Commonwealth v. Foley*, 38 A.3d at 888.

was no hearing required because there was no novel scientific evidence presented at the trial through Dr. Perlin and TrueAllele.[34] They maintained that this was simply a new form of calculating and analyzing data that was gathered using already-accepted scientific methods.[35] TrueAllele was calculating the same product rule likelihood ratios that were already generally accepted when calculated by human analysts.[36] This would mean that a Daubert hearing was not required because the rations were already generally accepted as scientific evidence.

To some degree, the prosecution's argument makes sense. The result that would be presented to the jury after TrueAllele analysis, the likelihood ratio, is the same ratio that would be presented if the DNA was analyzed by the FBI crime lab, or a state laboratory. However, the way that TrueAllele arrives at that probability is a significant departure from traditional analysis. One obvious distinction is that TrueAllele's calculations are done via computer program with no human input, as already discussed. Additionally, TrueAllele also analyzes more portions of the DNA and conducts more sophisticated calculations than a human analyst doing similar analysis and calculations. While a human would only look at sequences that met a certain threshold, TrueAllele looks at all the available sequences. However, it is unclear if this differing methodology warrants being labeled a "novel" science. Even the trial court was unsure about this and did not make an express determination when deciding to allow the evidence.[37]

Ultimately, the Superior Court found that there was no meaningful dispute in the scientific community about TrueAllele's methods. It further reasoned that it was generally accepted even though it had never been used in an American criminal case because it was used in

[34] *Id.*
[35] *Id*.
[36] For Acceptance of the product rule *See Commonwealth v. Blasioli*, 552 Pa. 149 (1998).
[37] *Commonwealth* v. Foley, 38 A.3d at 888

New York for other purposes and the United Kingdom used it to analyze its national database.[38] Therefore, the trial court did not abuse its discretion by allowing the testimony at trial without a *Frye* hearing, and Foley's conviction was upheld.[39] The abuse of discretion standard made a reversal unlikely, but an important opportunity was missed to explore the bounds of what constitutes novel science. In its decision, the appeal made no reference to the new technology and methods being used by Perlin in his calculations, and how this could potentially be construed differently than the existing product rule.[40] What would have been the harm of holding a hearing? The mere necessity of the hearing would not mean that the evidence would have been excluded. Instead, it would have allowed for more in-depth exploration of TrueAllele, how it makes it determinations, and how other people in the forensic DNA community view the program and its methods. Having a *Frye* hearing at trial level instead of allowing the evidence in through an existing backdoor would have been beneficial to all parties. For the defendant, they would have every opportunity to challenge TrueAllele's reliability. If the program was ultimately deemed valid, the prosecution would have a much more clear and solid precedent to admit the program in future cases.

Even though the technology was accepted without any *Frye* or *Daubert* hearings in Pennsylvania, TrueAllele's acceptance did face *Frye* and *Daubert* challenges in other states. In Ohio, a defendant challenged the acceptance of TrueAllele by arguing that it had only been accepted and validated to process single contributor samples, and had not been accepted to

[38] *Commonwealth v. Foley*, 38 A.3d at 888
[39] *Id.*
[40] *Id.*

process the more complex weak and multi-contributor samples.[41] Similar to *Foley*, initial analysis performed by the Cuyahoga County Medical Examiner and subsequently Sorensen Genomics was unable to yield any conclusive results on mixed samples found under the victim's fingernails and on a doorknob.[42] After these inconclusive results, the samples were sent to TrueAllele, where the program determined that Shaw's DNA was contained in both samples.[43]

The court then granted a motion for a *Daubert* hearing to determine the admissibility of TrueAllele's determinations. In the motion, the defendant relied heavily on testimony from Dr. Raj Chakraborty, a faculty member for the Scientific Working Group on DNA Analysis Methods (SWGDAM).[44] Dr. Chakraborty was previously responsible for approving the use of TrueAllele in New York, as cited in the *Foley* case, and cited by the prosecution in this case.[45] He testified that even though he had approved of TrueAllele, he only approved it for use in single-contributor sample cases in New York, and did not yet approve it for multi-contributor samples.[46] Dr. Chakriborty raised concerns about validation because TrueAllele has never revealed the source code that the program uses to make the calculations.[47] He believed that without having access to the source code, it was impossible for scientists to effectively validate TrueAllele because the results could not be replicated independently.[48] The defense also presented testimony from a

[41] *See* Order at 6-19, *Ohio v. Shaw*, CR-13-575691 (Oct. 10, 2014), http://www.cybgen.com/information/press-release/2014/TrueAllele-Casework-Ruled-Admissible-in-Ohio- Daubert-Challenge/admissibility.pdf
[42] *Id*.
[43] *Id*.
[44] *Id*.
[45] *Id*.
[46] *Id*.
[47] *Id*.
[48] *Id*.

second expert, Dr. Krane. He testified that an important part of the scientific process is the ability to replicate results. Scientists must share their results, as well as how they reached their results.

Dr. Perlin testified again on behalf of TrueAllele. He testified that a scientist can "get very close to duplicating by reading his work. But if the scientist has not purchased the system he cannot duplicate it because he does not have all of the engineering details."[49] Perlin further testified that the validity of the program was in its ability to get accurate results, rather than evaluating the actual source code. Despite Perlin's apparent admission that there was a clear obstacle to reproducing the results, the court decided to allow the evidence.[50] They held that TrueAllele used reliable scientific methods and concerns about accuracy or precision of the results was a matter of weight rather than admissibility.[51] The court reasoned that the technology met the "general acceptance" requirement due to its use in laboratories in other states and its admittance into evidence in other jurisdictions.[52]

The issue of replicability of results was an issue in both cases. However, both courts did not agree with defense arguments that replicability was impossible without further insight into how the program worked. In *Foley*, the court expressly rebuked any concern that the results could not be accurately verified without TrueAllele's source code, which determines how the program runs, and how it makes certain determinations in its analysis and calculations. The court stated: "TrueAllele has been tested and validated in peer-reviewed studies."[53] As proof that there was agreement in the scientific community, the court cited two papers that listed Dr. Perlin as the

[49] *Id*.
[50] *Id*.
[51] *Id*.
[52] *Id.*
[53] *Commonwealth v. Foley*, 38 A.3d at 889.

principal author.[54] These were published in peer reviewed journals, which meant they had been subject to some kind of external review.[55] However, there is a difference between review and replicability. The record is silent on the review process, but it makes no mention of how reviewing the article comprises of reproducing the results of the paper.

Generally, peer review focuses on the methodology used, the quality of the writing, and the logic of the conclusions of the article. Peer review does not imply that it is correct in its conclusions, or that the views of the article are widely accepted. It just means that the author met scientific standards conducting their research.[56] The *Daubert* court agreed with this assessment of peer review when determining reliability when they stated that publication "does not necessarily correlate with reliability.[57] Therefore, for the court, publication in a peer reviewed journal is certainly relevant in making a determination, but is not dispositive on its own.[58] Therefore, two peer reviewed articles authored by Dr. Perlin, the creator of TrueAllele, should not be sufficient to make the claim that there is no dispute about the methods or accuracy of the program, or that there is general acceptance in the scientific community. Nonetheless, TrueAllele appears to have evaded any potential *Daubert* or *Frye* challenges because its final result, the product rule likelihood ratio, is already generally accepted. Courts have also been willing to overlook any points of contention regarding the new technology that TrueAllele uses to reach those results.

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[54] *Id.*
[55] *Id.*
[56] *Id.*
[57] *Daubert v. Merrell Dow Pharm.*, Inc., 509 U.S. 579, 593 (1993).
[58] *Id* at 594.

B. The Boundaries of Admissibility

After courts decide whether TrueAllele is admissible as a novel (or already accepted) science, they must still decide when TrueAllele can be used reliably. The trial judge is assigned, "the task of ensuring that an expert's testimony both rests on a reliable foundation and is relevant to the task at hand."[59] This issue is best embodied by the landmark case *Kumho Tires,* which was decided shortly after *Daubert*.[60] In *Kumho*, there was no doubt that the plaintiff's expert, Carlson was a tire expert.[61] He worked at Michelin for 10 years and was a tire failure consultant in numerous cases.[62] However, the issue was whether it was possible for Carlson to make a determination on how the tire failed in the crash that was at issue in the case.[63] The court had to decide if a credible expert could make a reliable determination based solely on visual and tactile examination of the tire. Ultimately, it was upheld that the trial court did not abuse its discretion when it barred the witness from testifying.[64] This was because the judge felt that given the evidence presented to the expert, it was impossible for an expert to make a reliable determination, even though the expert had valid credentials.[65] Therefore, in order to be admissible, the science or methodology must be reliable and it must be able to make a reliable determination given the facts of the specific case where the testimony will be given.

In the realm of DNA analysis, this has become a concern because TrueAllele continues to push the boundaries of DNA analysis. TrueAllele may be reliable for analyzing high quality

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[59] *Id* at 597.
[60] *Kumho Tire Co. v. Carmichael*, 526 U.S. 137 (1999).
[61] *Id* at 154.
[62] *Id* at 154.
[63] *Id.*
[64] *Id.*
[65] *Id*.

single contributor samples. However, some defendants have challenged whether TrueAllele can reliably make determinations on more difficult samples, such as ones that have multiple contributors, or only contain trace amounts of DNA. Even if TrueAllele was found generally accepted or reliable in many jurisdictions limitations of the technology should be considered when deciding whether TrueAllele can do DNA analysis in a case.

This was one of the issues that was mentioned in the initial pretrial hearing in *Shaw*. Defendant Maurice Shaw was accused of kidnapping and murder. There were two DNA samples which contained a mixture of DNA from the victim and Shaw. Like the *Foley* case, traditional DNA analysis was not able to produce a confident match. However, Shaw placed more emphasis on TrueAllele's irrelevance to the task at hand, like *Kumho*. As previously discussed, part of the prosecution's argument in favor of allowing the evidence was that it had already been purchased by labs across the country and was planning to be adopted in state labs such as New York's lab.[66] To counter this argument, the defense called Dr. Chakraborty, a faculty member of SWGDAM, which had helped to approve New York's use of TrueAllele. Dr. Chakraborty testified that he only approved use of TrueAllele in New York for single-contributor samples.[67] He was unsure of TrueAllele's capability to do reliable analysis in the more complex samples such as the two presented in this case.[68] A second defense expert, Dr. Krane, also testified. Dr. Krane was a biological sciences professor at Wright State University and testified as a DNA expert witness in over 100 cases.[69] Dr. Krane analyzed the sample and argued that it was not a two-contributor

[66] *See* Order at 6-19, *Ohio v. Shaw*, CR-13-575691 (Oct. 10, 2014), http://www.cybgen.com/information/press-release/2014/TrueAllele-Casework-Ruled-Admissible-in-Ohio- Daubert-Challenge/admissibility.pdf
[67] *Id* at 15.
[68] *Id* at16.
[69] *Id* at 17.

sample as TrueAllele claimed. Instead, Krane believed three people contributed to the samples.[70] However, Krane was unable to declare any sort of match to Shaw in the sample. When asked about how TrueAllele could arrive at such a different and certain conclusion, Krane had no explanation.[71] This was the main reason for his doubt that TrueAllele could reliably analyze more complex samples.[72]

Despite the concerns of defense experts, the court decided that TrueAllele was admissible to analyze the sample. The court relied heavily on previous DNA precedents that favor admissibility and then allowing the jury to determine how much weight the evidence should receive.[73] This allows for a battle of the experts in court, where opposing parties are given the opportunity to replicate the results, or critique the methods used to obtain the results. [74] Under this approach, this meant that once TrueAllele was accepted as generally accepted (see III. A.) the task at hand question did not really matter. This approach allows for a more robust debate of experts at trial. However, it also fails to set any boundaries or limitations on when the software can be used. Without any acknowledgment of limitations of the program, it seems as though TrueAllele can be used to analyze any sample, and the jury will have to grapple with the accuracy of the analysis.

This issue was also seen in Maryland courts. The *Morten* case involved a revolver that was found in a yard after it was allegedly thrown by the defendant.[75] After the revolver was

[70] *Id.*
[71] *Id*.
[72] *Id*.
[73] *Id* at 20
[74] *Id*.
[75] *Morten v. State*, 242 Md. App. 537, 559 (2019)

recovered it was swabbed for fingerprints, but none were revealed.[76] The revolver was then given to Thomas Heibert, a DNA analyst for the Baltimore Police Department.[77] Only s very small trace amount of DNA was recovered from the gun.[78] Like the previous cases, when the DNA was analyzed traditionally, the results were inconclusive.[79] Heibert had analyzed the sample as a single-contributor sample, but could not confidently declare a match between the sample on the gun and the defendant. After this analysis was inconclusive, Heibert used TrueAllele to analyze the sample.[80] He also changed the analysis to try to get a determination that the defendant was a minor contributor to the sample instead of trying to determine that the DNA was a full match.[81] TrueAllele's analysis concluded that defendant's DNA was present in the sample.[82]

This case also took place during a time of uncertainty in DNA admissibility in Maryland. Maryland had a statute in effect that made DNA analysis automatically admissible if it met certain criteria. Namely, the methods used had to be approved by either The Technical Working Group on DNA Analysis Methods (TWGDAM), or the FBI's DNA Advisory Board.[83] This appeared to streamline DNA admissibility while still allowing for scientific critique. However, this became problematic because at the time of this case TWGDAM nor the FBI Advisory Board were no longer in existence, nor had they written any guidance on TrueAllele.[84] The defense

[76] *Id.*
[77] *Id.*
[78] *Id.*
[79] *Id.*
[80] *Id.*
[81] *Id.*
[82] *Id.*
[83] Md. Code Ann., Cts. & Jud. Proc. § 10-915
[84] *Morten v. State*, 242 Md. App. at 559.

subsequently moved to have the evidence suppressed, citing the novelty of TrueAllele and potential faults in its determination.[85]

At the hearing the defense took efforts to highlight the greater uncertainty of multiple contributor weak samples. Heibert classified the sample from the gun as a "low level mixture with a lot of uncertainty in the profile."[86] He went on to clarify that low level mixtures contain very small amounts of DNA and usually contain a mix of DNA from multiple people.[87] This particular sample had so little DNA that Heibert even acknowledged that it was impossible to determine whether the sample had suffered degradation because the sample was so small to start.[88] When asked about the boundaries of his own traditional analysis and the boundaries of TrueAllele, Heibert discussed that analysts were able to make their own determinations about when to do manual analysis and when to use TrueAllele.[89] However, TrueAllele is usually only used when traditional analysis is not possible.[90] However, he did not provide any insight into the potential upper limits of use for TrueAllele.

The defense relied on expert testimony from Dr. Word. She had received a Ph.D. in molecular biology and immunology and spent 15 years in a private lab doing DNA analysis for paternity and criminal cases.[91] She also worked as a consultant in DNA analysis, and had served on a Justice Department subcommittee regarding the future of DNA evidence.[92] In her full

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[85] *Id*.
[86] *Id* at 561-62.
[87] *Id.*
[88] *Id.*
[89] *Id.*
[90] *Id.*
[91] *Id* at 572.
[92] *Id.*

career, she estimated that she had reviewed well over one million samples.[93] Dr. Word testified in the pretrial hearings about concerns about the accuracy and capabilities of TrueAllele when dealing with complex samples. For instance, She testified that while TrueAllele's calculations for a two contributor sample included the defendant as a contributor, the program's three contributor analysis would have excluded him.[94] Dr. Word further argued that there was evidence to support that this was a sample containing more than two contributors.[95] Even Heibert admitted that choosing two person analysis was just his best assumption.[96] However, the court decided to air on the side of weight over admissibility and decided to allow the evidence at trial.[97] The court reasoned that the defense's issue with the program focused more on the assumptions made by Heibert when he put the samples into TrueAllele rather than the methods of the program itself. The question of boundaries again was unanswered.

It is understandable that courts would favor admissibility of evidence and allow the trier of fact to determine its significance and weight at trial. However, it is dangerous to establish no limits on admissibility. As already discussed, TrueAllele has been validated and generally accepted to be able to reliably analyze single samples, and several courts have been willing to extend that to weak samples containing two or more contributors. However, there should be some distinction between these different analyses. A method may be reliable for strong samples with minimal variables. However, as logic dictates, the more variables that are placed into

[93] *Id.*
[94] *Id.*
[95] *Id.*
[96] *Id.*
[97] *Id.*

analysis, the more complex and unreliable that analysis becomes. Therefore, there should be greater skepticism towards TrueAllele's analysis when it analyzes more complex samples.

IV. Confrontation at Trial and Accessibility

Based on most of the caselaw, TrueAllele is on solid admissibility footing. It has been admitted in most states, the federal court system, and abroad. With the possibility of pretrial suppression seemingly impossible, defendants must undermine the evidence at trial and allow the jury to decide whether TrueAllele is accurate and reliable. However, this has created new issues that require attorneys and courts to adapt. First, TrueAllele represents a new intersection of both DNA analysis and computer science. Although many prosecutors have placed human technicians on the stand to testify to findings, TrueAllele is responsible for the determinations. In order to effectively confront TrueAllele, an opposing expert must therefore be well versed in both DNA Analysis, as well as the underlying computer technology that makes TrueAllele possible. Second, courts must address the growing "black box" issue surrounding TrueAllele. Courts must strive for a balance between protecting proprietary material while allowing defendants to know how DNA in their case was analyzed.

A. Confronting TrueAllele at Trial

After Morten's pretrial suppression motion failed in Maryland, the case proceeded to trial. The defense relied on testimony from the same expert, Dr. Word to undermine TrueAllele's credibility. Dr. Word's testimony was the sole testimony for the defendant.[98] Additionally, the prosecution relied entirely upon finding the defendant's DNA on the revolver because it was

[98] *Id.*

their only way to tie the defendant to the crime scene.[99] During voir dire, Dr. Word testified to the same credentials as during the pretrial hearing. However, the prosecution revealed that Dr. Word had never gone through the full DNA analysis process using TrueAllele.[100] When Dr. Word was subsequently admitted as an expert, she was admitted as an expert in "forensic DNA analysis and interpretation" without objection from the prosecution.[101]

While this seemed like an insignificant distinction at the time, it would have important implications when Dr. Word testified. During the pretrial hearing, Dr. Word was able to testify to the weaknesses and uncertainty surrounding TrueAllele analysis. She was also able to cast doubt on the technician using the program and decisions he made when starting the analysis. However, her testimony at trial was a "muddle" with 30 objections, 26 being sustained.[102] There were also 16 bench conferences.[103] Since Dr. Word had never fully analyzed a sample with TrueAllele, she could only testify to its general existence as a method of DNA analysis. Since she had never used the program, she was not allowed to speak to its potential weaknesses, even though she testified about those weaknesses at the pre-trial hearing.[104] An objection was sustained when Dr. Word was asked about the reliability of DNA testing on small trace samples such as the one in the case.[105] An objection was sustained when she was asked about the implications of analyzing a sample for two contributors instead of three contributors.[106] An objection was also sustained when she was asked generally about the reliability of DNA analysis software, or whether there

[99] *Id* at 571.
[100] *Id* at 573-74.
[101] *Id*.
[102] *Id* at 575.
[103] *Id*.
[104] *Id* at 575-76.
[105] *Id*.
[106] *Id*. at 582.

were any tests regarding the limits of the program.[107] The trial court reasoned that the pre-trial hearing had already determined that TrueAllele was reliable, and its general reliability as a program could not be questioned again at trial.[108] Without any ability to present a proper defense against TrueAllele, the jury returned a verdict of guilty.

Morten subsequently appealed his conviction unrelated erroneous admittance of hearsay evidence at trial, as well as "erroneously being precluded from adequately challenging the DNA test results introduced against him."[109] The court vacated the conviction on the first issue, but also decided to address the issues regarding TrueAllele. This was a case of first impression and marked the first time the program was used in a Maryland criminal trial.[110] The Court of Special Appeals believed that Morten should have been able to continue to challenge the reliability of TrueAllele at trial and that reliability can contribute to weight. Specifically, they noted that there should be two avenues of challenging reliability at trial, theoretical reliability, and ad-hoc reliability. Theoretical reliability pertains to the reliability of the system. Essentially, the theoretical reliability of the methods is what is challenged in a *Daubert* or *Frye* hearing. However, even if the TrueAllele passed muster in a *Daubert* hearing, defendants are still allowed to continue to use evidence against reliability at the trial.[111]

The second type of reliability that can be challenged at the trial is ad-hoc reliability. This challenge focuses on the way that the test was performed specifically in that instance rather than the general reliability of the program.[112] In the *Morten* case, the challenge to ad-hoc reliability

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[107] *Id.*
[108] *Id.*
[109] *Id* at 541.
[110] *Id* at 558.
[111] *Id* at 577-78.
[112] *Id.*

was Heibert's decision to test for only two contributors in the sample instead of the three that Dr. Word suggested. Another ad-hoc challenge in this case was that the sample was too small to perform accurate analysis.[113] Since the defendant was deprived of the ability to challenge this evidence, it is implied that the court would have vacated the conviction on this issue as well.[114]

While the *Morten* case outlined how a defendant is permitted to challenge TrueAllele at trial, it did not address the potential issue of narrowing the ability of DNA experts to testify in TrueAllele cases. If courts mirror the narrow expert approach taken by the trial court, there will be very few experts available for defendants to challenge TrueAllele. Dr. Word had years of DNA analysis experience and other credentials. However, since she never used the program, she was not allowed to properly challenge the program. This would mean that only analysts who have worked with the program would be able to challenge its determinations in court. Consider the resume of Dr. Perlin, who is the creator of TrueAllele and testified on its behalf in many of the early *Daubert* and *Frye* proceedings, as well as early trials. He is an M.D. and has a Ph.Ds. in mathematics and computer science. It would be difficult for defendants to find experts who both his DNA and computer credentials. Using two separate experts would also not be ideal because the technical and DNA analysis aspects of the program could not be simultaneously discussed.

The solution to this issue would be to have more DNA analysts available who have used TrueAllele. However, access to the program is limited due to its proprietary nature. The cases already presented in this paper have shown numerous attempts to reveal the source code of TrueAllele, but it has never been revealed. The only way to thoroughly analyze the inner workings of the program would be to purchase a copy of the program from Cybergenetics, the

[113] *Id*.
[114] *Id*.

company that created TrueAllele. However, a copy of the program costs $60,000, a cost that almost any criminal defendant would be unable to afford.[115] Courts must balance the rights of defendants to have access to, and the ability to confront evidence presented against them with the rights of Cybergeneitcs to have their proprietary program protected.

While the source code has yet to be turned over to a defendant in a criminal trial in any jurisdiction, recent developments in California have suggested that TrueAllele's proprietary shield is not impenetrable. The first case where TrueAlelle was almost turned over to the defendant involved Martell Chubbs. He had been arrested in 2012 for a 1977 murder after TrueAllele analysis of a DNA sample led to a break in the case.[116] The sample analyzed by TrueAllele determined that Chubbs was "1.62 quintillion times more probable than a coincidental match."[117] Before trial, Chubbs made a discovery request for the source code of TrueAllele. The prosecution did not turn over the source code initially. Instead, the presented the defense with a copy of TrueAllele's report.[118] The prosecution also provided copies of articles written by Dr. Perlin regarding TrueAllele, manuals for how to use the program (even though the program itself was not provided) and a power point presentation on the program.[119]

After the source code was not turned over, the defense pressed forward with a motion to compel discovery of the program. The prosecution contested that turning over the source code would be "financially devastating" to Cybergenetics.[120] In the alternative, Cybergenetics would run further TrueAllele tests using defense-provided data. Additionally, they could meet with

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[115] *People v. Superior Court*, 2015 Cal. App. Unpub. LEXIS 105, at 7 (Jan. 9, 2015).
[116] *Id* at 2.
[117] *Id* at 4.
[118] *Id*.
[119] *Id.*
[120] *Id*.

defense experts to discuss the results in the case and explain how the system operates using one of the company's computers. Despite this attempt to assuage concerns, the Court decided to grant a subpoena for Dr. Perlin and the source code. Dr. Perlin did bring a copy of the code to California, but before it was turned over to the defense lawyers from Cybergenetics and the prosecution wanted TrueAllele recognized as a trade secret so that a protective order could be granted.[121] The protective order was granted in order to limit exposure at trial, but the prosecution still refused to turn over the source code. Therefore, the trial judge excluded the TrueAllele results citing Chubb's inability to confront the evidence at trial.[122] The prosecution then sought a writ of mandate to vacate the trial court ruling that the source code must be disclosed.[123]

California does have procedure in its evidence code for the disclosure of trade secrets at trial.[124] First, the party seeking protection must make a showing that there is in fact a trade secret. After that burden is satisfied, the other party must then show the necessity for disclosure at trial.[125] The issue of a trade secret was not in contention, so analysis focused on the necessity of disclosure. Chubbs submitted declarations from defense experts stating that the source code was essential to his defense.[126] He also relied on the fact that TrueAllele's DNA analysis was the only evidence that connected Chubbs to the victim.[127] However, the Appellate Court held that Chubbs did not make a sufficient showing that the code was necessary. The court found that the initial discovery material provided (the articles, TrueAllele manual, etc.) was sufficient for the

[121] *Id* at 11-12.
[122] *Id*.
[123] *Id*.
[124] *See* Cal. Evid. Code § 1060.
[125] *People v. Superior Court*, 2015 Cal. App. Unpub. LEXIS 105, at 14 (Jan. 9, 2015).
[126] *Id* at 24-25
[127] *Id*.

defense.[128] Additionally, the Court found that Chubbs did not make any showing on how access to the code would allow the defense to better challenge the program. For the court, the defense's mention of TrueAllele's reliance on likelihood ratios and probability undermined their own argument and demonstrated that they already understood how the program worked.[129] Therefore, the writ was issued, and the trial court could not compel disclosure of the source code.

This was one of the first instances where TrueAllele was almost compelled to disclose its code. Yet even when the TrueAllele analysis was the only evidence connecting the defendant to the scene of the crime, the court still found that the disclosure was unnecessary. However, the California framework for analysis provides a more comprehensive analysis than other jurisdictions. At the very least, it outlines the way that defendants can overcome a proprietary black box such as TrueAllele in the correct circumstances. Currently, it is unclear what facts would be needed show that disclosure was necessary. The most likely scenario would be one in which an error was uncovered in TrueAllele's programming. However, this fact would be difficult to uncover if only Cybergenetics and a few other labs are the only ones with access to the program's code. Another scenario might involve a vast discrepancy in two different computers running the same TrueAllele program. However, a case with these facts is yet to be presented.

V. Conclusion

TrueAllele's acceptance as reliable evidence in criminal cases was rushed. The first trial where it was used, *Foley*, did not even require a *Daubert* or *Frye* hearing before admitting this new type of analysis made by a computer. Even in jurisdictions where *Daubert* hearings were

[128] Id at 32.
[129] Id at 29.

conducted, there was little concern about the novelty of TrueAllele even though nobody outside Cybergeneitcs had seen the code. Even the validation studies presented to demonstrate reliability were mostly authored by Dr. Perlin, the program's creator. Questions also remain about the limitations of the program and when it can produce accurate results. This is not to say that TrueAllele is always unreliable or cannot be an important tool in the future. However, there should be more consideration before admitting the program's findings. TrueAllele is new technology that should be subject to thorough review and validation just like other new forms of expert testimony. TrueAllele also presents further challenges for defendants at trial. Defense attorneys will have to find new experts who have the credentials to challenge TrueAllele's computer programming and statistics as well as its DNA analysis. Defendants should also be allowed greater accessibility to the program so that they can better confront the evidence against them at trial. As technology continues becoming a greater part of all facets of life, implementation of that technology will continue to be a challenge in DNA analysis and other areas. It shows great promise for the future, but caution should be used when weighing admissibility in order to ensure defendants' rights are not trampled.