Texas Forensic Science Commission

Justice Through Science

FINAL REPORT ON COMPLAINT NO. 21.54 JAMES SMILEY (SIGNATURE SCIENCE, LLC; FORENSIC BIOLOGY/DNA)

April 22, 2022

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I. COMMISSION BACKGROUND

A. History and Mission of the Texas Forensic Science Commission

The Texas Forensic Science Commission ("Commission") was created during the 79th Legislative Session in 2005 with the passage of HB-1068. The Act amended the Code of Criminal Procedure to add Article 38.01, which describes the composition and authority of the Commission.[1] During subsequent legislative sessions, the Texas Legislature further amended the Code of Criminal Procedure to clarify and expand the Commission's jurisdictional responsibilities and authority.[2]

The Commission has nine members appointed by the Governor of Texas.[3] Seven of the nine commissioners are scientists or medical doctors and two are attorneys (one prosecutor nominated by the Texas District and County Attorney's Association and one criminal defense attorney nominated by the Texas Criminal Defense Lawyer's Association).[4] The Commission's Presiding Officer is Jeffrey Barnard, M.D. Dr. Barnard is the Chief Medical Examiner of Dallas County and Director of the Southwestern Institute of Forensic Sciences in Dallas.

B. Investigation of Complaints and Self-Disclosures

Texas law requires the Commission to "investigate, in a timely manner, any allegation of professional negligence or professional misconduct that would substantially affect the integrity of the results of a forensic analysis conducted by crime laboratory."[5] The Act also requires the Commission to: (1) develop and implement a reporting system through which a crime laboratory must report professional negligence or professional misconduct; and (2) require crime laboratories

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[1] *See*, Act of May 30, 2005, 79th Leg., R.S., ch. 1224, § 1 (2005).
[2] *See e.g.*, Acts 2013, 83rd Leg. ch. 782 (S.B. 1238) §§ 1-4 (2013); Acts 2015, 84th Leg. ch. 1276 (S.B. 1287) §§ 1-7 (2015); TEX. CODE CRIM. PROC. art 38.01 § 4-a(b).
[3] TEX. CODE OF CRIM. PROC. art. 38.01 § 3.
[4] *Id.*
[5] TEX. CODE CRIM. PROC. art. 38.01 § 4(a)(3).

that conduct forensic analyses to report professional negligence or professional misconduct to the Commission.[6]

The Commission's administrative rules set forth the process by which it determines whether to accept a complaint or self-disclosure for investigation as well as the process used to conduct the investigation.[7] The ultimate result is the issuance of a final report. The rules also include the process for appealing final investigative reports by the Commission and, separately, disciplinary actions by the Commission against a license holder or applicant.[8]

C. Laboratory Accreditation

The Texas Code of Criminal Procedure prohibits forensic analysis from being admitted in criminal cases if the crime laboratory conducting the analysis is not accredited by the Commission.[9] The term "forensic analysis" is defined as follows:

> "Forensic analysis" means a medical, chemical, toxicological, ballistic, or other expert examination or test performed on physical evidence, including DNA evidence, for the purpose of determining the connection of the evidence to a criminal action (except that the term does not include the portion of an autopsy conducted by a medical examiner or other forensic pathologist who is a licensed physician).[10]

The term "crime laboratory" includes a public or private laboratory or other entity that conducts a forensic analysis subject to Article 38.35 of the Texas Code of Criminal Procedure.[11] As part of its accreditation authority, the Commission may establish minimum standards relating to the timely production of forensic analysis; validate or approve specific forensic methods or methodologies;

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[6] *Id.* at § 4(a)(1)-(2) (2019). Additionally, pursuant to the Forensic Analyst Licensing Program Code of Professional Responsibility, members of crime lab management shall make timely and full disclosure to the Texas Forensic Science Commission of any non-conformance that may rise to the level of professional negligence or professional misconduct. See, 37 Tex. Admin. Code § 651.219(c)(5) (2018).
[7] *See*, 37 Tex. Admin. Code § 651.304-307 (2019).
[8] 37 Tex. Admin. Code § 651.309; *Id.* at § 651.216.
[9] TEX. CODE CRIM. PROC. art. 38.35 § (d)(1).
[10] TEX. CODE CRIM. PROC. art. 38.01 § 2(4).
[11] TEX. CODE CRIM. PROC. art. 38.35 § (a)(1).

and establish procedures, policies, and practices to improve the quality of forensic analysis in the state.[12] The Commission is permitted, at any reasonable time, to enter and inspect the premises or audit the records, reports, or other quality assurance matters of a crime laboratory that is accredited.[13]

D. Forensic Analyst Licensing

The Texas Code of Criminal Procedure requires the Commission to administer a forensic analyst licensing program by: (1) establishing the qualifications for a license; (2) setting fees for the issuance and renewal of a license; and (3) establishing the term of a forensic analyst license.[14] The licensing requirement applies to any "person who on behalf of a crime laboratory [accredited by the Commission] technically reviews or performs a forensic analysis or draws conclusions from or interprets a forensic analysis for a court or crime laboratory.[15] The licensing program took effect on January 1, 2019.[16]

The Commission is also required to maintain a Code of Professional Responsibility for Forensic Analysts and Crime Laboratory Management.[17] Pursuant to its licensing authority, the Commission may take disciplinary action against a license holder or applicant on a determination by the Commission that a license holder or applicant has committed professional misconduct or has violated Texas Code of Criminal Procedure Article 38.01 or an administrative rule or other order by the Commission.[18] If the Commission determines a license holder has committed professional misconduct or has violated an administrative rule or order by the Commission, the

[12] TEX. CODE CRIM. PROC. art. 38.01 § 4-d (b-1).
[13] TEX. CODE CRIM. PROC. art. 38.01 § 4-d(d).
[14] TEX. CODE CRIM. PROC. art. 38.01 § 4-a(d).
[15] TEX. CODE CRIM. PROC. art. 38.01 § 4-a(a)(2).
[16] *Id.* at § 4-a(b).
[17] *See*, Tex. Admin. Code § 651.219 (2020).
[18] TEX. CODE CRIM. PROC. art. 38.01 §4-c; 37 Tex. Admin Code § 651.216(b) (2019).

Commission may, (1) revoke or suspend the person's license; (2) refuse to renew the person's license; (3) reprimand the license holder; or (4) deny the person a license.[19]

E. Jurisdiction Applicable to this Complaint

The forensic discipline discussed in this final investigative report (DNA analysis) is subject to both laboratory accreditation and forensic analyst licensing requirements. Signature Science, LLC ("SigSci"), the laboratory that performed the forensic analysis in this case, is accredited by the Commission and the ANSI National Accreditation Board ("ANAB") under International Organization for Standardization ("ISO") accreditation standard 17025: 2017.[20] The DNA analyst who conducted the DNA mixture interpretation (Jamie Haas) holds a forensic analyst license in good standing.

F. Limitations of this Report

The Commission's authority contains important statutory limitations. For example, no finding by the Commission constitutes a comment upon the guilt or innocence of any individual.[21] The Commission's written reports are not admissible in civil or criminal actions.[22] The Commission has no authority to subpoena documents or testimony. The information gathered for this report was not subject to the standards for admission of evidence in a courtroom. No individual testified under oath, was limited by either the Texas or Federal Rules of Evidence (*e.g.*, against the admission of hearsay) or was subject to cross-examination under a judge's supervision.

[19] *Id.* at § 651.216(b)(1)-(4).
[20] *See*, http://www.txcourts.gov/fsc/accreditation/ for a list of accredited labs.
[21] *Id*. at § 4(g).
[22] *Id*. at § 11.

II. SUMMARY OF THE COMPLAINT

On September 8, 2021, James Smiley filed a complaint regarding the DNA analysis performed in his criminal case. Official records show Smiley pled guilty to two counts of sexual assault on January 5, 2021 and was sentenced to two years confinement. Smiley alleges: (1) he was wrongfully convicted; (2) the prosecution withheld evidence; (3) an unlicensed person performed forensic analysis in his case; (4) the laboratory was not functioning up to standards; (5) and the laboratory DNA reports are fraudulent and unreliable.

The complaint asserts the Austin Police Department Forensic Science Bureau ("APDFSB") performed the forensic analysis. Commission staff obtained the relevant laboratory reports and determined SigSci conducted the forensic analysis pursuant to an outsourcing agreement with APDFSB.

Several allegations in the complaint are outside the Commission's jurisdiction including claims of wrongful conviction, the disclosure obligations of prosecutors, and a request for retesting of certain evidence. Staff referred those matters to the Travis County District Attorney's Office (TCDAO). Staff also determined that one of the individuals who appeared in the case record submitted a marital name change; she was licensed by the Commission under a different name at the time the analysis in the case was performed. Thus, Smiley's allegation that an unlicensed person performed testing in his case is unfounded.

III. INVESTIGATIVE PROCESS

At its October 22, 2021, quarterly meeting, the Commission voted to form an investigative panel ("Panel") to assist in determining whether the allegations in the complaint are supported by the facts and circumstances, available data, and related documents. The Panel includes Bruce Budowle, Ph.D., Michael Coble, Ph.D., and Mark Daniel, Esq.

A. Document Review and Interviews

Once an investigative panel is created, the Commission investigation may include: (1) relevant document review; (2) interviews with members of the laboratory as needed to assess the facts and issues raised; (3) collaboration with the accrediting body and any other relevant agency; (4) requests for follow-up information as necessary; (5) retention of subject matter experts where necessary; and (6) any other steps needed to meet the Commission's statutory obligation.[23]

Commission staff reviewed relevant documents and spoke with the DNA analyst and DNA technical leader. Staff also communicated with representatives from the Travis County District Attorney's Office including the Assistant District Attorney who was assigned to the case.

IV. OBSERVATIONS AND FINDINGS

A. 2019 Manual Mixture Interpretation Results: Unsuitable for Comparison

The evidence submitted by law enforcement for testing in this case consisted of a tank top and underwear belonging to the sexual assault survivor, along with the relevant known DNA standards. Initially, Smiley's known standard was subjected to Y-STR testing for comparison in an unrelated case. SigSci reported the Y-STR results on January 17, 2019.

On April 29, 2019, SigSci issued a report stating semen was identified, and a presumptive test for blood on the underwear was positive. Also on April 29, 2019, SigSci reported a cutting from the crotch of the underwear was subjected to STR testing and compared to the known standards of Smiley and the survivor. DNA was extracted from the underwear cutting using a two-step method that attempts first to recover DNA from the non-sperm cells (designated EF) and second to recover DNA from the sperm cells (designated SF). The report states the following:

- Item 2.1-SF (Sperm cell fraction): The DNA profile obtained from this item is a **mixture of at least four individuals** with at least one male contributor. This

[23] 37 Tex. Admin. Code § 651.307 (2020).

mixture is potentially incomplete and is not suitable for comparison to known reference samples: therefore, no further conclusions can be made.

- Item 2-1-EF: (Non-sperm cell fraction): The DNA profile obtained from this item is a **mixture of at least three individuals** with at least one male contributor. This mixture is potentially incomplete and is not suitable for comparisons to known reference samples: therefore, no further conclusions can be made.

The April 29, 2019, DNA report also contained the following language:

- "The interpretation of DNA profiles (Item 2-1-SF and Item 2.1-EF) in this case may be aided by probabilistic genotyping software which SigSci LLC is in the process of validating. Should you require further analysis of these profiles utilizing probabilistic genotyping, please contact this laboratory.

- "Y-STR testing could provide additional information for Item 2-1-SF and 2-1-EF."

The report included an allele table related to the evidentiary items, the known standard of the survivor, and the known standard of the defendant.

B. 2020 STRmix™ Reinterpretation: Smiley Excluded

On June 25, 2020, APDFSB contacted SigSci with a request for reinterpretation using probabilistic genotyping software. Internal email communications provided by TCDAO indicate the request was initiated by the Austin Police Department after discussions regarding additional testing with the Assistant District Attorney assigned to the case.

On August 17, 2020, SigSci reported the STR results and conclusions after data re-interpretation utilizing STRmix™ probabilistic genotyping software on the DNA profiles previously obtained from items 2-1-EF/SF and a comparison to the results previously obtained from the known standards of the survivor and the defendant. SigSci reported:

- Item 2.1-SF (Sperm cell Fraction): The DNA profile previously obtained from this item was interpreted as a **mixture of four individuals** with at least one male contributor and with [the survivor] as an assumed contributor. **James Smiley is excluded** as a contributor to this profile.

- Item 2-1-EF (Non-sperm cell fraction): The DNA profile previously obtained from this item was interpreted as a **mixture of three individuals** with at least one male

contributor and with the survivor as an assumed contributor. **James Smiley is excluded** as a contributor to this profile.

V. COMPLEX DNA MIXTURE INTERPRETATION

The primary role of a DNA analyst in a forensic laboratory is to review and interpret data obtained from known and evidentiary samples generated by polymerase chain reaction (PCR) amplification of short tandem repeat (STR) markers typed via capillary electrophoresis (CE). Based on the data that emerge from the DNA testing process, the analyst then provides information to the trier of fact regarding the potential association between a person of interest's DNA profile and the DNA profile extracted from the evidentiary item(s). A degree of subjective interpretation has always been present when analyzing DNA profiles containing multiple contributors (*i.e.,* a DNA mixture) and deciding which loci and/or alleles at a locus to include in statistical analysis, as well as what statistical weight to afford an association (if any).

To address these challenges, forensic DNA analysts must have extensive expertise in the principles of profile interpretation and an appreciation for the complexity of the samples and the possibility of missing data (allele dropout and other stochastic effects). The issue becomes even more pronounced as the number of contributors increases in a mixture and the quality of the profile decreases (due to low amounts of DNA, DNA degradation, PCR inhibition, etc.).

As technology evolved over time to detect smaller and smaller amounts of DNA, the data generated has also become increasingly more complex, posing significant challenges in interpretation. In response, many laboratories within the forensic DNA community have transitioned (or are in the process of transitioning) to probabilistic genotyping software systems which use biological modeling and statistical theory to weigh probable genotype combinations

from DNA typing results and assign likelihood ratios.[24] Probabilistic genotyping software, when properly utilized, is better equipped to interpret complex DNA mixture data reliably and accurately than manual methods. It is important to note, as with any technology, that probabilistic genotyping systems have limitations that must be properly understood to guard against misinterpretation or overstatement.

The Commission accepted Mr. Smiley's complaint for investigation because the reported results related to the DNA profile obtained from the evidentiary items changed from "not suitable for comparison" to an *exclusion* of Smiley as a possible contributor after STRmix™ reinterpretation. The Commission seeks to determine whether SigSci's initial "not suitable for comparison" conclusion was supported by the data generated at the time. The Commission further seeks to reinforce what should be a commonly accepted principle among the forensic DNA community. Even when a DNA mixture does not lend itself to interpretation under the laboratory's standard operating procedure due to its complexity, the mixture should still be assessed for exclusionary purposes. Failure to assess mixture data for exclusionary purposes may result in a laboratory possessing but not communicating exculpatory information to the trier of fact, which risks depriving the parties of the opportunity to make important decisions about the criminal action with the best available information.

A. The Murder of Aaron Scheerhoorn and Wrongful Conviction of Lydell Grant

In the late hours of December 10, 2010, Aaron Scheerhoorn banged on the door of a nightclub in Houston, screaming for help and opening his shirt to show that he had been stabbed. A man was chasing him and continued to stab him in the presence of several witnesses. Scheerhoorn later died from his wounds. Six out of the seven witnesses identified Lydell Grant as

[24] *See generally*, DNA Mixture Interpretation: A NIST Foundational Review 2.4.3 (draft report 2022).

the person who stabbed Scheerhoorn. Grant was convicted of murder and sentenced to life in prison.[25]

At trial, a DNA analyst from the Houston Police Department Crime Laboratory testified that she had performed DNA analysis of the victim's fingernails collected during autopsy. The analyst performed DNA testing on the right fingernail scrapings/clippings and obtained a mixture of DNA from at least two individuals. The victim could not be excluded as a contributor to the major component of the mixture. The report, which was introduced at trial, stated the following:

> "No conclusions will be made regarding Lydell Grant as a possible contributor to this DNA mixture."

During her testimony, the DNA analyst explained that this reported conclusion meant she was "not able to make a clear determination if [Lydell Grant] was a contributing individual to that mixture." She testified initially that she "could not make a conclusion." However, the prosecutor followed with this question:

> Q: "So in that circumstance, you could not exclude [Lydell Grant] as a possible contributor to that DNA?"
>
> A. "Correct."
>
> [Volume 5; p. 254]

On cross-examination, the defense attorney briefly explored the reported conclusions related to the fingernail scraping in the following dialogue:

> A. "[The victim] was a major contributor [to the mixture obtained from the fingernail], yes.
>
> Q. You can't make any conclusions about the other contributor, is that right?
>
> A. Correct.
>
> Q. So, you can't associate Lydell Grant with—as being part of that mixture; is that correct?

[25] *Grant v. State*, 2014 Tex. App. 3516 (Tex. App. - Houston [1st Dist.] 2014).

A. Correct, I could not make any conclusions."

[Vol. 5; p. 256-257]

While incarcerated, Grant sought assistance from the Innocence Project of Texas (IPTX). IPTX accepted Grant's case and retained an expert to review the DNA mixture results. IPTX asserted that Grant *should have been excluded* as a contributor to the DNA mixture recovered from the fingernail scrapings of the victim. IPTX also asserted there was an unknown (foreign) male profile present that was not associated with the known DNA profile of Grant or the victim. Commissioners Bruce Budowle and Michael Coble reviewed the same information and reached the same conclusion; sufficient data were present to exclude Grant at the time of original analysis but the DNA analyst failed to do so.

IPTX also sought assistance from Cybergenetics, the creator of TrueAllele® probabilistic genotyping software. TrueAllele® analysis of the DNA mixture from the fingernail scraping of the victim definitively excluded Grant as a contributor and confirmed the presence of an unknown male profile. The unknown male profile was uploaded to CODIS under a cooperative agreement between Cybergenetics and a law enforcement crime laboratory in South Carolina. The CODIS search resulted in a hit to Jermarico Carter, a known offender. After a joint investigation by the Houston Police Department and law enforcement agencies in Georgia, Carter was arrested. Once in custody, he made statements to the police implicating himself in Scheerhoorn's murder.

On May 19, 2021, the Texas Court of Criminal Appeals found Lydell Grant "actually innocent" of the murder of Aaron Scheerhoorn.[26]

[26] *Ex parte Grant*, 622 S.W.3d (Tex. Cr. App. 2021).

B. Gap Between Historical Laboratory Practice and Published Literature

The probabilistic genotyping results in Lydell Grant's case highlight a common historic practice among forensic DNA laboratories when performing manual mixture interpretation. If the DNA analyst, following the laboratory's written protocol, determined a mixture profile was too complex to interpret, the analyst would simply "INC" the profile (*i.e.,* call it inconclusive or uninterpretable) without taking the additional step of assessing the data for exclusionary purposes. Reporting an inconclusive result for a complex mixture was viewed by many in the forensic DNA community as a "conservative approach" that supported the community's collective desire to avoid erroneous inclusions. While in many cases this "conservative approach" was an appropriate restraint given the complexity of the data and the risk of misinterpretation, there is nothing "conservative" about masking clearly exculpatory data with an inconclusive finding. For cases interpreted manually, the risk of unintentionally holding exculpatory information is present for all otherwise uninterpretable mixtures *unless* the analyst conducts a proactive assessment of the profile data for exclusionary purposes.

One of the factors that may contribute to a hesitancy among DNA analysts to perform any comparison once a mixture is deemed too complex to interpret is the longstanding admonishment that DNA analysts refrain from "suspect driven" bias. Profile interpretation is considered "suspect driven" when the analyst, for example, decides whether a locus should be used for statistical calculation based on the alleles observed in the known profile, rather than determining *a priori* which loci have a low probability of allele dropout. This practice was problematic historically because in some cases it biased the interpretation toward a higher statistical association than would be warranted had the evidentiary data been evaluated independently. Against this backdrop, it is

understandable why DNA analysts hesitate to do anything with a profile once the mixture is designated as indistinguishable.

However, the hesitancy to proceed carries significant risk that a laboratory will inadvertently fail to communicate exculpatory information to stakeholders. Once a DNA analyst evaluates a mixture profile and determines it is too complex to deconvolute based on the number of contributors, the quality of the DNA or other factors, the analyst has performed the required *a priori* assessment. While the quantity of DNA contributed by each individual may be so close as to prevent the analyst from determining which of the allele pairings represent which contributors at a given locus, the analyst may still be able to conclude that given the assessed number of contributors and the totality of the observed alleles, it is not possible for the person of interest to be a contributor. In such a situation, the data support an exclusionary result, and the laboratory has an obligation to ensure this information is communicated so that affected stakeholders may evaluate any potential impact on the criminal case.

Published literature in the area of DNA mixture interpretation has long emphasized the need for DNA analysts to inspect otherwise uninterpretable mixture profiles for exclusionary data. For example, in a 2016 paper providing instruction to the forensic DNA community on mixture interpretation using the Combined Probability of Inclusion (CPI), Bieber, et al. offered the following guidance:

> Once the mixture has been evaluated, both the qualified and unqualified loci should be inspected for potential exclusionary evidence. For the qualified loci, exclusionary evidence may be based on the absence of alleles or the absence of deconvoluted genotypes in the mixture compared with those of the known reference profile. If the deconvoluted genotypes of the mixture are

> different from the genotype of the known comparison profiles, then an exclusion interpretation is supported.[27]

What is particularly noteworthy about this scientific paper is that the authors collaborated on the manuscript *for the express purpose* of providing clear guidance regarding mixture interpretation to DNA analysts *before* most labs had transitioned to probabilistic genotyping. The Commission paid to have this paper included in an open access journal so that all DNA analysts could readily view and download the paper at no cost.

Well before the 2016 Bieber, et al. paper, scientific literature on DNA mixture interpretation emphasized the principle that analysts should include a step to evaluate the profile for exclusionary data even when the mixture is otherwise uninterpretable. For example, the authors of a 2009 paper on DNA mixture interpretation published in the Journal of Forensic Sciences offered the following:

> While every effort should be made to reliably draw typing information from mixed samples, some mixtures…may not lend themselves to interpretation using a laboratory's prescribed procedures. Although not always, these tend to be three or more person mixtures where quantitative deconvolution becomes more complex…. Alternatively, at times and depending on the complexity, such mixtures may yield DNA typing information only for exclusionary purposes….
>
> An example statement can be:
>
> The STR typing results for specimen Q1 indicate the presence of DNA from three or more individuals. The DNA profile obtained from specimen Q1 does not satisfy the Laboratory's inclusionary reporting criteria and therefore may be utilized only for exclusionary purposes. Based upon the STR typing results, specimen K1 is

[27] Bieber et al., F.R., Buckleton, J.S., Budowle, B., Butler, J.M., & Coble, M.D. 2016. Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion. *BMC Genetics*, 17:(1), 125 (2016).

excluded as a potential contributor to the mixture of DNA obtained from specimen Q1.[28]

C. Why Smiley Should Have Been Excluded Even Without STRmix™

SigSci's standard operating procedures allow for an exclusionary interpretation where the evidence and reference sample(s) have different genotypes at some or every locus interpreted and/or the reference sample contains alleles that are not observed in the evidence, and the unobserved alleles cannot be due to degradation/inhibition within the evidentiary sample.[29] However, the protocol does not direct the analyst to inspect the profile for exclusionary data after identifying the mixture as too complex for interpretation.

The analyst in this case did not take the additional step of assessing the DNA profile obtained from a cutting of the survivor's underwear for exclusionary purposes once she deemed it an uninterpretable mixture. If the analyst had, she would have observed data supporting exclusion. For example, the data observed at the SE33 locus include seven alleles from the SF fraction. An additional allele (not attributable to the victim) is observed from the EF fraction. Smiley does not have any of these eight alleles. Under the presumption of four contributors to the evidentiary sample (note this was also the number of contributors in the STRmix™ reinterpretation) Smiley is unequivocally excluded. With four contributors to a mixture, the maximum number of alleles that could be observed is eight. If one were to invoke a post-hoc explanation that assumes more than four contributors, the mixture should not have been entered into STRmix™ under SigSci's SOP, as the software has not been validated for more than four contributors.

[28] Budowle, B., Onorato, A.J., Callaghan, T.F., Manna, A.D., Gross, A.M., Guerreri, R.A., . . . McClure, D.L. 2009. Mixture Interpretation: Defining the Relevant Features for Guidelines for the Assessment of Mixed DNA Profiles in Forensic Casework, *J. Forensic Sci.* Vol. 54, No. 3 (2009).
[29] FDSOP-19, Version 11, Effective Date: 19 December 2017 at 25.

In performing an introspective review of the manual interpretation, it is important to note that the STRmix™ results excluding Smiley are intuitively supported. When conditioned on the female survivor's known profile, and compared to Smiley's known profile, 13/20 loci returned likelihood ratios less than one. Even disregarding locus SE33, which returned a likelihood ratio of zero, the evidence favors the explanation that the contributors to the mixture include the female alleging sexual assault plus three unknown contributors *over* the alternative explanation that the contributors to the mixture include the female survivor plus Smiley and two unknown contributors *by a factor of 46 billion*. These data clearly favor exclusion of Smiley and should be conveyed as such to relevant stakeholders in the criminal justice system.

D. Evaluation of Professional Negligence or Misconduct

When the Commission accepts a complaint involving an accredited discipline like DNA analysis, Texas law requires that the investigative report describe whether professional negligence or misconduct occurred in the case under review.[30] Neither "professional negligence" nor "professional misconduct" is defined by statute. The Commission has defined both terms in its administrative rules.

Professional Misconduct means:

> The forensic analyst or crime laboratory, through a material act or omission, deliberately failed to follow a standard of practice that an ordinary forensic analyst or crime laboratory would have followed, and the deliberate act or omission would substantially affect the integrity of the results of a forensic analysis. An act or omission was deliberate if the forensic analyst or crime laboratory was aware of and consciously disregarded an accepted standard of practice.[31]

Professional Negligence means:

> The forensic analyst or crime laboratory, through a material act or omission, negligently failed to follow the standard of practice that

[30] Tex. Code Crim. Proc. art. 38.01 §4(b)(1)(B).
[31] 37 Tex. Admin. Code § 651.302(7) (2020).

> an ordinary forensic analyst or crime laboratory would have followed, and the negligent act or omission would substantially affect the integrity of the results of a forensic analysis. An act or omission was negligent if the forensic analyst or crime laboratory should have been but was not aware of an accepted standard of practice.[32]

There is no evidence to support a finding of professional misconduct in this case.

Assessing professional negligence is difficult because it is a context-driven analysis that depends on the weight afforded to various factors. The Commission recognizes the criminal justice system is not well-served by punitive oversight that discourages analysts from admitting mistakes for fear of adverse consequences. A professional negligence assessment necessarily requires the Commission to determine whether there was an "accepted standard of practice" that the analyst should have followed but did not. In forensic laboratories, the main resource guiding analytical activities is the laboratory's standard operating procedure. In this case, the analyst followed the laboratory protocol which indicated that indistinguishable mixtures of four or more contributors should be designated as too complex for comparison. The protocol did not direct the analyst to inspect an indistinguishable mixture for exclusionary data.

SigSci is far from alone in its omission of an exclusionary assessment step for otherwise uninterpretable mixtures. If the Commission were to issue a finding of professional negligence against the DNA analyst in this case, the same finding would apply to countless other laboratories and DNA analysts across the country. In light of these observations, the Commission concludes that a finding of professional negligence against the DNA analyst is not supported.

However, the Commission is cognizant of the gap between the principles stated in published scientific literature and implementation of the concepts in many operational laboratories. This gap is a troubling phenomenon that exists in many forensic disciplines. The forensic DNA

[32] *Id* at § 651.302(8).

community has a responsibility to ensure the information contained in scientific literature is well understood by all practitioners. As set forth in the Code of Professional Responsibility for Forensic Analysts and Crime Laboratory Management adopted after SigSci's manual DNA mixture procedure was developed, crime laboratories and forensic analysts must commit to continuous learning in the forensic discipline and stay abreast of the scientific literature to maintain professional competency.[33]

E. Exclusion Assessment Step in Otherwise Uninterpretable DNA Mixtures

There are two foundational concepts DNA analysts must master to perform an assessment for exclusionary purposes of otherwise uninterpretable data. Understanding these concepts is essential *even after* the laboratory transitions to probabilistic genotyping, as one cannot critically evaluate the STRmix™ output without them.[34]

First, the analyst must know how to properly assign the number of contributors to a mixture and understand the limitations and/or risks associated with under- or over-estimating the number of contributors.[35] Second, the analyst must be able to consider the potential genotypes for each locus in deciding whether an exclusion is supported. Simplistic allele matching with no consideration of potential genotypes given the totality of the profile risks impacting accurate and robust interpretation. A DNA analyst may conclude a DNA mixture is unsuitable for interpretation due to the fact that similar amounts of DNA were contributed to the evidentiary sample by multiple donors, and the alleles detected cannot be attributed unequivocally to a single source(s). Even in such a case, the analyst should still proceed to assess the data for exclusionary purposes.

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[33] 37 Tex. Admin. Code § 651.219(b)(2) (2020).
[34] For a guide to understanding DNA mixture interpretation using probabilistic genotyping and likelihood ratios, *see* JO-ANNE BRIGHT & MICHAEL COBLE, FORENSIC DNA PROFILING: A PRACTICAL GUIDE TO ASSIGNING LIKELIHOOD RATIOS (2020).
[35] *Id.* at 177-179, discussing the effect of the misassignment of the number of contributors on resulting likelihood ratios.

Depending on the DNA profile, an exclusionary interpretation may be based on the non-observance of alleles or deconvoluted genotypes in the mixture at informative loci in comparison with the genotypes of the known reference profile of the person of interest. If the deconvoluted genotypes of the mixture are different from the genotype of the known comparison profiles, then an exclusion interpretation may be supported. While one may consider using the person of interest's profile to conduct an assessment for exclusionary purposes as a form of suspect-driven bias, this criticism should be rejected because the risk of sitting on clearly exculpatory data (as in the Smiley and Grant examples) far outweighs concerns about using the known profile at this final stage of interpretation.

Data evaluation for exclusionary purposes must take into account the molecular weight of each locus as needed to determine whether the data support exclusion. Foundational concepts must be considered, such as the fact that lower molecular weight markers tend to amplify better with degraded DNA than higher molecular weight markers. If, for example, a DNA analyst observes alleles and genotypes at lower molecular weight markers that cannot be explained by the person of interest, there may be support for an exclusion. A failure to exclude based upon the rationale that a person of interest's alleles "must have dropped out" at a low molecular weight marker is not supported just because the person of interest's allele(s) were observed at higher molecular weight markers. Allele dropout due to degradation does not increase from large to small size molecular weight markers.

VI. RECOMMENDATIONS

The recommendations in this section apply to SigSci as well as any other Texas laboratory whose manual DNA mixture interpretation approach omits an exclusion assessment step for otherwise uninterpretable DNA mixtures.

1) Any laboratory that has not included an exclusion assessment step in its manual mixture interpretation protocol should be willing to reinterpret previously reported inconclusive mixtures upon request.

2) Any laboratory that currently performs manual mixture interpretation should ensure its DNA mixture interpretation protocol includes sufficient conceptual guidance regarding how to assess uninterpretable mixtures for exclusionary purposes. The guidance should be based on information contained in published scientific literature. Texas laboratories may seek feedback from the Commission on these protocols.

3) All laboratories should ensure their analysts understand factors to consider in assessing otherwise uninterpretable mixtures for exclusionary purposes discussed in Section V above. Additional training should be provided as necessary to establish competency.

4) All analysts should review and understand the scientific literature cited in this report, regardless of whether the laboratory has transitioned to probabilistic genotyping.