IN THE UNITED STATES COURT OF APPEALS
FOR THE ARMED FORCES

U N I T E D S T A T E S, Appellee	)	APPELLEE'S ANSWER TO APPELLANT'S PETITION FOR GRANT OF REVIEW
v.	)	
Major (O-4) **ANTIWAN M. HENNING,** United States Army, Appellant	)	Crim. App. Dkt. No. 20150410 USCA Dkt. No. 16-0026/AR

JIHAN WALKER
Captain, Judge Advocate
Branch Chief, Government
Appellate Division
U.S. Army Legal Services Agency
9275 Gunston Road
Fort Belvoir, VA 22060
(703) 693-0783
jihan.e.walker.mil@mail.mil
U.S.C.A.A.F. Bar No. 36340
Lead Counsel for Appellee

DANIEL D. DERNER
Major, U.S. Army
Acting Deputy Chief, Government
Appellate Division
U.S.C.A.A.F. Bar No. 36331

Index of Brief

Table of Cases and Other Authorities.....iii

Issue Presented.....ii, 1

WHETHER THE ARMY COURT APPLIED THE WRONG STANDARD OF REVIEW TO THIS ARTICLE 62, UCMJ, APPEAL WHEN IT FOUND THE MILITARY JUDGE MADE ERRONEOUS FINDINGS OF FACT AND ERRONEOUS CNOCLUSIONS OF LAW.

Statement of Statutory Jurisdiction.....1

Statement of the Case.....2

Statement of Facts.....2

Summary of the Argument.....10

Standard of Review.....10

Law and Argument.....10

A. The CCA applied the correct standard of review in this case.....11

B. The military judge made several clearly erroneous findings of fact.....16

C. The military judge unreasonably applied the law to the facts in this case by impermissibly usurping the factfinder's role.....22

D. The military judge unreasonably applied the law to the facts because the probative value of the DNA evidence was not substantially outweighed by unfair prejudice.....29

Conclusion.....35

Certificate of Compliance.....36

Table of Cases and Other Authorities

Supreme Court of the United States

Daubert v. Merrell Dow Pharms., 509 U.S. 579 (1993).....*passim*

GE v. Joiner, 522 U.S. 136 (1997).....22

Kumho Tire Co. v. Carmichael, 526 U.S. 137 (1999).....29

United States Court of Appeals for the Armed Forces

United States v. Ashby, 68 M.J. 108 (C.A.A.F. 2007).....35

United States v. Baker, 70 M.J. 283 (C.A.A.F. 2011).....15

United States v. Billings, 61 M.J. 163 (C.A.A.F. 2005).....22

United States v. Buford, 74 M.J. 98 (C.A.A.F. 2015).....10, 12

United States v. Cossio, 64 M.J. 254 (C.A.A.F. 2007)....12-13, 15

United States v. Ellis, 68 M.J. 341 (C.A.A.F. 2010).....12

United States v. Flesher, 73 M.J. 303 (C.A.A.F. 2014).....12, 14

United States v. Griffin, 50 M.J. 278 (C.A.A.F. 1999).....14

United States v. Houser, 36 M.J. 392 (C.M.A. 1993).....14, 30

United States v. Kaspers, 47 M.J. 176 (C.A.A.F. 1997).....22, 24

United States v. Marks, 35 M.J. 64 (C.M.A. 1992).....32

United States v. Nimmer, 43 M.J. 252 (C.A.A.F. 1995).....28

United States v. Sanchez, 65 M.J. 145 (C.A.A.F. 2007).....
.....11, 22, 31

United States v. Stellato, __ M.J. __ (C.A.A.F. 20 Aug. 2015)....
.....15

United States v. Youngberg, 43 M.J. 379 (C.A.A.F. 1995)....27, 29

Service Courts

United States v. Bell, 72 M.J. 543 (Army Ct. Crim. App. 2013)....29

United States v. Henning, ARMY 20150410, 2015 CCA LEXIS 376 (Army Ct. Crim. App. 2015).....*passim*

United States v. Teeter, 12 M.J. 716 (A.C.M.R. 1981).....31

United States Courts of Appeals and District Courts

Amorgianos v. Amtrak, 303 F.3d 256 (2d Cir. 2002).....31

United States v. Chischilly, 30 F.3d 1144 (9th Cir. 1994).....33

United States v. Graves, 465 F. Supp. 2d. 450 (E.D. Pa. 2006)....31, 33

United States v. Jakobetz, 955 F.2d 786 (2d Cir. 1992).....33

Uniform Code of Military Justice

UCMJ art. 25, 10 U.S.C. § 825 (2006).....34

UCMJ art. 62, 10 U.S.C. § 862 (2006).....2

UCMJ art. 67, 10 U.S.C. § 867 (2006).....2

Military Rules of Evidence

Mil. R. Evid. 401 (2012).....30

Mil. R. Evid. 403 (2012).....30

Regulations

Dep't of Army, Pam. 27-9, Legal Services: Military Judges' Benchbook, para. 7-9-1 (10 Sept. 2014).....34

IN THE UNITED STATES COURT OF APPEALS
FOR THE ARMED FORCES

U N I T E D S T A T E S, Appellee	)	APPELLEE'S ANSWER TO APPELLANT'S PETITION FOR GRANT OF REVIEW
v.	)	
Major (O-4) **ANTIWAN M. HENNING,** United States Army, Appellant	)	Crim. App. Dkt. No. 20150410
	)	USCA Dkt. No. 16-0026/AR

TO THE JUDGES OF THE UNITED STATES COURT OF APPEALS
FOR THE ARMED FORCES

Issue Presented

WHETHER THE ARMY COURT APPLIED THE WRONG STANDARD OF REVIEW TO THIS ARTICLE 62, UCMJ, APPEAL WHEN IT FOUND THE MILITARY JUDGE MADE ERRONEOUS FINDINGS OF FACT AND ERRONEOUS CONCLUSIONS OF LAW.

Statement of Statutory Jurisdiction

The United States Army Court of Criminal Appeals (CCA) reviewed this case pursuant to Article 62, Uniform Code of Military Justice, 10 U.S.C. § 862 (2012) [hereinafter UCMJ]. If appellant establishes good cause, this Honorable Court may exercise jurisdiction over this case under Article 67(a)(3), UCMJ, which permits review in "all cases reviewed by a Court of Criminal Appeals in which, upon petition of the accused and on

good cause shown, the Court of Appeals for the Armed Forces (C.A.A.F.) has granted review."[1]

Statement of the Case

On 29 April 2015, the military judge issued a ruling to exclude evidence that appellant "is a possible contributor to the genetic material recovered from [the victim's] underwear . . . ."[2] On 1 May 2015, the government filed a written notice of appeal pursuant to Rule for Courts-Martial [hereinafter R.C.M.] 908 as the military judge's ruling "exclude[d] evidence that is substantial proof of a fact material in the proceeding."[3] After reviewing the briefs from both parties and hearing oral argument, the CCA granted the government's appeal and set aside the military judge's erroneous ruling.[4]

Statement of Facts

A. Background facts.

Appellant is charged with committing rape and other sexual assaults.[5] Appellant entered the victim's bedroom while she was

---

[1] 10 U.S.C. § 867(a)(3).
[2] Appellate Exhibit (AE) XII, p. 7.
[3] AE XIII; UCMJ art. 62(a)(1)(B).
[4] *United States v. Henning*, ARMY 20150410, 2015 CCA LEXIS 376, at *3, 24 (Army Ct. Crim. App. 3 Sep. 2015)(mem. op.).
[5] Charge Sheet. All references to the record will be submitted to appellant for inclusion in the Joint Appendix (JA) should a JA be necessary. For the court's convenience, excerpts from the record are enclosed in the Appendix.

sleeping next to her husband.[6] The victim awoke to appellant touching her breast with his hand.[7] He also penetrated her vagina with his tongue and penis.[8] Due to his level of intoxication, the victim's husband did not wake-up during the assaults.[9] Appellant denies any sexual contact with the victim.[10]

The deoxyribonucleic acid (DNA) evidence in this case came from the genetic material in the victim's underwear.[11] Ms. Hanna tested and analyzed this genetic material.[12] The military judge found that Ms. Hanna is "qualified to testify about forensic DNA testing and analysis."[13] Ms. Hanna is a forensic specialist in the DNA Biology section of the Kansas City Policy Crime Laboratory (KCPCL) and has served in that position for approximately ten years.[14] She has a bachelor of science in genetics and a master's degree in forensic science with a concentration in DNA analysis.[15] She is a member of multiple forensic science associations and receives continuous education within her field, specifically relating to DNA statistical

---

[6] App. Ex. XII, p. 1, para. 1.
[7] App. Ex. XII, p. 1, para. 1.
[8] App. Ex. XII, p. 1, para. 1.
[9] App. Ex. XII, p. 1, para. 1; Article 32 Tr. at 20-21.
[10] App. Ex. XII, p. 1, para. 1.
[11] R. at 17-18.
[12] R. at 17-18.
[13] App. Ex. XII, p. 5.
[14] App. Ex. IX, encl. 8.
[15] App. Ex. IX, encl. 8.

analysis.[16] Finally, she has testified as an expert in Missouri courts and federal court.[17]

B. The testing procedures in this case.

Ms. Hanna's testing procedures included extracting the DNA and then amplifying it, which is a process that makes millions of copies of the DNA for analysis.[18] Afterwards, she utilized instrumentation to detect and separate the mixtures for analysis.[19] Ms. Hanna analyzed the genetic material from the victim's underwear prior to comparing the sample to *any* of the known samples, such as appellant's sample.[20] As a result, Ms. Hanna made specific determinations about the sample she tested and the particular formula applicable to the sample prior to making any comparisons.[21]

First, Ms. Hanna assumed allelic dropout occurred in the sample.[22] A person receives two alleles at each locus (*i.e.*, location): one allele comes from the mother and the other allele comes from the father.[23] An allelic dropout means data is missing from the genetic information that was detected; the

---

[16] App. Ex. IX, encl. 8.
[17] App. Ex. IX, encl. 8.
[18] R. at 31-32.
[19] R. at 32.
[20] R. at 32, 99; App. Ex. VIII, encl. 5, p. 52, para. 6.2.8.
[21] R. at 32, 99; App. Ex. VIII, encl. 5, p. 52, para. 6.2.8.
[22] R. at 21, 23, 25.
[23] R. at 37-38.

allele is present but cannot be seen.[24] The template DNA Ms. Hanna tested was only 1 nanogram, which is small.[25] She injected a type of fluorescence into this sample to identify whether an allele was present at a particular locus.[26] The laboratory sets a certain threshold for the fluorescence units.[27] When dealing with a small amount of DNA, such as the template DNA in this case, the biochemical reaction in the testing process can mask some of the results.[28] This is called "preferential amplification."[29] For example, if the 16 allele is smaller than the 22 allele, the biochemical reaction in processing this small amount of DNA makes it easier for the analyst to identify only one of the alleles.[30] When you have small amounts of DNA, "you get a preferential amplification of the short fragments versus the large fragments and when you don't have very much of the DNA to begin with you end up with only one of them being present in your results."[31] This is also referred to as the stochastic threshold, meaning that it is possible that results are there

---

[24] R. at 39.
[25] R. at 19, 39-40.
[26] R. at 37.
[27] R. at 38.
[28] R. at 89-90.
[29] R. at 89-90.
[30] R. at 89-90.
[31] R. at 89-90.

but have not reached a detectable level, in part due to the testing process.[32]

Second, Ms. Hanna assumed one or more potential individuals contributed to the genetic material.[33] Although she did not know whether it was one contributor or two because one or two individuals could have contributed to the sample, Ms. Hanna explained that it was not scientifically valid for three or more contributors given the small size of the sample.[34]

The DNA laboratory employs quality control mechanisms and Ms. Hanna documented the procedural steps she utilized in the testing and analysis.[35]

C. KCPCL's statistical formula.

After determining the appropriate assumptions to make given the sample, Ms. Hanna applied the alleles present statistic, which is a formula KCPCL adopted and has been utilizing for the past fifteen years.[36] The formula accounts for the scientific assumptions applicable to the circumstances of this case: one or more potential individuals contributed to the genetic material and an allelic dropout occurred.[37] In her analysis, Ms. Hanna accounted for allelic dropout and limited the number of

---

[32] R. at 89-90.
[33] R. at 19, 21, 47.
[34] R. at 24, 47-48.
[35] R. at 17-18, 32-33, 35.
[36] R. at 30, 34-35, 101-102.
[37] R. at 19, 21, 47.

potential contributors in the sample to two contributors.[38] In calculating the alleles present, Ms. Hanna calculated the allele detected and any other possible allele.[39] This allowed her to account for two potential contributors.[40]

Finally, Ms. Hanna compared the sample she tested to appellant's sample.[41] Appellant cannot be excluded as a potential contributor to the sample of the genetic material from the victim's underwear.[42] Ms. Hanna concluded that "the expected frequency of potential contributors to the alleles present in [the sample] is 1 in 220 unrelated individuals."[43] Furthermore, in the same sample, the DNA analysis excluded the other male individuals who were present on the night of the offenses.[44] Ms. Hanna's testing and analysis was subject to a technical review by an expert who agreed with her conclusions.[45]

---

[38] R. at 21, 23-25, 40, 47-48.
[39] R. at 19-20, 24.
[40] R. at 200.
[41] R. at 32, 99; App. Ex. VIII, encl. 5, p. 52, para. 6.2.8.
[42] R. at 42; App. Ex. VI, encl. 2.
[43] App. Ex. VI, encl. 2.
[44] R. at 50; App. Ex. VI, encl. 2. Appellant was excluded as a potential contributor to a separate sample of genetic material from the victim's underwear. App. Ex. VI, encl. 2. In this separate sample, the victim's husband cannot be excluded as a potential contributor. App. Ex. VI, encl. 2.
[45] R. at 36, 96.

The defense expert produced its own electropherograms or images of the data in this case.[46] The defense expert reanalyzed the data and relies upon the same information as Ms. Hanna.[47]

D. Acceptance of KCPCL's statistical formula within the scientific community.

The laboratory publishes their testing procedures and statistical formulae, including the alleles present statistic used in this case.[48] Their procedures and statistical formulae have been subjected to extensive peer review and KCPCL has met the expected standards in the scientific community.[49]

Mr. Scott Hummel serves as the Chief Criminalist of the DNA Biology Section at the KCPCL and has served as a supervisor and technical leader at the KCPCL since 2009.[50] The military judge found that Mr. Hummel is "qualified to testify about forensic DNA testing and analysis."[51] Mr. Hummel is responsible for the quality assurance protocols for the laboratory and he reviewed the reports and circumstances of this case.[52] Mr. Hummel testified that the laboratory receives audits under three sets of guiding standards including the quality assurance standards issued by the Federal Bureau of Investigation (FBI) in

---

[46] R. at 14.
[47] R. at 33, 53.
[48] R. at 34-35.
[49] R. at 35.
[50] R. at 81; App. Ex. IX, encl. 10.
[51] App. Ex. XII, p. 5.
[52] R. at 81, 96.

conjunction with the Scientific Working Group for DNA Analysis Methods (SWGDAM).[53] Although these guidelines are not mandatory, auditors and accreditors have evaluated the alleles present statistic and approved its use at KCPCL under the SWGDAM guidelines.[54]

The alleles present statistic is generally accepted in the scientific community and is "used in forensic sciences."[55] Moreover, the SWGDAM guidelines do not preclude KCPCL's formula.[56] In fact, KCPCL's formula is contemplated in the SWGDAM guidelines. Although KCPCL uses different terminology to describe their formula, the KCPCL experts testified that the formula is a modified unrestricted random match probability (RMP) statistic, which is expressed in the SWGDAM guidelines.[57] Even the defense expert conceded that the "formulas in [KCPCL's] operating procedures and their interpretation guidelines are clearly consistent with and derived from SWGDAM guidelines."[58]

Additional facts pertaining to this assignment of error will be addressed accordingly.

---

[53] R. at 88.
[54] R. at 20-21, 35, 66-67, 85-85, 101-02.
[55] R. at 32, 89.
[56] R. at 21, 89.
[57] R. at 21, 101; App. Ex. IX, encl. 11, pp. 12, 16.
[58] R. at 104-05.

Summary of Argument

In an appeal pursuant to Article 62, UCMJ, an appellate court may review de novo a legal determination in ultimately concluding a military judge abused his discretion. The CCA applied the correct standard of review in this case because the military judge made several erroneous legal determinations that formed the basis of his ruling. Moreover, the military judge made clearly erroneous findings of fact and impermissibly usurped the factfinder's role. Since the CCA applied the correct standard of review and the military judge's ruling was manifestly erroneous, appellant has not established good cause for a grant of review in this case.

Standard of Review

Since the issue presented by the defense is whether the CCA applied the correct standard of review in this case, the legal principles governing the standard of review will be addressed *infra*.

Law and Argument

Typically, this court pierces through the CCA's analysis and reviews a military judge's decision directly in an appeal pursuant to Article 62, UCMJ.[59] The military judge's ruling excluding expert testimony on the DNA analysis in this case was

[59] *United States v. Buford*, 74 M.J. 98, 100 (C.A.A.F. 2015).

manifestly erroneous because DNA analysis is not a novel science and the government established a proper foundation for its admission. Specifically, the government established: the government expert is qualified; the subject matter of her testimony will assist the fact finder; the testimony is based on the expert's personal knowledge; the DNA evidence and analysis is relevant; KCPCL's formula is testable, has been subject to peer review, is subject to standard operating procedures, and is generally accepted within the scientific community; and the probative value of the DNA evidence and analysis is not substantially outweighed by a danger of unfair prejudice. The defense concedes the government satisfied most of this foundation[60] but challenges the reliability of KCPCL's formula. However, the appellate defense counsel presented the issue in terms of whether the CCA applied the correct standard of review. Appellant has not established good cause for a grant of review in this case because the CCA applied the correct standard of review in concluding that the military judge's ruling was manifestly erroneous.

A. The CCA applied the correct standard of review in this case.

A military judge's decision to admit or exclude expert testimony is reviewed for an abuse of discretion.[61] A military

---

[60] Appellant's Br. 11.

[61] *United States v. Sanchez*, 65 M.J. 145, 148 (C.A.A.F. 2007).

judge abuses his discretion when his findings of fact are clearly erroneous, his decision is influenced by an erroneous view of the law, or his application of the law to the facts is unreasonable.[62]

Under Article 62, UCMJ, if a case involves mixed questions of law and fact, an appellate court reviews a question of law de novo and an appellate court is not bound by a military judge's finding of fact if it is clearly erroneous.[63] Accordingly, an appellate court may review de novo a legal determination in ultimately concluding a military judge abused his discretion. For example, in *United States v. Buford*, this court reviewed de novo a military judge's legal determination that a third party collected evidence as a government agent.[64] This court made a de novo determination that the third party did not act as a government agent and held that the "military judge erred when she reached a legal determination to the contrary."[65] After conducting this de novo review, this court held that the military judge "abused her discretion when she used [an] erroneous conclusion of law as the basis for [her ruling.]"[66]

---

[62] *See United States v. Flesher*, 73 M.J. 303, 311 (C.A.A.F. 2014); *accord United States v. Ellis*, 68 M.J. 341, 344 (C.A.A.F. 2010).
[63] *See United States v. Cossio*, 64 M.J. 254, 256 (C.A.A.F. 2007).
[64] *Buford*, 74 M.J. at 102.
[65] *Id.*
[66] *Id.* at 99, 102.

As another example, in *United States v. Cossio*, this court reviewed de novo the legal question of whether the government moved towards trial with reasonable diligence under Article 10, UCMJ.[67] In concluding the government proceeded to trial with reasonable diligence, this court upheld the CCA's decision to set aside the military judge's erroneous ruling.[68]

In this case, the CCA held the military judge's ruling was manifestly erroneous because the military judge made two clearly erroneous findings of fact, overstepped his gatekeeping role, and made erroneous legal determinations.[69] Appellant confuses questions of law with questions of fact. Findings of fact are restricted to "things, events, deeds, or circumstances that 'actually exist.'"[70] However, questions of law are distinguishable and involve a "'legal effect, consequence, or interpretation.'"[71]

Similar to the facts in *Buford* and *Cossio*, the military judge's ruling in this case was based, in part, on erroneous legal determinations.[72] For example, the military judge made an erroneous legal determination that KCPCL's formula was

---

[67] *Cossio*, 64 M.J. at 256-57.
[68] *Id.* at 258.
[69] *Henning*, 2015 CCA LEXIS 376, at *13-24.
[70] *Cossio*, 64 M.J. at 257.
[71] *Id.*
[72] The military judge's ruling was also based on clearly erroneous findings of fact and an unreasonable application of the law to the facts, which will be addressed *infra*.

unreliable.[73] The reliability of any scientific formula is determined by numerous factors under the *Daubert* framework[74] to include: i) the science can be (and has been) tested, ii) the science has been subjected to peer review and publication, iii) there is a known or potential error rate, iv) there are existing maintenance or standard operating procedures, and v) the science is accepted within the relevant scientific community.[75] Therefore, the military judge's erroneous legal determination in this case was a legal question involving "legal effect, consequence, or interpretation." Indeed, an appellate court reviews de novo whether a military judge properly performed the required gatekeeping function of Military Rule of Evidence [hereinafter Mil. R. Evid.] 702 and followed this *Daubert* framework.[76]

---

[73] App. Ex. XII, p. 5.
[74] *United States v. Griffin*, 50 M.J. 278, 284 (C.A.A.F. 1999). This court established in *United States v. Houser* six prongs to assess the admissibility of expert testimony: 1) the qualifications of the expert, 2) the subject matter of the testimony, 3) the basis for the expert opinion, 4) the relevance of the testimony, 5) the reliability of the science, and 6) the probative value of the evidence under a Mil. R. Evid. 403 balancing test. *United States v. Houser*, 36 M.J. 392, 397-400 (C.M.A. 1993). "Although *Houser* was decided before *Daubert*, the two decisions are consistent, with *Daubert* providing more detailed guidance on the fourth and fifth *Houser* prongs to relevance and reliability." *Griffin*, 50 M.J. at 284.
[75] *Daubert v. Merrell Dow Pharms.*, 509 U.S. 579, 593-94 (1993).
[76] *Flesher*, 73 M.J. at 311.

Finally, appellant erroneously alleges the CCA "impermissibly found facts to support its overall conclusion."[77] Although an appellate court cannot "find its own facts or substitute its own interpretation of the facts" in an appeal pursuant to Article 62, UCMJ, the court is not bound by a military judge's clearly erroneous findings of fact.[78] In *United States v. Baker*, the CCA erred by finding an additional fact after the court "held the facts set forth by the military judge were not clearly erroneous and adopted those facts in its opinion."[79] Similarly, in *United States v. Stellato*, the CCA "adopted the military judge's findings of fact."[80] Therefore, this court stated that "[b]y finding no clear error, the CCA was bound by the military judge's fact-finding . . . ."[81] Here, in contrast to *Baker* and *Stellato*, the CCA did not adopt the military judge's findings of fact. Instead, the CCA properly found that the military judge made clearly erroneous findings of fact that were not supported in the record.[82]

---

[77] Appellant's Br. 5.
[78] *Cossio*, 64 M.J. at 256.
[79] *United States v. Baker*, 70 M.J. 283, 287, 290 (C.A.A.F. 2011).
[80] *United States v. Stellato*, __ M.J. __, slip op. at 14 (C.A.A.F. 20 Aug. 2015).
[81] *Stellato*, __ M.J. __, slip op. at 19.
[82] *Henning*, 2015 CCA LEXIS 376, at *12-15 ("This finding and its corresponding conclusion are clearly erroneous and unsupported by the record.").

B. The military judge made several clearly erroneous findings of fact.

The military judge erroneously found that KCPCL "used a statistical calculation in this case that does precisely what the [SWGDAM] Guidelines state is 'precluded.'"[83] However, the SWGDAM guidelines contemplate KCPCL's formula as the guidelines encourage laboratories to use their professional judgment and expertise to update their procedures and formulae as needed with written manuals that are "sufficiently detailed that other forensic DNA analysts can review, understand in full, and asses the laboratory's policies and practices."[84] Indeed, the SWGDAM guidelines expressly caveat their formulae with the practical reality that "[d]ue to the multiplicity of forensic sample types and the potential complexity of DNA typing results, it is impractical and infeasible to cover every aspect of DNA interpretation by a preset rule."[85]

Moreover, both KCPCL witnesses, qualified experts,[86] testified that the SWGDAM guidelines do not preclude their

---

[83] App. Ex. XII, p. 2, para. 5.
[84] App. Ex. IX, encl. 11, p. 1-2. Ms. Hanna explained that the SWGDAM guidelines are "not something that is set" and that they require an analyst to use a formula that is "backed up" by the assumptions applicable to the evidentiary sample. R. at 20-21.
[85] App. Ex. IX, encl. 11, p. 1.
[86] The military judge properly found the experts were qualified and appellant concedes they are qualified stating, "[t]he first four *Houser* factors are not in dispute." App. Ex. XII, p. 5; Appellant's Br. 11.

formula.[87] Of significance, the defense expert conceded that the "formulas in [KCPCL's] operating procedures and their interpretation guidelines are clearly consistent with and derived from the SWGDAM guidelines."[88]

Finally, although KCPCL uses different terminology to describe their formula, it is a modified unrestricted RMP statistic, which is expressed in the SWGDAM guidelines.[89] The SWGDAM guidelines describe a modified RMP formula stating, "this document also applies the term RMP to mixture calculations where the number of contributors is assumed (this has sometimes been referred to as a 'modified RMP')."[90] The formula discussed in paragraph 5.2.2.3 of the SWGDAM guidelines is essentially the alleles present statistic formula KCPCL applied in this case.[91] Under the section entitled RMP, the SWGDAM guidelines state:

> In a mixture having at a locus alleles P, Q, and R, assumed to be from *two contributors*, where all three alleles are *below the stochastic threshold*, the interpretation may be that the two contributors could be a heterozygote-homozygote pairing where all alleles were detected, a heterozygote-heterozygote pairing where all alleles were detected, or a heterozygote-heterozygote pairing where a fourth allele *might have dropped out*. In this case, the RMP must account for all heterozygotes and homozygotes represented by these three alleles, but also

---

[87] R. at 21, 89.
[88] R. at 105.
[89] R. at 21, 101.
[90] App. Ex. IX, encl. 11, p. 12.
[91] App. Ex. IX, encl. 11, p. 16, para. 5.2.2.3.

> all heterozygotes that include one of the detected alleles. The RMP for this interpretation could be calculated as $(2p - p^2) + (2q - q^2) + (2r - r^2) - 2pq - 2pr - 2qr$.[92]

Similar to KCPCL's formula, this formula in the SWGDAM guidelines applies to a circumstance in which there are two potential contributors.[93] Additionally, Ms. Hanna testified that there were alleles below the stochastic threshold in this case similar to the formula from the SWGDAM guidelines.[94] Lastly, both formulae account for allelic dropout.[95]

Simply put, the military judge's finding of fact was clearly erroneous as it was unsupported in the record. The military judge based this clearly erroneous finding of fact on layer upon layer of clearly erroneous findings of fact.

For example, the military judge erroneously found that "Ms. Hanna did not conclude, one way or another, whether allelic dropout had occurred in the sample."[96] However, Ms. Hanna repeatedly explained that she accounted for allelic dropout in her analysis.[97] She is a qualified expert and she analyzed the genetic material from the victim's underwear prior to comparing

---

[92] App. Ex. IX, encl. 11, p. 16, para. 5.2.2.3 (emphasis added).
[93] R. at 23-24, 40, 47-48; App. Ex. IX, encl. 11, p. 16, para. 5.2.2.3.
[94] R. at 40.
[95] R. at 21, 23, 25; App. Ex. IX, encl. 11, p. 16, para. 5.2.2.3.
[96] App. Ex. XII, p. 3, para. 6.
[97] R. 21, 23, 25.

the sample to *any* of the known samples, such as appellant's sample.[98] She applied a formula that is based on the assumption that allelic dropout occurred and she stated, "there is a dropout occurring . . . ."[99] Therefore, her decision to apply a formula that accounts for allelic dropout reflects her determination that allelic dropout, in fact, occurred. Indeed, *no* expert concluded that allelic dropout did not occur. The defense expert conceded that KCPCL's formula "is predicated on the fact that dropout did occur"[100] and he also stated, "there is a good chance that [allelic] dropout may have occurred."[101] Therefore, the CCA properly concluded that the military judge's finding was clearly erroneous and unsupported by the record.[102]

As another example, the military judge erroneously found that "if you assume two contributors to the sample in this case, then the [appellant] could not have contributed all five alleles detected; the second person would have had to contribute at least one of the alleles (and possibly more). This is true regardless whether allelic dropout had occurred."[103] First, *no* expert provided this testimony. Appellant acknowledges that "it

---

[98] R. at 32, 99; App. Ex. VIII, encl. 5, p. 52, para. 6.2.8.; App. Ex. XII, p. 5.
[99] R. at 21, 23, 25.
[100] R. at 57.
[101] R. at 76-77.
[102] *Henning*, 2015 CCA LEXIS 376, at *14.
[103] App. Ex. XII, p. 6.

is true the experts did not state this expressly" but argues "logically the military judge's thinking makes sense based on the [SWGDAM] guidelines and the evidence."[104] This is an example of the military judge conducting his own analysis of the evidence, discussed *infra*. The military judge and appellant misunderstand allelic dropout. An allelic dropout means data is missing from the genetic information that was detected; the allele is present but cannot be seen.[105] Accordingly, it is possible for two individuals to contribute to a sample but only one person's alleles are detected. Ms. Hanna applied a formula that accounted for more than one contributor.[106] In fact, the defense expert conceded a statistic that assumes more than one contributor to the sample is scientifically sound, stating, "so now we're formally entertaining and using a statistic that would require more than one contributor, but none the less that is something that could be done."[107]

Finally, the military judge erroneously found that an assumption of two potential contributors to the genetic material in this case "would presumably result in a different formula producing a different statistic than the one KCPCL developed (1

---

[104] Appellant's Br. 19, n.3.
[105] R. at 39.
[106] R. at 23-24, 40, 47-48.
[107] R. at 75.

in 220)."[108] This clearly erroneous finding was directly contradicted by the military judge's personal exchange with Ms. Hanna. The military judge specifically asked Ms. Hanna whether the formula accounted for two potential contributors:

> Q. So hypothetically if *one person* contributed two alleles and *another person* contributed three alleles in order to be included as a possible match you have to have all five despite the fact that - -
> A. You'd have to share—you'd have to have the same alleles just by chance.
> Q. And the probability or the percentage calculation *somehow accounts for this*?
> A. *Yes*, what's taking in consideration of just looking at what alleles are there.[109]

Again, Ms. Hanna stated multiple times that KCPCL's formula was limited to only two potential contributors.[110] While technically there was an unknown number of contributors because one individual could have contributed all the alleles to the sample or two individuals could have contributed a combination of alleles to the sample,[111] Ms. Hanna made clear that it was not scientifically valid to assume more than two contributors to the sample in this case (*i.e.*, an infinite number of contributors).[112]

---

[108] App. Ex. XII, p. 6.
[109] R. at 50 (emphasis added).
[110] R. at 23-24, 39-40, 47-48.
[111] R. at 24.
[112] R. at 47-48. Some of Ms. Hanna's testimony was disjointed because the military judge inexplicably allowed the defense to cross-examine her first despite the fact that the government bore the burden of proof at the motions hearing.

C. The military judge unreasonably applied the law to the facts in this case by impermissibly usurping the fact finder's role.

As the CCA recognized, a military judge must respect the differing roles for the judge and jury. The military judge is a gatekeeper who may exclude junk science and an expert opinion "which is connected to existing data only by the *ipse dixit* of the expert . . . where there is simply too great [of] an analytical gap between the data and the opinion proffered."[113] However, the military judge's inquiry should not focus on the expert's ultimate conclusions but on the expert's principles and methodology.[114] The question for the military judge is not whether he finds one expert correct and more persuasive than another expert.[115] Courts recognize there is a range in which experts may reasonably disagree.[116] The military judge's role is to "screen all evidence for minimum standards of admissibility and to let the factfinder determine which evidence is more persuasive."[117] Accordingly, even in extreme cases of "shaky" scientific evidence, "[v]igorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of

---

[113] *GE v. Joiner*, 522 U.S. 136, 146 (1997); *accord United States v. Billings*, 61 M.J. 163, 168 (C.A.A.F. 2005).
[114] *Sanchez*, 65 M.J. at 149-50.
[115] *United States v. Kaspers*, 47 M.J. 176, 178 (C.A.A.F. 1997)(internal citations omitted).
[116] *Sanchez*, 65 M.J. at 150.
[117] *Kaspers*, 47 M.J. at 178 (internal citations omitted).

proof are the traditional and appropriate means of attacking shaky but admissible evidence."[118]

In this case, the military judge usurped the factfinder's role by substituting his own interpretation of the science for the explanations provided by qualified experts. The CCA observed that the military judge "became his own expert, conducted his own analysis of the evidentiary DNA data and application of the SWGDAM guidelines in a manner not addressed by any of the experts."[119] Appellant argues that the military judge was "free to apply the evidence to KCPCL's formula in order to question its reliability—which is exactly what the military judge did here."[120] However, the military judge is not a qualified expert in DNA testing and analysis. He lacks the requisite training, education, and experience to correctly apply this scientific evidence to KCPCL's formula. As discussed *supra*, the military judge concluded that an assumption of two potential contributors to the genetic material in this case "would presumably result in a different formula producing a different statistic than the one KCPCL developed (1 in 220)"[121] contrary to the expert testimony from Ms. Hanna[122] and the

---

[118] *Daubert*, 509 U.S. at 596.
[119] *Henning*, 2015 CCA LEXIS 376, at *19.
[120] Appellant's Br. 18-19.
[121] App. Ex. XII, p. 6.
[122] R. at 50.

defense expert's concession that a statistic that assumes more than one contributor is scientifically sound.[123]

Moreover, the military judge usurped the factfinder's role by adopting a portion of the defense expert's testimony who as appellant states "the military judge found compelling."[124] However, the military judge's role as gatekeeper was not to assess which expert was more compelling. Rather, his gatekeeping function under Mil. R. Evid. 702 and the *Daubert* framework required him to "screen all evidence for minimum standards of admissibility and to let the factfinder determine which evidence is more persuasive."[125]

Both government and defense experts rely upon the same data and information; they merely differ in their interpretation of that data.[126] Ms. Hanna conducted the testing, documented the procedures used, and her results are "reviewed and everybody can replicate [it]."[127] Indeed, the defense expert produced its own electropherograms or images of the same data.[128] The defense expert reanalyzed this data and relies upon the same information as Ms. Hanna.[129] The defense expert also agreed that appellant

---

[123] R. at 75.
[124] Appellant's Br. 13.
[125] *Kaspers*, 47 M.J. at 178 (internal citations omitted).
[126] R. at 33, 42-43, 60-61.
[127] R. at 36.
[128] R. at 14.
[129] R. at 33, 53.

possesses the same five alleles detected in the evidentiary sample.[130]

Most importantly, the defense expert conceded there are three scientifically valid ways to interpret the data, stating:

> What I would prefer to say is that there are essentially three ways that one might look [at this case, five alleles at four loci]. If an individual has two alleles and yet only one is observed at that locus in an evidence sample, one might conclude that the individual cannot be excluded because dropout had occurred. Another is that the individual - - another possible conclusion is that the individual is actually excluded because dropout did not occur, and a third conclusion might be to refrain from drawing a conclusion . . . it's simply safest to walk away and say that we don't care to draw a conclusion at all.[131]

The defense expert adopted the third interpretation, stating that he is only comfortable concluding that the data is inconclusive, which is his personal opinion.[132] The military judge erroneously adopted the second interpretation of the data. He stated, "if you assume no allelic dropout occurred, [appellant] must be excluded as a contributor regardless of the

---

[130] R. at 56, 67-70. Although appellant disputes this fact, the defense expert explained that appellant has all five of the alleles detected in the evidentiary sample and appellant also has two other alleles that were not detected. R. at 69. The defense expert stated that "at the end of this process there were seven opportunities to match. Five of those alleles are found . . . ." R. at 69.

[131] R. at 70.

[132] R. at 61.

number of contributors."[133] He continued his analysis by providing his opinion of which alleles would be present in the sample if no allelic dropout occurred.[134] Again, *no* expert adopted this interpretation.[135]

Ms. Hanna adopted the first interpretation and the CCA properly concluded that her opinion is "connected by a long-used, reproducible, announced, audited, and written formula."[136] Appellant concedes that the CCA's determination of Ms. Hanna's opinion "may be true" but argues "only if the requirement for establishing the scientific reliability of a method is reliance upon the originator (nee [sic] benefactor) of that methodology."[137] Appellant further argues "that is simply not how it works."[138] Appellant cites no legal authority for the proposition that an expert's explanation of the methodology and scientific principles forming the basis of her scientific opinion is insufficient to establish the reliability factor in the *Daubert* framework. Indeed, in *United States v. Youngberg*,

---

[133] App. Ex. XII, p. 6.
[134] App. Ex. XII, p. 6.
[135] Although the defense expert stated he was more comfortable not making a conclusion, he conceded that there is a "good chance" that allelic dropout may have occurred due to the small size of the sample. R. at 72, 76.
[136] *Henning*, 2015 CCA LEXIS 376, at *17.
[137] Appellant's Br. 18.
[138] Appellant's Br. 18.

this court found the government expert's testimony sufficient to establish the reliability of DNA evidence.[139]

Ms. Hanna is a qualified expert in DNA testing and analysis,[140] which appellant does not dispute.[141] The analytical steps she applied in KCPCL's formula are traceable and reliably flow from the assumptions she made in this case.[142] The DNA testing and analysis was subject to a technical review by another expert who agreed with Ms. Hanna's conclusions.[143] The laboratory publishes their testing procedures and statistical formulae, including the alleles present statistic used in this case.[144] Their procedures and statistical formulae have been subjected to extensive peer review and KCPCL has never failed.[145] For example, the American Society of Crime Lab Directors Laboratory Accreditation Board has issued multiple accreditation certificates to KCPCL throughout the past fifteen years.[146] In

---

[139] *United States v. Youngberg*, 43 M.J. 379, 387 (C.A.A.F. 1995). In *Youngberg*, the expert's testimony included: the process of DNA testing, its general acceptance in the scientific community, the testing could be duplicated, and was reliable. *Id.*

[140] App. Ex. XII, p. 5; App. Ex. IX, encl. 8 (Ms. Hanna's curriculum vitae).

[141] Appellant's Br. 11.

[142] R. at 21, 30.

[143] R. at 36, 96. In a technical review, another expert evaluates all of the data, conclusions, reports, and notes to "ensure there is an appropriate and sufficient basis for the scientific conclusions." R. at 96; App. Ex. IX, encl. 12.

[144] R. at 34-35.

[145] R. at 35.

[146] App. Ex. IX, encls. 3-7.

addition, KCPCL receives an audit every year and an external audit at least once every two years.[147] The laboratory has been using the alleles present statistic for approximately fifteen years and the laboratory has been audited and inspected on approximately ten different occasions.[148] These auditors and accreditors evaluated the alleles present statistic and approved its use as the laboratory has passed all of the audits.[149]

In fact, the military judge found that KCPCL's formula was testable and subject to peer review.[150] The *Daubert* court recognized that peer review and publication is a component of "'good science' in part because it increases the likelihood that substantive flaws in methodology will be detected."[151] The extensive peer review and vetting of the alleles present statistic demonstrates that it is "good science." If there was

---

[147] R. at 35, 86.
[148] R. at 21, 102. The laboratory receives audits under three sets of guiding standards: the international standards used across the world, supplemental standards to these international standards, and the quality assurance standards issued by the FBI in conjunction with the SWGDAM. R. at 88. Auditors review individual cases and case work produced by each analyst at KCPCL. R. at 86-87. Auditors have previously reviewed case files applying the alleles present statistic used in this case and KCPCL's manual, which includes all statistical formulae, equations, and guidelines. R. at 35, 87.
[149] R. at 35, 101-02.
[150] App. Ex. XII, p. 5.
[151] *Daubert*, 509 U.S. at 594; *see also United States v. Nimmer*, 43 M.J. 252, 259 (C.A.A.F. 1995)("Publication increases the likelihood that substantive flaws in methodology will be detected.").

a substantive flaw in KCPCL's methodology, the auditors and accrediting bodies within the scientific community would have identified it.[152]

Therefore, the experts' difference in the interpretation of the data falls within the reasonable range in which experts may disagree. By adopting a portion of the defense expert's testimony in his ruling—an interpretation no expert adopted, the military judge improperly exceeded his role as gatekeeper and invaded the factfinder's role.[153]

D. The military judge also unreasonably applied the law to the facts because the probative value of the evidence was not substantially outweighed by unfair prejudice.

Under Mil. R. Evid. 403 and the sixth *Houser* prong, "[l]ogically relevant and reliable expert testimony 'may be excluded if its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or

---

[152] R. at 35, 101-02.

[153] The military judge also erred in the application of the law to the facts of this case, in part, because he placed an undue reliance upon the lack of known error rates. Courts have cautioned against placing an undue reliance upon error rates. *See United States v. Bell*, 72 M.J. 543, 554 (Army Ct. Crim. App. 2013)(recognizing that error rates "'neither necessarily nor exclusively appl[y] to all experts in every case.'")(quoting *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 138 (1999)). Indeed, the government presented *no* evidence of error rates for the DNA evidence admitted in *Youngberg*. *Youngberg*, 43 M.J. at 386-87.

misleading the members.'"[154] The military judge misapplied the law to the facts because the probative value of this evidence is high and the military judge failed to consider any of the safeguards established in *Daubert* that reduce the risk of unfair prejudice. With a proper application of the *Daubert* safeguards, the probative value of the DNA analysis in this case is not substantially outweighed by unfair prejudice.

Appellant argues that the defense expert testified that "the statistical significance of KCPCL's ratio was 'very weak.'"[155] First, this testimony does not constitute a legal determination of the probative value of this evidence. Under Mil. R. Evid. 401, evidence is logically relevant if "it has any tendency to make a fact [of consequence] more or less probable than it would be without the evidence . . . ."[156] Here, appellant cannot be excluded as a potential contributor to a sample of the genetic material from the victim's underwear.[157] Accordingly, the DNA evidence has a tendency to make a fact of consequence—that sexual contact between appellant and the victim occurred—more probable. Second, courts have been "reluctant to enunciate a threshold that delineates the level of statistical

---

[154] *Houser*, 36 M.J. at 399-400 (quoting Mil. R. Evid. 403); *see also, Daubert*, 509 U.S. at 595 (noting the applicability of the 403 balancing test).
[155] Appellant's Br. 21.
[156] Mil. R. Evid. 401.
[157] R. at 42.

significance required for DNA evidence to be admissible."[158] Indeed, even DNA evidence of a "low statistical value is probative to show that [an accused] cannot be excluded as a contributor to the DNA sample."[159]

The CCA properly made a legal determination that the probative value of this evidence is high because appellant cannot be excluded as a potential contributor.[160] Furthermore, in this same sample, the DNA analysis excluded the other male individuals who were present on the night of the offenses.[161] Appellant argues the military judge "erred on the side of exclusion" and the CCA "erred on the side of inclusion."[162] However, as a matter of law, Mil. R. of Evid. 403 favors admission.[163] Courts applying the sixth *Houser* factor also strike a balance in favor of admission given the "'liberal admissibility standards of the federal and military rules and the express teachings of *Daubert*.'"[164] The military judge misapplied the law by "err[ing] on the side of exclusion."

---

[158] *United States v. Graves*, 465 F. Supp. 2d 450, 458 (E.D. Pa. 2006).
[159] *Id.*
[160] R. at 42.
[161] R. at 50.
[162] Appellant's Br. 20-21.
[163] *United States v. Teeter*, 12 M.J. 716, 725 (A.C.M.R. 1981)("In weighing the probative value of evidence against the dangers of prejudicial impact, the general rule is that the balance should be struck in favor of admission.").
[164] *Sanchez*, 65 M.J. at 152 (quoting *Amorgianos v. Amtrak*, 303 F.3d 256, 267 (2d Cir. 2002)).

Next, the military judge misapplied the law in stating that the DNA analysis is too favorable to the government because by using the statistic (1 in 220), only seven people from the city population could be potential contributors to the genetic material.[165] However, as a matter of law, "the mere fact that [evidence] support[s] the prosecution's case against [an appellant] does not make [the] evidence unduly prejudicial."[166] Moreover, the DNA analysis is not misleading because Ms. Hanna properly limited the scope of her results. She does not claim that appellant is *the* contributor to the genetic material.[167] Rather, appellant is a potential contributor and she freely admitted that she is not asserting "it's this one person and this is their profile."[168]

Moreover, the military judge misapplied the law in stating that the expert testimony will lead to a mini-trial. This case involves serious allegations that deserve the factfinder's full attention. Appellant is charged with rape and committing other acts of sexual assault.[169] He denies the sexual contact occurred.[170] Since the DNA evidence is probative in determining whether appellant committed these criminal acts, the evidence

---

[165] App. Ex. XII, p. 6.
[166] *United States v. Meeks*, 35 M.J. 64, 69 (C.M.A. 1992).
[167] R. at 20.
[168] R. at 20.
[169] Charge Sheet.
[170] App. Ex. XII, p. 1, para. 1.

will not be a waste of time for the factfinder and the CCA properly reasoned these issues are the essence of the trial.[171]

Finally, the military judge misapplied the law by stating that "the panel members will put aside the 'technical' issue they do not understand and default to the more straightforward conclusion of 'included as a possible contributor' [b]ecause DNA evidence is powerful (and ubiquitous on television and the movies). . . ."[172] However, in evaluating DNA evidence, courts reason that "[a]lthough scientific and statistical evidence may seem complicated, we do not think a jury will be so dazzled or swayed as to ignore evidence suggesting that an experiment was improperly conducted or that testing procedures have not been established."[173] "Where the [court] provides careful oversight, the potential prejudice of the DNA evidence can be reduced to the point where [its] probative value outweighs it."[174] Therefore, "[e]ven DNA evidence with relatively low statistical significance may be admitted as probative evidence, provided that certain safeguards are afforded."[175] Appropriate safeguards include "[v]igorous cross-examination, presentation of contrary

---

[171] *Henning*, 2015 CCA LEXIS 376, at *22.
[172] App. Ex. XII, p. 6.
[173] *United States v. Jakobetz*, 955 F.2d 786, 797 (2d Cir. 1992).
[174] *Graves*, 465 F. Supp. 2d at 458 (quoting *United States v. Chischilly*, 30 F.3d 1144, 1158 (9th Cir. 1994)).
[175] *Id.*

evidence, and careful instruction on the burden of proof" as established in *Daubert*.[176]

The CCA properly concluded the military judge erred because he failed to consider the neutralizing effect of the safeguards established in *Daubert*. For example, appellant's defense counsel fully understands the nuances of the DNA evidence in this case and he effectively cross-examined the experts on the science during the motions hearing.[177] The defense expert communicated the defense interpretation of the DNA evidence in easy to understand, laymen's terms during the motions hearing.[178]

Moreover, the military judge failed to even consider using the voir dire process and instructions to inform the panel members on the appropriate way to evaluate the DNA evidence in this case. A military panel is intelligent, educated, sophisticated, and possess an appropriate judicial temperament as each member must meet the criteria set forth in Article 25, UCMJ.[179] Finally, the Military Judges' Benchbook provides an instruction on expert testimony that the military judge could have further tailored to serve as another safeguard in this case.[180] Under the law, "[a]bsent evidence to the contrary, the

---

[176] *Daubert*, 509 U.S. at 596.
[177] R. at 17-31, 46-49, 94-96.
[178] R. at 52-80.
[179] UCMJ art. 25.
[180] Dep't of Army, Pam. 27-9, Legal Services: Military Judges' Benchbook, para. 7-9-1 (10 Sept. 2014).

members are presumed to follow the military judge's instructions."[181]

In sum, all of these safeguards reduce any potential prejudice to the point where the probative value of the DNA analysis in this case far outweighs it.

Conclusion

The CCA applied the correct standard of review in this case because the military judge made several erroneous legal determinations that formed the basis of his ruling; he made clearly erroneous findings of fact; and he impermissibly usurped the factfinder's role. Since the CCA applied the correct standard of review and the military judge's ruling was manifestly erroneous, appellant has not established good cause for a grant of review in this case.

WHEREFORE, the Government respectfully requests that this Honorable Court deny appellant's petition for review.

JIHAN WALKER
Captain, JA
Chief, Branch IV
U.S.C.A.A.F. Bar No. 36340

DANIEL D. DERNER
Major, JA
Acting Deputy Chief,
Government Appellate Division
U.S.C.A.A.F. Bar No. 36331

[181] *United States v. Ashby*, 68 M.J. 108, 123 (C.A.A.F. 2009).

CERTIFICATE OF COMPLIANCE WITH RULE 24(d)

1. This brief complies with the type-volume limitation of Rule 24(c) because:

This brief contains **9,493** words.

2. This brief complies with the typeface and type style requirements of Rule 37 because:

This brief has been typewritten in 12-point font, mono-courier new typeface using Microsoft Word Version 2013.

JIHAN WALKER
Captain, JA
Chief, Branch IV
Government Appellate Division
Attorney for Appellee
23 October 2015

Appendix

UNITED STATES ARMY COURT OF CRIMINAL APPEALS

Before
COOK[1], HAIGHT, and WEIS[2]
Appellate Military Judges

UNITED STATES, Appellant
v.
Major ANTIWAN M. HENNING
United States Army, Appellee

ARMY MISC 20150410

Headquarters, Combined Arms Center & Fort Leavenworth
Charles L. Pritchard, Jr., Military Judge

For Appellee: Captain Jennifer K. Beerman, JA (argued); Lieutenant Colonel Jonathan F. Potter, JA; Major Aaron R. Inkenbrandt, JA; Captain Jennifer K. Beerman, JA (on brief).

For Appellant: Captain Jihan Walker, JA (argued); Major A.G. Courie III, JA; Major Janae M. Lepir, JA; Captain Jihan Walker, JA (on brief).

3 September 2015

MEMORANDUM OPINION AND ACTION ON APPEAL
BY THE UNITED STATES FILED PURSUANT TO
ARTICLE 62, UNIFORM CODE OF MILITARY JUSTICE

HAIGHT, Judge:

BACKGROUND

Although the science involved in this government appeal is beyond the ken of even relatively experienced jurists, as well as the typical layperson, the facts are simple.

The alleged victim, SLN, reported that appellee raped her. Major (MAJ) Henning denied any and all sexual contact with SLN. Genetic material was

---

[1] Senior Judge COOK took final action in this case prior to his departure from the court and retirement.

[2] Judge WEIS took final action in this case while on active duty.

recovered from the underwear SLN wore the evening in question. The Kansas City Police Crime Laboratory (KCPCL) conducted deoxyribonucleic acid (DNA) testing on that genetic material. After testing and analysis, the KCPCL reported that MAJ Henning could not be excluded as a potential minor contributor to the tested sample. Furthermore, the KCPCL is of the opinion that approximately 1 in 220 unrelated individuals in the general population would be a match to the minor contributor's profile. Major Henning was charged with the rape of, and other sexual crimes against, SLN.

The defense moved to "prohibit the government from offering any expert testimony concerning MAJ Henning being a possible contributor of genetic material recovered from the underwear of [SLN]." The defense asserted that the DNA analysis conducted by the KCPCL and which the government seeks to introduce "does not meet the requirements for expert testimony established by [Military Rule of Evidence] 702, *United States v. Houser* [36 M.J. 392 (C.M.A. 1993)], and *Daubert v. Merrell Dow* [*Pharms.*, 509 U.S. 579 (1993)]." After an Article 39(a) session, the military judge granted the defense motion and ruled that "[e]vidence that [MAJ Henning] is a possible contributor to the genetic material recovered from [SLN]'s underwear is excluded." The government, pursuant to Rule for Courts-Martial [hereinafter R.C.M.] 908 and Article 62, UCMJ, appeals the decision of the military judge.

After oral argument and consideration of the government appeal, we find the military judge abused his discretion in his ruling to exclude.

ARTICLE 39(a), UCMJ, HEARING

For purposes of this motion, the defense called Ms. Jessica Hanna, the KCPCL employee who conducted the DNA testing in this case. From a sample identified during serological screening of SLN's underwear, Ms. Hanna extracted DNA, amplified and analyzed that DNA, and was able to identify a "major profile" from a female as well as a "minor profile" from a male. This minor profile or genetic information revealed "five alleles at four different locations [loci]." Major Henning's DNA also has those same five alleles at those same four loci. Therefore, he cannot be excluded as a potential contributor.[3] Then, Ms. Hanna applied a statistical formula labeled an "alleles present statistic" in order to determine the weight of Major Henning's DNA match or, in other words, the frequency of those in the general population with DNA that could possibly match the minor profile. The calculated frequency was 1 in 220.

[3] This is particularly pertinent as, according to KCPCL, the two other males present in SLN's home on the night in question were both excluded after comparison to the DNA profile.

The defense also called Dr. Krane, an expert in the field. While having significant concerns with the KCPCL's calculated ratio of 1 in 220, Dr. Krane acknowledged that it was "factually correct" that Major Henning's genetic information does match the minor profile to the extent that the profile only revealed five alleles at four loci. In other words, Dr. Krane confirmed that Major Henning's DNA does, in fact, have those same identified five alleles at those four identified specific loci. Furthermore, Dr. Krane did not dispute that the minor profile derived from the genetic information recovered from the sample found in SLN's underwear accurately reflected the presence of those five alleles at those four loci. Therefore, Dr. Krane did not question any of the scientific testing performed or the resulting data; his critique dealt with the appropriate statistical significance that should be attached to those results.

Dr. Krane identified various bases for his overall concern. First, the minor profile at issue was derived from an exceedingly small amount of DNA. Second, similar to the first basis, five points of comparison does not provide much information concerning the other points where Henning's DNA might not match. Third, the KCPCL's "alleles present statistic" assumes allelic dropout,[4] because if allelic dropout had not occurred, then Major Henning would effectively be excluded. But, Dr. Krane later acknowledged twice that "the less template DNA that you start with, the more likely locus dropout and allelic dropout there will be." Fourth, as the statistical analysis was applied to a "minor profile" with low peaks, as opposed to a "major profile" with high peaks, the interpretation thereof must not only account for allelic dropout and drop-in but also take into consideration "stutter peaks" and how those stutters could possibly be allelic peaks of a "minor contributor." For this instance, Dr. Krane testified that the 1 in 220 statistic is "very weak by DNA profiling standards . . . but that number would have been less impressive still if those stutter peaks had been added into the calculation." Finally, Dr. Krane is of the opinion that in scenarios such as the present, where there is a combination of the two factors of "unknown number of contributors" and "possible or assumed allelic dropout," "then all bets are off" and the safer course of action would be to report the findings as "inconclusive."

Succinctly, when asked what conclusions could be drawn from the results of the KCPCL's DNA testing in this case, Dr. Krane stated:

> What I would prefer to say is that there are essentially three ways that one might look at such a circumstance. If an individual has two alleles and yet only one is observed at that locus in an evidence sample, one might conclude that the individual cannot be excluded because dropout

[4] Allelic dropout is the failure to detect an allele within a sample or failure to amplify an allele during the polymerase chain reaction process.

> had occurred. Another is that the individual -- another possible conclusion is that the individual is actually excluded because dropout did not occur, and a third conclusion might be to refrain from drawing a conclusion and say that we can't say if dropout or what the likelihood that dropout has or has not occurred is, therefore, since we can't decide which of those two possibilities is most likely or how to capture that into some sort of statistic it's simply safest to walk away and say that we don't care to draw a conclusion at all.

The government called Mr. Scott Hummel, the Chief Criminalist of the DNA Biology Section at the KCPCL. In that capacity, he is responsible for quality assurance at the lab. Generally, the KCPCL is accredited by the American Society of Crime Lab Directors, Laboratory Accreditation Board and is also externally audited to ensure its personnel, policies, and procedures are in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) guidelines, the FBI-issued quality assurance standards, as well as the international standards used by the scientific community "not in just this country, but across the world." Specifically, the KCPCL is currently accredited, and all of its "statistical formulas, equations, guidelines," to include the "alleles present statistic," along with particular case files in which such equations were used were provided to and reviewed by the accrediting body.

Mr. Hummel defended the formula used in this case. He explained the formula, which accounts for an unknown number of contributors and allelic dropout, is a "modification of an unrestricted random match probability" and does not violate SWGDAM guidelines. To the contrary, according to Mr. Hummel, this "possible permutation or calculation" is actually contemplated by or alluded to in those guidelines. Furthermore, Mr. Hummel testified that the KCPCL's analysis does consider and take into account "stutter peaks" and their possible interplay with "minor contributor allelic peaks."

Dr. Krane was recalled. He was specifically asked if the KCPCL's formulas are "somehow not following the SWGDAM guidelines," to which he responded, "I think it would be best to say I'm saying something a little bit different. I'm saying that they're not being applied appropriately. The formulas in their operating procedures and their interpretation guidelines are clearly consistent with and derived from the SWGDAM guidelines."

THE MILITARY JUDGE'S RULING

Faced with a classic battle of the experts, the military judge granted the defense motion and excluded "[e]vidence that the Accused is a possible contributor

to the genetic material recovered from Mrs. [SLN]'s underwear." The military judge found, *inter alia*, as fact:

1. "The Accused's DNA matched five alleles at four loci in the minimal minor profile from the underwear."
2. "SWGDAM is the definitive authority on reliable procedures and methods for forensic DNA testing and analysis."
3. "The SWGDAM Guidelines are mostly that: guidelines."
4. "The Guidelines clearly state that RMP [Random Match Probability statistical calculations] and CPE/I [Combined Probability of Exclusion or Inclusion statistical calculations] are incompatible with each other.
5. "KCPCL used a statistical calculation in this case that does precisely what the Guidelines state is 'precluded,'" that is, a combination of RMP and CPE/I.
6. "The amount of human, male DNA used in the testing process in this case that resulted in the conclusion that the Accused was included as a potential contributor to the genetic material in Mrs. [SLN]'s underwear was the equivalent to three or four human cells."
7. In accordance with Dr. Krane's testimony, "because this was an exceedingly small quantity," "because of the possibility of allelic dropout or drop-in (e.g., through contamination)," and because this was a minimal minor sample, this was "the most difficult sample that could be interpreted."
8. "Ms. Hanna did not conclude, one way or another, whether allelic dropout had occurred in the sample."

After reciting the law and standards pertaining to the admission of expert testimony and his role as gatekeeper, the military judge then concluded:

1. "There is no real argument about the first four *Houser* [36 M.J. 392] factors in this case: they are satisfied."
2. "KCPCL's testing procedures (i.e., the extraction of DNA from an evidentiary sample and the identification therefrom of a constellation of specific alleles at specific loci) are not in question; they are reliable under a *Daubert* analysis."
3. "However … the 'modified' formula KCPCL applied to draw conclusions about potential contributors in this case" was not shown to be reliable.
4. The KCPCL's "formula has never made it into (much less mentioned by) the SWGDAM Guidelines" and "appears wholly contradictory" to the guidelines as they "reject KCPCL's approach."
5. The "Guidelines preclude the combination of CPE/I and RMP calculations in a given sample."
6. An apparent flaw with the KCPCL's formula is "if you assume two contributors to the sample in this case, then the Accused could not have

contributed all five of the alleles detected; the second person would have had to contribute at least one of the alleles (and possibly more). This is true regardless whether allelic dropout had occurred."

7. The formula the KCPCL used did not rely on a conclusive determination whether allelic dropout had occurred.
8. "This battle of the experts would certainly be a mini-trial within the trial, with multiple experts being called and recalled to rebut one another on a highly technical issue the panel members will likely have a difficult time understanding."
9. "Using the 1 in 220 statistic, in a population as small as Weston, Missouri (1,641 in the 2010 census (citation omitted)), only 7 people could be contributors to the genetic material in Mrs. [SLN]'s underwear."
10. Because the "Government is sure to point out that of those seven possible people, only one was in Mrs. [SLN]'s house, . . . the probative value is substantially outweighed by the danger of unfair prejudice, misleading the panel members, and waste of time."

LAW AND DISCUSSION

On appeal, "[w]e review de novo the question of whether the military judge properly performed the required gatekeeping function of [Military Rule of Evidence] 702" and "'properly followed the *Daubert* framework.'" *United States v. Flesher*, 73 M.J. 303, 311 (C.A.A.F. 2014) (citing *United States v. Griffin*, 50 M.J. 278, 284 (C.A.A.F. 1999)). However, the decision by the military judge to exclude expert testimony is reviewed for an abuse of discretion. *United States v. Sanchez*, 65 M.J. 145, 148 (C.A.A.F. 2007). "A military judge abuses his discretion when: (1) the findings of fact upon which he predicates his ruling are not supported by the evidence of record; (2) if incorrect legal principles were used; or (3) if his application of the correct legal principles to the facts is clearly unreasonable." *United States v. Ellis*, 68 M.J. 341, 344 (C.A.A.F. 2010). Additionally, "[a]n abuse of discretion exists where reasons or rulings of the military judge are clearly untenable and . . . deprive a party of a substantial right such as to amount to a denial of justice." *United States v. Travers*, 25 M.J. 61, 62 (C.M.A. 1987) (internal quotation marks and citations omitted); *see also Flesher*, 73 M.J. at 311. Also, because this case came to this court by way of a government appeal under Article 62, UCMJ, we are limited to reviewing the military judge's decision only with respect to matters of law and are bound by the military judge's findings of fact unless they were clearly erroneous. We cannot find our own facts or substitute our own interpretation of the facts. *United States v. Cossio*, 64 M.J. 254, 256 (C.A.A.F. 2007) (citing *United States v. Mizgala*, 61 M.J. 122, 127 (C.A.A.F. 2005)).

We determine the military judge made two clearly erroneous findings of fact as well as multiple erroneous conclusions when applying the law and acting in his gatekeeper role.

Military Judge's Findings of Fact

The military judge found, as fact, that the "alleles present statistic" formula utilized by the KCPCL is expressly precluded by the SWGDAM guidelines. This finding is in error. First, as everybody agreed, to include the military judge, the male minor DNA profile was derived from an exceedingly small sample. Page 1 of the SWGDAM guidelines reads, "Some aspects of these guidelines may be applicable to low level DNA samples." This prolonged caveat continues, "Due to the multiplicity of forensic sample types and the potential complexity of DNA typing results, it is impractical and infeasible to cover every aspect of DNA interpretation by a preset rule." In fact, laboratories are encouraged to use their professional judgment, expertise, and experience to review their standard operating procedures, update their procedures as needed, and utilize written procedures for interpretation of analytical results.

That is precisely what the KCPCL has done. Based upon its collective expertise and judgment and in accordance with SWGDAM guidelines, it has incorporated in its DNA Analytical Procedure Manual an "alleles present statistic." This formula "accounts for allelic drop-out and makes no assumption regarding the number of contributors."[5]

The aforementioned formula has been used by the KCPCL for 15 years, and the KCPCL, along with its manuals, procedures, and written methods of statistical calculations, has been audited and inspected "about ten different times" to ensure it is not running afoul of the SWGDAM guidelines or the FBI's Quality Assurance Standards for Forensic DNA Testing Laboratories. Finally, paragraph 4.1 of the SWGDAM guidelines mandates, "The laboratory must perform statistical analysis in support of any inclusion that is determined to be relevant in the context of a case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis." The KCPCL did not mix preset and firm RMP and CPE/I formulae. It modified an RMP calculation in accordance with their assumptions, as is its scientific prerogative. Other scientists may feel it "safer" to do otherwise, but that does not mean the formula is expressly forbidden by the applicable guidelines.

The military judge also found, "Ms. Hanna did not conclude, one way or another, whether allelic dropout had occurred in the sample." This finding and its corresponding conclusion are clearly erroneous and unsupported by the record. When statistically analyzing the minor profile, the KCPCL assumed allelic dropout and then necessarily concluded that this dropout occurred when reporting the frequency ratio. Both of the witnesses from the KCPCL testified clearly and repeatedly that the "alleles present statistic" accounts for allelic dropout and is

[5] The "alleles present statistic" is the calculation of the alleles present at each genetic location accounting for possible drop-out of the sister allele in a genotype.

utilized in those scenarios where allelic dropout is assumed. In fact, one of Dr. Krane's main criticisms of the KCPCL's analysis in this case is that it was premised upon the assumption and conclusion that allelic dropout had, in fact, occurred. Dr. Krane explained that "[Ms. Hanna]'s statistic is predicated on the fact that dropout did occur. Her inclusion of Major Henning as a possible contributor is predicated on the idea that dropout must have occurred. . . . If dropout had not occurred . . . then Major Henning is actually excluded as a possible contributor."

Military Judge's Conclusions of Law

The military judge concluded the government had not shown the statistical evaluation applied by the KCPCL in this case to be "reliable." In determining that the military judge abused his discretion in so concluding, we do not do so lightly. We may not apply a review more "stringent" than abuse of discretion to a trial court's decision to receive or exclude evidence and similarly may not reverse unless the trial ruling was "manifestly erroneous." *GE v. Joiner*, 522 U.S. 136, 142-43 (1997). Likewise, we acknowledge a "court of appeals applying 'abuse of discretion' review to such rulings may not categorically distinguish between rulings allowing expert testimony and rulings which disallow it," nor was the military judge required "to admit opinion evidence which is connected to existing data only by the *ipse dixit* of the expert." *Id*. at 142, 146. That said, we find the military judge's exclusion of any and all evidence that MAJ Henning is a possible contributor to the genetic material recovered from SLN's underwear was manifestly erroneous.

In this case, both parties present experts who agree on the underlying science of DNA extraction, matching, and comparison and also agree on the underlying data that was generated, that is, five alleles present at four loci. They disagree, however, on what is to be concluded from that data. *Daubert* is clear:

> The inquiry envisioned by [Federal Rule of Evidence] 702 is, we emphasize, a flexible one. Its overarching subject is the scientific validity -- and thus the evidentiary relevance and reliability -- of the principles that underlie a proposed submission. The focus, of course, must be solely on principles and methodology, not on the conclusions that they generate.

Daubert, 509 U.S. at 594-95. The proffered frequency ratio of 1 in 220 is not connected to the presence of those specific five alleles at those specific four loci by the *ipse dixit* of Ms. Hanna; rather, it is connected by a long-used, reproducible, announced, audited, and written formula.

In excluding evidence of the statistical significance of the matching minor profile, the military judge expressly adopted Dr. Krane's conclusion that this would

be attaching weight to an "exceedingly small quantity" and is "the most difficult sample that could be interpreted." Dr. Krane did not testify that no conclusions could be drawn from the minor profile; he testified it would be "safer" to not draw any conclusions from such a profile. Our superior court has addressed a scenario where experts in the field differ in their interpretation of the underlying facts and how much weight, if any, should be given to those facts in deriving an opinion. *See Sanchez*, 65 M.J. at 151. In that case, it is made clear that any requirement that experts agree on a certain interpretation "would be at odds with the liberal admissibility standards of the federal [and military] rules and the express teachings of *Daubert*." *Id*. at 152 (quoting *Amorgianos v. Amtrak*, 303 F.3d 256, 267 (2d. Cir. 2002)). Furthermore,

> A review of the caselaw after *Daubert* shows that the rejection of expert testimony is the exception rather than the rule . . . . The trial court's role as gatekeeper is not intended to serve as a replacement for the adversary system. As the Court in *Daubert* stated: "Vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate means of attacking shaky but admissible evidence."

United States v. Billings, 61 M.J. 163, 169 (C.A.A.F. 2005) (citation omitted). At worst, the KCPCL's approach was *shaky* science; it was definitely not *junk* science and should not be excluded. *See Sanchez*, 65 M.J. at 153 (citing *Kumho Tire Co. v. Carmichael*, 526 U.S. 137, 152 (1999)).

A trial judge certainly can and should form an opinion as to the reliability of differing scientific approaches when performing his role as gatekeeper. However, here, the military judge overstepped his bounds and conducted his own scientific analysis and statistical evaluation. In the "*Conclusions*" portion of his ruling, the military judge points out his perceived flaws in the KCPCL's formula and then proceeds to discuss the possibilities of heterozygous or homozygous alleles at various loci and how those eventualities would potentially impact the appropriate statistical approach. The problem lies in his statement, "First, if you assume two contributors to the sample in this case, then the Accused could not have contributed all five of the alleles detected; the second person would have had to contribute at least one of the alleles (and possibly more). This is true regardless whether allelic dropout had occurred." Not only do we question the scientific and mathematical validity of the above statement, it is wholly unsupported in the record. None of the experts testified consistent with the military judge's base premise. Accordingly, we are left with the distinct impression that in this battle of the experts, the military judge became his own expert, conducted his own analysis of the evidentiary DNA data and application of the SWGDAM guidelines in a manner not addressed by any

of the experts, and consequently impermissibly assumed a role far different than that of gatekeeper.

In the same portion of his ruling, the military judge criticized the government for providing "no evidence of error rates with regard to KCPCL's formula or what the statistical cutoff is for inclusion as a possible contributor (e.g., is 1 in 100,000 a permissible statistic to be included?)." Regardless of the obvious observations that a pure numerical cutoff line would, by definition, go to the weight of a factual finding as opposed to its validity or admissibility and that a statistical cutoff is a distinct concept from an error rate, we again look to *Sanchez*. "Nothing in the precedents of the Supreme Court or this Court requires that a military judge either exclude or admit expert testimony because it is based in part on an interpretation of facts for which there is no known error rate or where experts in the field differ in whether to give, and if so how much, weight to a particular fact." *Sanchez*, 65 M.J. at 151.

We now turn to the military judge's Military Rule of Evidence 403 balancing in which he found the probative value of the KCPCL's "statistical conclusion" is "substantially outweighed by the danger of unfair prejudice, misleading the panel members, and waste of time." We find three parts of his balancing to be manifestly erroneous.

First, the military judge found the probative value of the statistical conclusion, the 1 in 220 ratio, to be minimal. There is a disconnect between the concerns the military judge harbored with respect to the reliability of the KCPCL's formula and his blanket exclusion of evidence that MAJ Henning is a *possible* contributor to the discovered genetic material. In accordance with the options found in the SWGDAM guidelines and in line with Dr. Krane's suggestion, the most favorable conclusion the defense could have hoped for was that comparison of MAJ Henning's DNA to the minor profile was either inconclusive or uninterpretable. But, even in that event, because per SWGDAM, "statistical analysis is not required for exclusionary conclusions," that would still potentially leave evidence that the other males in the house that night in question are excluded as contributors to the male minor profile found in SLN's underwear. In other words, in this case, the importance of the numerical ratio may be relatively minimal. But, in light of the categorical exclusion of other potential suspects, any evidence that MAJ Henning is a possible contributor, even to a small degree, would still be highly probative.

Second, the military judge concludes this "battle of the experts would certainly be a mini-trial within the trial, with multiple experts called and recalled to rebut one another on a highly technical issue the panel members will likely have a difficult time understanding." We echo the Supreme Court in that this view "seems to us to be overly pessimistic about the capabilities of the jury and of the adversary system generally. Vigorous cross-examination, presentation of contrary evidence, and careful instruction on the burden of proof are the traditional and appropriate

means of attacking shaky but admissible evidence." *Daubert*, 509 U.S. at 596. The questions of whether SLN was assaulted and by whom do not constitute the subjects of any "mini-trial;" rather, they are the very essence of *the* trial.

Third, inconsistent with his prior conclusion that the probative value of the KCPCL's "resulting statistical conclusion" is minimal, the military judge then applied the 1 in 220 ratio against the population of the city where the alleged crime occurred and concluded that his calculation that only seven people in that city could be contributors is a significant and unfairly prejudicial statistic. The military judge observed, "The Government is sure to point out that of those seven possible people, only one was in Mrs. [SLN]'s house." In this case, we find that evidence that an accused's DNA possibly matches that of genetic material found at the scene of the alleged crime to indeed be prejudicial, but not even remotely unfairly so. Once a proper foundation is laid, not only is DNA testing sufficiently reliable and admissible, but evidence of statistical probabilities of an alleged match is admissible as well. *See United States v. Allison*, 63 M.J. 365 (C.A.A.F. 2006).

CONCLUSION

"The military judge's role as evidentiary gatekeeper does not require him to admit only evidence that he personally finds correct and persuasive and to exclude that which he finds incorrect or unpersuasive. Rather, the judge's role is to screen all evidence for minimum standards of admissibility and to let the factfinder determine which evidence is more persuasive." *United States v. Kaspers*, 47 M.J. 176, 178 (C.A.A.F. 1997). We possess, as a reviewing court, "a definite and firm conviction that the [military judge] committed a clear error of judgment in the conclusion [he] reached upon a weighing of the relevant factors" and thus find an abuse of discretion. *See Houser*, 36 M.J. at 397 (quoting Magruder, J, *The New York Law Journal* at 4, col. 2 (March 1, 1962), quoted in *Quote It II: A Dictionary of Memorable Legal Quotations* 2 (1988)).

The appeal of the United States pursuant to Article 62, UCMJ, is granted. The ruling of the military judge to exclude evidence that MAJ Henning is a possible contributor to the genetic material recovered from SLN's underwear on the bases that the KCPCL's formula and its application in this case are unreliable and unfairly prejudicial is set aside. The record will be returned to the military judge for action not inconsistent with this opinion

Senior Judge COOK and Judge WEIS concur.

FOR THE COURT:

MALCOLM H. SQUIRES, JR.
Clerk of Court

CHARGE SHEET

I. PERSONAL DATA

1. NAME OF ACCUSED (Last, First, Middle Initial)	2. SSN	3. GRADE OR RANK	4. PAY GRADE
HENNING, Antiwan M.	354-62-5065	MAJ	O-4

5. UNIT OR ORGANIZATION	6. CURRENT SERVICE	
	a. INITIAL DATE	b. TERM
Headquarters and Headquarters Company, Combined Arms Center, Fort Leavenworth, Kansas	5 Dec 2002	INDEF

7. PAY PER MONTH			8. NATURE OF RESTRAINT OF ACCUSED	9. DATE(S) IMPOSED
a. BASIC	b. SEA/FOREIGN DUTY	c. TOTAL		
$7,149.60	$0.00	$7,149.60	None	N/A

II. CHARGES AND SPECIFICATIONS

10. CHARGE I: VIOLATION OF THE UCMJ, ARTICLE 120

SPECIFICATION 1: In that Major (O-4) Antiwan M. Henning, U.S. Army, did, at or near Weston, Missouri, on or about 7 September 2013, commit a sexual act upon Mrs. Sarah L. Nightengale, to wit: penetrating her vulva with his penis, by unlawful force, to wit: moving her to the floor and pulling down her panties and penetrating her vulva with his penis.

SPECIFICATION 2: In that Major (O-4) Antiwan M. Henning, U.S. Army, did, at or near Weston, Missouri, on or about 7 September 2013, commit a sexual act upon Mrs. Sarah L. Nightengale, to wit: penetrating her vulva with his tongue, by unlawful force, to wit: pulling her panties to the side and penetrating her vulva with his tongue.

SPECIFICATION 3: In that Major (O-4) Antiwan M. Henning, U.S. Army, did, at or near Weston, Missouri, on or about 7 September 2013, commit sexual contact upon Mrs. Sarah L. Nightengale, to wit: touching her breast with his hand when the accused knew or reasonably should have known that Mrs. Sarah L. Nightengale was asleep.

(END OF CHARGES)

III. PREFERRAL

11a. NAME OF ACCUSER (Last, First, Middle Initial)	b. GRADE	c. ORGANIZATION OF ACCUSER
HAEUSSLER, Frederic D.	O-4	HHC, Combined Arms Center

d. SIGNATURE OF ACCUSER	e. DATE (YYYYMMDD)
	20140814

AFFIDAVIT: Before me, the undersigned, authorized by law to administer oath in cases of this character, personally appeared the above named accuser this 14th day of August, 2014, and signed the foregoing charges and specifications under oath that he/she is a person subject to the Uniform Code of Military Justice and that he/she either has personal knowledge of or has investigated the matters set forth therein and that the same are true to the best of his/her knowledge and belief.

JOSEPH A. MORMAN	HHC, CAC
Typed Name of Officer	*Organization of Officer*
O-3	Trial Counsel
Grade	*Official Capacity to Administer Oath (See R.C.M. 307(b)_ must be commissioned officer)*

Signature

12.

On 14 AUGUST , 2014 , the accused was informed of the charges against him/her and of the name(s) of the accuser(s) known to me *(See R.C.M. 308(a)). (See R.C.M. 308 if notification cannot be made.)*

Frederic D. Haeussler	HHC, Combined Arms Center
Typed Name of Immediate Commander	*Organization of Immediate Commander*
O-4	
Grade	
Signature	

IV. RECEIPT BY SUMMARY COURT-MARTIAL CONVENING AUTHORITY

13.

The sworn charges were received at 1630 hours, 14 August , 2014 at Headquarters, Special Troops
Designation of Command or

Battalion, Fort Leavenworth, Kansas 66027 .
Officer Exercising Summary Court-Martial Jurisdiction (See R.C.M. 403)

FOR THE [1] _____

Karen S. Hanson	Commander
Typed Name of Officer	*Official Capacity of Officer Signing*
O-5	
Grade	
Signature	

V. REFERRAL; SERVICE OF CHARGES

14a. DESIGNATION OF COMMAND OF CONVENING AUTHORITY	b. PLACE	c. DATE *(YYYYMMDD)*
HQs, USACAC and Fort Leavenworth	Fort Leavenworth, KS	20141121

Referred for trial to the General court-martial convened by Court-Martial Convening Order Number 10, this headquarters

dated 6 May , 2014 , subject to the following instructions: [2]

none

By Command of Lieutenant General Robert B. Brown
Command or Order

LESLIE A. ROWLEY	Deputy Staff Judge Advocate
Typed Name of Officer	*Official Capacity of Officer Signing*
O-5	
Grade	
Signature	

15.

On 21 November , 2014 , I (caused to be) served a copy hereof on (each of) the above named accused.

JOSEPH A. MORMAN	CPT
Typed Name of Trial Counsel	*Grade or Rank of Trial Counsel*
Signature	

FOOTNOTES: 1 - When an appropriate commander signs personally, inapplicable words are stricken.
2 - See R.C.M. 601(e) concerning instructions. If none, so state.

CHARGE SHEET

I. PERSONAL DATA

1. NAME OF ACCUSED (Last, First, Middle Initial)	2. SSN	3. GRADE OR RANK	4. PAY GRADE
HENNING, Antiwan M.	354-62-5065	MAJ	O-4

5. UNIT OR ORGANIZATION	6. CURRENT SERVICE	
Headquarters and Headquarters Company, Combined Arms Center, Headquarters, United States Army Garrison, Fort Leavenworth, Kansas 66027-2300	a. INITIAL DATE: 05 December 2002	b. TERM: INDEF

7. PAY PER MONTH			8. NATURE OF RESTRAINT OF ACCUSED	9. DATE(S) IMPOSED
a. BASIC	b. SEA/FOREIGN DUTY	c. TOTAL		
$7,149.60	$0.00	$7,149.60	NONE	N/A

II. CHARGES AND SPECIFICATIONS

10. THE ADDITIONAL CHARGE : VIOLATION OF THE UCMJ, ARTICLE 120 (After 28 Jun 12).

The Specification: In that Major Antiwan M. Henning, U.S. Army, did at or near Weston, Missouri, on or about 7 September 2013, commit a sexual act upon Mrs. Sarah L. Nightengale, to wit: penetrating her vulva with his tongue, by causing bodily harm to her, to wit: by wrongully pulling her underwear to the side.

(END OF CHARGES)

III. PREFERRAL

11a. NAME OF ACCUSER (Last, First, Middle Initial)	b. GRADE	c. ORGANIZATION OF ACCUSER
HAEUSSLER, Frederic D.	O-4	HHC, Combined Arms Center

d. SIGNATURE OF ACCUSER	e. DATE (YYYYMMDD)
[signature]	2014 11 17

AFFIDAVIT: Before me, the undersigned, authorized by law to administer oath in cases of this character, personally appeared the above named accuser this 17th day of November, 2014, and signed the foregoing charges and specifications under oath that he/she is a person subject to the Uniform Code of Military Justice and that he/she either has personal knowledge of or has investigated the matters set forth therein and that the same are true to the best of his/her knowledge and belief.

JOSEPH A. MORMAN	HHC, CAC
Typed Name of Officer	*Organization of Officer*
O-3	Trial Counsel
Grade	*Official Capacity to Administer Oath (See R.C.M. 307(b)_ must be commissioned officer)*

[signature]

Signature

12.
On 17 Novembes , 2014 , the accused was informed of the charges against him/her and of the name(s) of the accuser(s) known to me *(See R.C.M. 308(a)). (See R.C.M. 308 if notification cannot be made.)*

Frederic D. Haeussler	HHC, Combined Arms Center
Typed Name of Immediate Commander	*Organization of Immediate Commander*

O-4
Grade

Signature

IV. RECEIPT BY SUMMARY COURT-MARTIAL CONVENING AUTHORITY

13.
The sworn charges were received at 1335 hours, 17 Nov 14 , _____ at Headquarters, Special Troops
Designation of Command or

Battalion, Fort Leavenworth, Kansas 66027 .
Officer Exercising Summary Court-Martial Jurisdiction (See R.C.M. 403)

FOR THE [1] _____

Karen S. Hanson	Commander
Typed Name of Officer	*Official Capacity of Officer Signing*

O-5
Grade

Signature

V. REFERRAL; SERVICE OF CHARGES

14a. DESIGNATION OF COMMAND OF CONVENING AUTHORITY	b. PLACE	c. DATE *(YYYYMMDD)*
HQs, USACAC and Fort Leavenworth	Fort Leavenworth, KS	20141121

Referred for trial to the General court-martial convened by Court-Martial Convening Order Number 10, this headquarters , dated 6 May , 2014 , subject to the following instructions: [2] to be tried in conjunction with the original charge preferred on 14 August 2014

By Command of Lieutenant General Robert B. Brown
Command or Order

LESLIE A. ROWLEY	Deputy Staff Judge Advocate
Typed Name of Officer	*Official Capacity of Officer Signing*

O-5
Grade

Signature

15.
On 21 November , 2014 , I (caused to be) served a copy hereof on (each of) the above named accused.

JOSEPH A. MORMAN	CPT
Typed Name of Trial Counsel	*Grade or Rank of Trial Counsel*

Signature

FOOTNOTES: 1 - When an appropriate commander signs personally, inapplicable words are stricken.
2 - See R.C.M. 601(e) concerning instructions. If none, so state.

PROCEEDINGS OF A GENERAL COURT-MARTIAL

The military judge called the Article 39(a) session to order at Fort Leavenworth, Kansas, at 0902 hours, 4 December 2014, pursuant to the following order:

Court-Martial Convening Order Number 10, Headquarters, Combined Arms Center and Fort Leavenworth, Fort Leavenworth, Kansas, dated 6 May 2014.

[END OF PAGE]

DEPARTMENT OF THE ARMY
HEADQUARTERS
U.S. ARMY COMBINED ARMS CENTER AND FORT LEAVENWORTH
FORT LEAVENWORTH, KANSAS 66027-2300

GENERAL COURT-MARTIAL CONVENING ORDER NUMBER 10 — 6 May 2014

Pursuant to the authority of General Order number 16, Headquarters, Department of the Army, dated 20 December 2002, a General Court-Martial is convened with the following members detailed as the "Primary Panel" and shall meet at the courtroom, 415 Custer Ave, Building 244, Fort Leavenworth, Kansas 66027, unless otherwise directed:

* COL DREW R. MEYEROWICH, 0432, IN, LD&E, (20090601)
COL DAVID P. KOMAR, 6055, FA, CDID, (20090901)
COL TIMOTHY P. SULLIVAN, 4613, FA, MCTP, (20120301)
* LTC ZAID I. Y. ABDULRAHMAAN, 4071, LG, MCTP, (20101101)
LTC JOHN D. DALBEY, 6671, AR, LD&E, (20110101)
* LTC RENE YBARRA, 7324, EN, MCTP, (20110601)
LTC TONY L. DEDMOND JR., 0427, AD, MCTP, (20130901)
*MAJ TRACIE M. HENRYNEILL, 2795, LG, LD&E, (20090401)
*MAJ MANUEL GONZALEZ, 0172, FA, MCCO, (20110901)

1SG ANTHONY W. BRAGG, 2554, 31E, HHC, 705TH MP BN, (20110801)
MSG GREGORIO VILLANUEVAOCHOA, 6973, 68W, HHC, USDB, (20091101)
SFC BRUCE L. SMITH, 8619, 31E, 165TH MP CO, (20090801)
SFC SEAN L. HOOKER, 8101, 31B, 500TH MP CO, (20121001)
SFC AMANDA S. JENKINS, 5226, 92Y, 291ST MP CO, (20130701)

Pursuant to the authority of General Order number 16, Headquarters, Department of the Army, dated 20 December 2002, a General Court-Martial is convened with the following members detailed as the "Alternate Panel" and shall meet at the courtroom, 415 Custer Ave, Building 244, Fort Leavenworth, Kansas 66027, unless otherwise directed:

LTC RYAN D. STRONG, 3544, MI, LD&E, (20091101)
LTC THOMAS GOLDNER, 1371, IN, LD&E, (20100201)
LTC MICHAEL J. CATHEY, 4705, LG, LD&E, (20100901)
LTC GLENN R. MOSHER, 8442, FA, LD&E, (20101101) (BASD: 19930720)
LTC RICHARD B. DAVENPORT, 4569, PO, LD&E, (20101101) (BASD: 19930728)
LTC RANDY T. JOHNSON, 1289, AV, USACAC - FT. LVN, (20110201)
LTC MICHAEL L. ESSARY, 0315, AD, MCTP, (20111101) (BASD: 19940423)
LTC JEFFREY E. REDECKER, 7621, AC, MCTP, (20111101) (BASD: 19941015)
LTC ADAM M. CHALMERS, 8693, EN, MCTP, (20131201)
LTC AMANDA B. AKERSVORNHOLT, 7560, LG, LD&E, (20140301)
MAJ CEDRIC L. J. BURDEN, 9611, IN, MCTP, (20071101)
MAJ MARIA A. STEWART, 9841, AG, USACAC - FT. LVN, (20071201) (BASD: 19930415)
MAJ RODNEY D. JOHNSON, 8374, MP, MCTP, (20071201) (BASD: 19980103)
CPT JENNIFER A. EVANS, 4250, MS, MEDDAC, (20080701)
CPT BRIAN L. SMITH, 4164, MI, MCTP, (20090601)
CPT KATHRYN A. CRANE, 7659, MC, HHC, 40TH MP BN, (20120608)
CPT SARAH L. JABO, 2315, SP, HHC, 40TH MP BN, (20131201)

CONTINUATION SHEET FOR General Court-Martial Convening Order Number 7, 10 a
Headquarters, United States Army Combined Arms Center and Fort Leavenworth, Fort Leavenworth, Kansas 66027-2300

MSG RONNY O. DACOSTA, 7948, 79S, USACAC - FT. LVN, (20090201)
MSG LUIS OLMOJIMENEZ, 4078, 31E, HHC, USDB, (20101001)
MSG ERIC MAINU, 7796, 51C, MCTP, (20130701)
SFC BRIAN A. WALLACE, 9095, 31E, HHC, USDB, (20080501)
SFC GRANT L. PRATT, 0932, 68W, MEDDAC, (20081101) (BASD: 19941030)
SFC DOUGLAS C. APPELGREN, 7645, 31E, HHC, JRCF, (20081101) (BASD: 19970820)
SFC AARON R. HEIZER, 0425, 31E, 526TH MP CO, (20081201)
SFC NICHOLAS A. HOAD, 4330, 31E, HHC, JRCF, (20090801)
SFC DANNY L. LICCIARDI JR., 3424, 56M, USACAC - FT. LVN, (20100701)
SFC RENE M. SALAZAR, 3375, 31E, HHC, USDB, (20101001)
SFC BRIAN S. WILDMAN, 8615, 31E, 256TH MP CO, (20101201)
SFC DUSTIN A. CLAYTON, 2785, 11B, MCTP, (20120501)
SFC SHAWN D. BRYANT, 5690, 31B, 500TH MP CO, (20120801)
SFC CEDRIC M. WILSON, 1887, 42A, HHC, 15TH MP BDE, (20130201)
SFC SAMANTHA KELLY, 4338, 42A, USACAC - FT. LVN, (20140301)
SSG JIM K. MEDINA GARCIA, 5137, 42A, MCTP, (20051101)
SSG ROGELIO O. AGUILAR JR., 4887, 68X, HHC, JRCF, (20081101)
SSG ERICA R. HALLADAY, 4712, 68X, HHC, USDB, (20090101)
SSG ALEJANDRA JOHNSON, 9623, 31E, HHC, 15TH MP BDE, (20110301)
SSG ALDRIN M. TEJADA, 9898, 12H, HHC, 40TH MP BN, (20111201)
SSG SHALYNN A. EVANS, 3619, 51C, MCTP, (20120101)
SSG NATHANIEL BENTON JR., 3253, 31E, HHC, 40TH MP BN, (20120601)

*Temporarily excused when enlisted panel is requested.

This Court-Martial Convening Order supersedes General Court-Martial Convening Order Number 1, dated 6 February 2014. All cases previously referred to General Court-Martial by Court-Martial Convening Order 1, dated 6 February 2014, as amended by Court-Martial Convening Order Number 3, this headquarters, dated 7 March 2014, as amended by Court-Martial Convening Order Number 6, this headquarters, dated 29 April 2014, as amended by Court-Martial Convening Order Number 7, this headquarters, dated 29 April 2014, in which the proceedings have not begun, will be brought to trial before the court-martial hereby convened, effective the date of 6 May 2014.

BY COMMAND OF LIEUTENANT GENERAL BROWN:

LUISA SANTIAGO
LTC, JA
Deputy Staff Judge Advocate

DISTRIBUTION:
1 – Each Member
1 – Adjutant General
1 – Military Judge
1 – Defense Counsel

MJ: This Article 39(a) session is called to order.

TC: Your Honor, this court-martial is convened by General Court-Martial Convening Order Number 10, Headquarters, United States Army Combined Arms Center and Fort Leavenworth, dated 6 May 2014, copies of which have been furnished to the military judge, counsel, and the accused, and which will be inserted into the record at this point.

The charges have been properly referred to this court for trial and were served on the accused on 21 November 2014. The five day statutory waiting period has expired.

The prosecution is ready to proceed with the arraignment in the case of the United States versus Major Antiwan M. Henning.

The accused and the following persons detailed to this court are present:

COLONEL JEFFERY R. NANCE, MILITARY JUDGE;

CAPTAIN JOSEPH A. MORMAN, TRIAL COUNSEL; and

CAPTAIN RUSSELL D. WARDLOW, DEFENSE COUNSEL.

Ms. Ruth Vaughn has been detailed reporter for this court and has been previously sworn.

I have been detailed to this court-martial by Colonel John S.T. Irgens, Staff Judge Advocate, US Army Combined Arms Center and Fort Leavenworth.

I am qualified and certified under Article 27 Bravo and sworn under Article 42 Alpha, Uniform Code of Military Justice. I have not acted in any manner that might tend to disqualify me in this case.

MJ: All right, thank you, Trial Counsel.

Defense Counsel, have you received Section III disclosures to your satisfaction?

DC: Yes, Your Honor.

MJ: Major Henning, you have the right to be represented by Captain Wardlow who's your detailed military defense counsel. He is provided to you at no expense to you. You also have the right to request a different military lawyer to represent you, and if the person you requested were reasonably available, he or she would be detailed to represent you free of charge as well. If your request for this other military lawyer were granted, you wouldn't have the right to keep the services of Captain Wardlow on your case because you're only entitled to one free military lawyer. You could request his superiors to allow him to stay on the case, but your request would not have to be granted.

Now in addition you may be represented by a civilian attorney. A civilian attorney would have to be provided by you at no expense to the government. If you were represented by a civilian attorney, you could keep your military attorney or attorneys on your case to assist your civilian attorney or you could excuse your

military attorney and be represented only by your civilian attorney. All of that that I just explained to you is your rights to counsel or your rights to representation. Do you understand those?

ACC: Yes, sir.

MJ: Any questions about those?

ACC: No, sir.

MJ: By whom do you wish to be represented?

ACC: Captain Wardlow and Mr. James Brun.

MJ: And Mr. James Brun?

ACC: Yes, sir; Bravo-Romeo-Uniform-November.

MJ: Okay, and I'll note that Mr. Brun is not here today. Have you retained him, meaning that have you paid a retainer to him?

ACC: Yes, sir, I have.

MJ: All right. As we discussed in the RCM 802 session which was held prior to this session, present at which were counsel for both sides and the military judge, Mr. Brun needs to make a--file a notice of appearance before the court. He can provide that to Captain Wardlow or provide it directly to me and Ms. Vaughn, whichever he prefers to do, but he's not here today for this arraignment session, so, Major Henning, do you consent to being represented for purposes of this arraignment session only by Captain Wardlow?

ACC: Yes, sir.

MJ: Captain Wardlow, would you state your qualifications and by whom you've been detailed please?

DC: Sir, I've been detailed to this court-martial by Major Frank E. Kostik, Senior Defense Counsel, U.S. Army TDS Fort Leavenworth Field Office. I am qualified and certified under Article 27 Bravo and sworn under Article 42 Alpha, Uniform Code of Military Justice. I have not acted in any manner which might tend to disqualify me in this court-martial.

MJ: All right, thank you, Captain Wardlow.

Before we--well, I have been properly certified and sworn and detailed myself to this court-martial. I am not aware of any matter which might be a grounds for challenge against me. Does either side desire to question or challenge me?

DC: No, Your Honor.

TC: No, Your Honor.

MJ: Counsel for both sides appear to have the requisite qualifications and all personnel required to be sworn have been sworn.

Before trial counsel announces the general nature of the charges, I noted one typographical error on the charge sheet. On the original charges it says "Charge I". That should just be "The Charge". It's just a numbering thing, so, Defense, do you object to having that administrative change made to the charge sheet?

DC: No, Your Honor.

MJ: So when we're done here, Trial Counsel, just line through the Roman numeral I and write the word "The" above "Charge" and put your initials out in the margin of the original charge sheet that Ms. Vaughn has.

TC: Yes, Your Honor.

MJ: All right, now you may announce the general nature of the charges.

TC: Your Honor, the general nature of the charges in this case are two specifications of rape, after 28 June 2012; one specification of sexual assault, after 28 June 2012; and one specification of abusive sexual contact.

The original charge and the additional charge were preferred by Major Frederic D. Haeussler and forwarded with recommendations as to disposition by Major Frederic D. Haeussler, Lieutenant Colonel Karen S. Hanson, and Colonel Timothy R. Wulff.

The Article 32 Bravo investigation was conducted on 1 October 2014.

MJ: And who was the Article 32 investigating officer?

TC: Lieutenant Colonel Crumley, sir, Tom Crumley.

MJ: The additional charge you make as a violation of what? Is what general nature--what is the general nature of the additional charge?

TC: Sir, the additional charge would be sexual assault, after 28 June 2012.

MJ: I think the additional charge as it's referred is a rape. It's referred as a rape as far as I can tell. A rape is any person subject to this chapter who commits a sexual act upon another person by using unlawful force against that person.

TC: Sir, I believe the addition charge alleges bodily harm.

MJ: Oh, I'm sorry, that's right. It does allege a bodily harm. Okay, you are correct. And in Specification 3 of The Charge you have as a----

TC: Sir, that would be abusive sexual contact, sir.

MJ: Okay, that is correct.

Major Henning, you have the right to be tried by a court consisting of at least five officer members. That is a court composed of commissioned and/or warrant officers, and in your case it would just be commissioned officers because they all have to be senior in rank to you. Do you understand that?

ACC: Yes, sir.

MJ: If you're tried by a court with members, the members would vote by secret written ballot and at least two-thirds of them would have to agree before you could be found guilty of any offense, and if you are found guilty of any offense, then two-thirds of the members would have to agree on any sentence in your case, and if that

sentence were to include confinement for more than 10 years, then three-fourths of the members would have to agree. Now you also have the right to request to be tried by military judge alone. If your request for trial by me alone were approved, there wouldn't be any court members and I alone would determine whether or not you're guilty of any offense, and if I found you guilty of any offenses, I alone would determine an appropriate sentence for you.

Do you understand the difference between a trial before members and a trial by military judge alone?

ACC: Yes, sir.

MJ: And do you understand the choices that you have?

ACC: Yes, sir.

MJ: And what type of court do you wish to be tried?

DC: Sir, the defense would wish to defer entry of----

MJ: Forum selection?

DC: Yes, sir.

MJ: Okay, forum selection is deferred. Because forum selection is deferred the court is not assembled, but the accused will nevertheless be arraigned.

DC: Yes, sir.

TC: All parties to the trial have been furnished a copy of the charge and the additional charge. Does the accused want it read?

DC: The accused waives the reading.

MJ: The reading of the charges may be omitted.

[THE CHARGE SHEET FOLLOWS AND IS NOT A NUMBERED PAGE.]

[END OF PAGE]

TC: Both the charge and the additional charge is signed by Major Frederic D. Haeussler, a person subject to the Code as accuser, is properly sworn to before a commissioned officer of the armed forces authorized to administer oaths, and is properly referred to this court for trial by Lieutenant General Robert B. Brown, the Convening Authority.

MJ: All right. Accused and defense counsel please rise.

[The accused and defense counsel stood.]

MJ: Major Antiwan M. Henning, I now ask you how do you plead. Before receiving your plea, I advise you that any motion to dismiss or grant other relief should be made at this time. You may be seated, Major Henning. Captain Wardlow will do the talking from this point on.

DC: Sir, Major Henning requests to defer entry of pleas and motions.

MJ: Okay. Pleas and motions are deferred.

Major Henning, what has just happened--thank you, Captain Wardlow. What has just happened is called an arraignment and an arraignment has certain legal consequences, one of which I'd like to explain to you now. Under ordinary circumstances you have the right to be present at every phase of your trial. However, now that you have been arraigned if you're voluntarily absent on the day the trial is scheduled to begin, which is the 2nd of March, the trial could go

forward all the way up through and including sentencing, if necessary, without you being present. Do you understand that?

ACC: Yes, sir.

MJ: So it's critical that you keep your chain of command and your defense counsel apprised of your whereabouts at all times between now and when this case goes to trial. As I mentioned, the case is scheduled for the 2nd of March. I issued a pretrial order yesterday, setting the case for the case for the 25th of February with a motions hearing on the 23rd of January.

In the R.C.M. 802 session defense counsel let me know that he was not aware that Mr. Brun would not be available on that week that I had set the case for trial when Captain Wardlow submitted the electronic docket request, and so that caused me to end up setting the date at a time that Mr. Brun would not be available. Based upon what Captain Wardlow represented to me, based upon his discussion with Mr. Brun, Mr. Brun is available the following week, the 2nd of March and so I moved the trial ahead three or four days on the docket to begin on the 2nd of March when Mr. Brun will be available. The motions hearing date is still on the 23rd [sic] of March and Captain Wardlow is going to go back to Mr. Brun and find out if that date is suitable for him, and if not, we'll find another date to do the motions hearing in this case.

Is that an accurate reflection of what was discussed in the R.C.M. 802 session, Counsel?

DC: Yes, Your Honor.

TC: Yes, Your Honor.

MJ: Including what I talked about earlier about Mr. Brun's notice of appearance and so forth?

DC: Yes, Your Honor.

TC: Yes, Your Honor.

MJ: All right, anything else to take up before we adjourn this Article 39(a) session?

DC: No, Your Honor.

TC: No, Your Honor.

MJ: All right, this Article 39(a) session is adjourned.

[The Article 39(a) session adjourned at 0917 hours 4 December 2014.]

[END OF PAGE]

[The 39(a) session convened at 0832 hours 24 April 2015.]

MJ: This Article 39(a) session is called to order. All parties present when the court recessed are again present, except Colonel Jeffery Nance, whom I have replaced as military judge [**LTC Charles L. Pritchard**]; **Mr. James Brun** is now present as civilian defense counsel. Mr. Brun, please announce your qualifications.

CDC: Your Honor, I'm an attorney and licensed to practice law in the states of Kansas and Missouri and the federal courts in Kansas and Missouri. I'm a member in good standing of the bars in Kansas and Missouri. I have not acted in any manner which might tend to disqualify me in this court-martial.

[The civilian defense counsel was sworn by the military judge.]

MJ: I've been properly certified and sworn, and detailed myself to this court-martial. I'm not aware of any matter that might be a ground for challenge against me. Does either side desire to question or challenge me?

CDC: No, Your Honor.

TC: No, Your Honor.

MJ: Counsel for both sides appear to have the requisite qualifications and all personnel required to be sworn have been sworn.

The court held various R.C.M. 802 conferences with counsel by email, discussing docketing, potential motions and the interplay

between them. A defense request for enlargement of time to file motions, which the court granted; a defense request for continuance for the motions hearing based on expert availability, which the court granted; and Mr. Brun's notice of appearance.

On 3 April I held an 802 conference with counsel in person where the government indicated they would move to dismiss Specification 2 of the charge. We discussed witness/accused for the motions, changes in the parties in the convening orders, and the fact that the government agreed to produce an adequate substitute for the evidence the defense sought to compel, and that the defense was withdrawing its motion to compel.

My understanding is that the defense expert produced its own electropherograms from the Kansas City Police Crime Lab data and that the crime lab was going to review those electropherograms to determine if they accurately reflect the digital data the crime lab analyst used.

This morning I held an 802 counsel--802 with counsel in person where we discussed continuing the trial by one week to accommodate a personal issue of the defense expert witness. Trial is now scheduled for 12 to 15 May.

Counsel, does that accurately summarize the various 802 conferences?

DC: Yes, Your Honor.

between them; a defense request for enlargement of time to file motions, which the court granted; a defense request for continuance of the motions hearing based on expert availability, which the court granted; and Mr. Brun's notice of appearance.

On 3 April I held an 802 conference with counsel in person where the government indicated they would move to dismiss Specification 2 of the charge. We discussed witness issues for the motions, changes in the parties and the convening orders, and the fact that the government agreed to produce an adequate substitute for the evidence the defense sought to compel, and that the defense was withdrawing its motion to compel.

My understanding is that the defense expert produced its own electropherograms from the Kansas City Police Crime Lab data and that the crime lab was going to review those electropherograms to determine if they accurately reflect the digital data the crime lab analysts used.

This morning I held an 802 counsel--802 with counsel in person where we discussed continuing the trial by one week to accommodate a personal issue of the defense expert witness. Trial is now scheduled for 12 to 15 May.

Counsel, does that accurately summarize the various 802 conferences?

DC: Yes, Your Honor.

TC: Yes, Your Honor.

MJ: Government, please announce the changes to the convening order.

TC: Your Honor, the change to the convening order is that General Court-Martial Convening Order Number 1, Headquarters, United States Army Combined Arms Center and Fort Leavenworth, dated 17 December of 2014, copies of which have been provided to the military judge, counsel, and the accused.

MJ: Major Henning, Judge Nance explained your forum rights to you. That is the different compositions of the court-martial by which you may elect to be tried. Do you need me to repeat those rights?

ACC: No, thank you--no, sir.

MJ: Do you understand the choices that you have?

ACC: Yes, sir.

MJ: By what type of court do you wish to be tried?

ACC: Panel.

MJ: Officer panel? The accused was previously arraigned. Defense, are you prepared to proceed on your motions?

DC: Yes, Your Honor.

MJ: All right. Go ahead.

[The following page is CMCO Number 1, mentioned previously on this page and is an unnumbered page.]

General Court-Martial Convening Order Number 10 was the last of the series for 2014.

DEPARTMENT OF THE ARMY
HEADQUARTERS
U.S. ARMY COMBINED ARMS CENTER AND FORT LEAVENWORTH
FORT LEAVENWORTH, KANSAS 66027-2300

GENERAL COURT-MARTIAL CONVENING ORDER NUMBER 1 — 17 December 2014

Pursuant to the authority of General Order number 16, Headquarters, Department of the Army, dated 20 December 2002, a General Court-Martial is convened with the following members detailed as the "Primary Panel" and shall meet at the courtroom, 415 Custer Ave, Building 244, Fort Leavenworth, Kansas 66027, unless otherwise directed:

COL PAUL P. REESE, 6939, AR, MCCOE, (20130101)
*COL GREGORY H. PENFIELD, 3572, AR, LD&E, (20140301)
*COL JEFFREY A. MERENKOV, 0355, IN, USACAC - FT. LVN, (20140401)
*LTC KATHLEEN B. FARREN, 7696, AV, LD&E, (20111101)
LTC DAVID L. SHOFFNER, 9732, CH, MCTP, (20111104)
*LTC ERIC R. OLSON, 0063, IN, NSC, (20121201)
*LTC ANDREW H. LANIER IV, 9994, AR, LD&E, (20130501)
MAJ JEROME A. KING, 2020, EN, MCTP, (20091101)
MAJ ALICIA L. PRUITT, 6162, AG, USACAC - FT. LVN, (20120201)

CSM KEITH R. WHITCOMB, 3607, 12A, LD&E, (20080701)
MSG KENNETH E. ROMINE, 1474, 42A, GARRISON, (20071201)
1SG ADAM R. PATTERSON, 9368, 31E, 165TH MP CO, (20130301)
SFC JEREMY M. SCHULTZ, 1604, 11B, USACAC - FT. LVN, (20070801)
SFC DEVON A. MARTELLOTTI, 1164, 31E, HHC, JRCF, (20110101)

Pursuant to the authority of General Order number 16, Headquarters, Department of the Army, dated 20 December 2002, a General Court-Martial is convened with the following members detailed as the "Alternate Panel" and shall meet at the courtroom, 415 Custer Ave, Building 244, Fort Leavenworth, Kansas 66027, unless otherwise directed:

COL HENRY A. ARNOLD III, 3063, IN, LD&E, (20071001)
COL MYRON J. REINEKE, 0143, IN, MCTP, (20100401)
COL CHRISTOPHER N. PRIGEE, 0677, AR, USACAC - FT. LVN, (20110601)
COL STEPHEN T. MILTON, 4605, AC, MCCOE, (20111001)
COL GORDON A. RICHARDSON, 7238, FA, MCTP, (20120701)
COL ERICA C. NELSON, 4955, MP, HHD, 15TH MP BDE, (20130401)
COL ANNA R. FRIEDERICHMAGGARD, 5904, LG, LD&E, (20130801)
COL JAMES G. ERBACH, 9174, AV, MCTP, (20140101)
COL TY D. BONNER, 8537, IN, MCTP, (20140201)
COL PAUL M. SALTYSIAK, 5181, LG, MCCOE, (20140301)
COL WILLIAM H. KACZYNSKI, 7691, AV, TRAC, (20140701)
LTC STEVEN D. ROSSON, 3652, MI, LD&E, (20070401)
LTC LUIS D. SOLANO, 9852, EN, MCCOE, (20090407)
LTC RYAN D. STRONG, 3544, MI, LD&E, (20091101)
LTC HENRY C. YOUNG JR., 0465, LG, LD&E, (20100101)
LTC BRYAN K. DESPAIN, 9035, AG, MCCOE, (20110103)
LTC NICHOLAS A. JOSLIN, 6512, FA, LD&E, (20110501) (BASD: 19940308)
LTC RICHARD S. CORREZ, 1486, AR, MCCOE, (20110501) (BASD: 19940705)

CONTINUATION SHEET FOR General Court-Martial Convening Order Number 1, Headquarters, United States Army Combined Arms Center and Fort Leavenworth, Fort Leavenworth, Kansas 66027-2300

LTC ALBERT C. HILL JR., 6834, FA, MCCOE, (20111101) (BASD: 19910611)
LTC ANDREW H. WARNINGHOFF, 2555, LG, LD&E, (20111101) (BASD: 19990517)
LTC SCOTT L. UNSWORTH, 0101, IN, MCCOE, (20120601)
LTC BRIAN V. DELEON, 9209, AD, MCCOE, (20130301)
LTC NIHOLAS E. AYERS, 7630, AR, LD&E, (20130601)
LTC FRANK L. NIETO, 3732, AD, MCCOE, (20130701)
LTC CURTIS L. JOHNSON, 0395, LG, LD&E, (20140201)
CSM HENRY M. MONTOYA, 4022, 25X, LD&E, (20080901)
MSG VERNA F. BELLAMY, 2284, 92G, HHD, 15TH MP BDE, (20090801)
MSG RYAN B. NAGY, 6724, 11Z, MCTP, (20100401)
MSG JUSTIN L. SMITH, 0871, 31E, HHC, JRCF, (20111201) (BASD: 19960917)
1SG SHELETHEA Y. BAILEY, 3074, 31E, 291ST MP CO, (20111201) (BASD: 19980424)
MSG DAVID D. ROWE, 4523, 92G, HHC, USDB, (20140601) (BASD: 19930623)
MSG JASON B. WAITKOSS, 8632, 25B, MCCOE, (20140601) (BASD: 19960613)
SFC LEE A. MOSS, 3916, 35F, MCTP, (20040501)
SFC TRAVIS K. SULLIVAN, 9274, 31E, 165TH MP CO, (20080601)
SFC HEATH A. MCLAUGHLIN, 3081, 19K, MCCOE, (20090901)
SFC GARY W. FINK, 6086, 35F, MCTP, (20101101)
SFC BRIAN S. WILDMAN, 8615, 31E, 291ST MP CO, (20101201)
SSG RAYMOND A. RODRIGUEZ, 8824, 31B, 500TH MP DET, (20071001)
SSG WILLIAM E. PRUITT, 3081, 31E, 165TH MP CO, (20080801)
SSG DAVID A. BEATON, 1683, 31B, 500TH MP DET, (20130601)

*Temporarily excused when enlisted panel is requested.

BY COMMAND OF LIEUTENANT GENERAL BROWN:

Leslie A Rowley

LESLIE A. ROWLEY
LTC, JA
Deputy Staff Judge Advocate

DISTRIBUTION:
1 – Each Member
1 – Adjutant General
1 – Military Judge
1 – Defense Counsel

DC: Prior to calling the witness though I just wanted to make sure that we can get Dr. Krane on the phone.

TC: Your Honor, prior to calling the witness the government would like to move to dismiss Specification 2 of Charge I.

MJ: Okay, on what grounds?

TC: Your Honor, the Specification of the Additional Charge is charged in the alternative and therefore the government moves to dismiss Specification 2.

MJ: [Reading silently] Okay, defense have any objection?

DC: No, Your Honor.

MJ: All right, Specification 2 of Charge I, yes?

TC: Yes, sir.

MJ: All right, Specification 2 of Charge I is dismissed under R.C.M. 907(d)(3)(b). Go ahead.

[Dr. Daniel Krane was called telephonically]

Dr. Krane: Hello, this is Dan Krane.

DC: Sir, this is Captain Wardlow. You're on a speaker phone in a courtroom at Fort Leavenworth. Are you available to participate in the hearing now?

Dr. Krane: Yes, I am. I'm ready and waiting.

DC: All right, sir, so what--so if you could just stand by we're going to call the first witness, okay, and please let us know if you can't hear at any point, okay?

Dr. Krane: I will certainly do that. Thank you.

DC: And, sir, the defense calls Miss Jessica Hanna.

Dr. Krane, sir, can you hear me from here? Dr. Krane?

Dr. Krane: Yes, I can hear you.

DC: Okay, thank you.

JESSICA HANNA, civilian, was sworn as a witness for the defense, was sworn, and testified as follows:

DIRECT EXAMINATION

Questions by the trial counsel:

Q. You are Miss Jessica Hanna?

A. I am.

Q. And could you please state your current city and state of residence?

A. I live in Kansas City, Missouri.

TC: Thank you.

Questions by the defense counsel:

Q. Miss Hanna, you're employed by the Kansas City--KCPCL, Kansas City Police Criminal Laboratory?

A. Correct.

Q. And you actually performed the testing involved with the case for Major Antiwan Henning?

A. Yes, I performed some testing.

Q. Okay. Part of that testing was the testing on what was eventually labeled as the----

[The court reporter indicated she could not hear the witness and the mic was adjusted.]

Q. So, Miss Hanna, you performed the DNA analysis on the stains that were identified during the serological screening of the underwear that was collected in this case, correct?

A. Correct.

Q. And you identified several profiles, one of them--a couple major profiles as well as what was labeled as a 3.2 minor profile, right?

A. Minor genetic information.

Q. Okay. I would like to talk about that minor profile, but I'm just going to--for your convenience I'm just going to refer to that as the minor profile, okay?

A. Okay.

Q. Now, at this point--well, from your testing you can't actually determine how many minor--how many contributors there were that made up that minor profile, correct?

A. In the testing it was very minimal, so we're not comfortable stating it was one or more than one contributor; correct.

Q. Okay, so in terms of the conclusions that you can draw you--you can say it was one or more, but you can't be more specific than that?

A. Correct.

Q. Okay. How much template DNA was used in terms of generating that profile and analyzing that profile?

A. Can I look at my notes?

Q. Yes.

A. [Looking through notes] The total template DNA was 1 nanogram and that's all--that's the human amount used.

Q. And could you describe for the court the statistical analysis that you performed in generating a random match probability or a modified random match probability for that minor profile?

A. So for the minor profile because we say that it's more or more than one, we don't say it's just one, I did a--what we call an alleles presence statistic, so what you do is you use that allele so that information that's in each of the locus and you take into account a person that has that and any other possible allele in the population, and that's used at each of those locations.

Q. And then how do you arrive at the final number?

A. So each of the locations you get a locus frequency and this is how you do any kind of statistic, and each of those locations are

Q. Okay, so in terms of the conclusions that you can draw you--you can say it was one or more, but you can't be more specific than that?

A. Correct.

Q. Okay. How much template DNA was used in terms of generating that profile and analyzing that profile?

A. Can I look at my notes?

Q. Yes.

A. [Looking through notes] The total template DNA was 1 nanogram and that's all--that's the human amount used.

Q. And could you describe for the court the statistical analysis that you performed in generating a random match probability or a modified random match probability for that minor profile?

A. So for the minor profile because we say that it's more or more than one, we don't say it's just one, I did a--what we call an alleles presence statistic, so what you do is you use that allele so that information that's in each of the locus and you take into account a person that has that and any other possible allele in the population, and that's used at each of those locations.

Q. And then how do you arrive at the final number?

A. So each of the locations you get a locus frequency and this is how you do any kind of statistic, and each of those locations are

then multiplied together to get the profile frequency or the genetic information frequency.

Q. And how does the issue of not knowing the number of contributors, how does that factor into your statistical analysis?

A. In this case it makes it actually a more conservative statistic because I'm taking into the assumption that whoever--anybody that could have that allele and any other allele in the population would be included in that instead of just saying it's this one person and this is their profile.

Q. And is there a--is there a source, sort of a standard source that your laboratory uses in terms of guiding it for what--well, strike that question. Do you know what the SWGDAM guidelines are for genetic testing and genetic analysis?

A. Yes.

Q. So where would your lab identify where the guidelines allow for the kind of calculation that you did in this case? Can you point us to what source of authority your lab uses to use the analysis that you just described?

A. Okay. This might be a long winded answer, but we do use SWGDAM as a guideline. It's a guideline that's used throughout the community--or community. It's not something that is set. In the guideline it states that not every example can be stated of exactly what you do; that you have to do whatever your assumptions say that

you do, so we do a modified version of things that are listed in the guidelines and do what we call an alleles present statistic. Nothing in the guidelines say that you can't do it. It gives indications of ideas that you can use for this and it's what we've done and used for over 15 years for this type of statistic.

Q. Would you say that the statistical calculation you did was a modified random match probability?

A. If you get into the terms that SWGDAM uses versus what we use at our laboratory, yes, it's a--like--it's a modified version of the unrestricted one.

Q. Okay. Are you aware that SWGDAM states that a modified random match probability requires an assumption or a known value for the number of contributors for a sample?

A. That's why it's a modified version, so what we're doing is we're basing--our statistic is backing up what our assumptions are, so my assumptions are that I don't know the number of contributors and that there is a dropout occurring, so what I am doing is making a statistic that goes with those assumptions that we follow. So in SWGDAM it says you have to base your statistic based on your assumptions, and so what my--those were my assumptions and this is the way to do a statistic based on my assumptions.

Q. Right, but SWGDAM specifically says when you have--you could only use a modified RMP when you actually assume a particular number of contributors, right?

A. They actually say the unrestricted. They don't use the term "modified", so we're modifying it.

Q. Okay.

A. They're saying unrestricted random match probability, so we're modifying that to be able to take in account--there is a portion of the SWGDAM guidelines that talk about going into allelic dropout with random match probability, and, again, it's modified version that we do where our assumptions--our statistic is backing what our assumptions say, so there's the way that we can give weight to what our assumptions and conclusions are.

Q. So maybe you can help me then because what I looked at, and again speaking as a layman, I looked at the interpretation guidelines, you know, the 2010 version, the most recent version of those guidelines, page 12 states "while the random match probability is commonly thought of in terms of single source profile the application of this formula to evidentiary profiles inherently includes an assumption of the number of contributors to the DNA sample. As such this document also applies to the term RMP to mixture calculations where the number of contributors is assumed and this has sometimes been referred to as a modified RMP", so they're

using it in that term. What are you doing or what did you do that was different?

A. So we didn't make--we didn't make a conclusion on the number of contributors. My assumption is that it--anybody--that is one or more than one contributor, so I'm not making a conclusion on that. So, statistically I'm taking into account any dropout that could possibly be occurring instead of saying that all those alleles are there and it's that one person, so that's what's different in my statistic of taking into--taking in that it might be more than one person.

Q. But didn't the ultimate number you came up with assume that it was all from the same person?

A. No, it did not.

Q. How did you account for the fact that there could have been a contributor, for instance, of the five loci, another person could have contributed to one or more of those loci?

A. So alleles present statistics, so each of those locations to be matching that you have to have at least one of those alleles that's showing at each location. Statistically what we're taking into account is each one of those alleles and anything else that could possibly be would be included in that, so it does put into--that those--that a person has to have each one of those, but it doesn't say that's the same person and if you look at specifically--

let's see, the THO1 locus where there's two alleles, typically if you had one person you would say those two go to that same person because each person has one from their mom, one from their dad. You have two things of genetic information. In this case I'm saying I don't know if it's one or more than one, so those two pieces of genetic information aren't put together saying that this person is a 6, 9. They're actually calculated separately that this person could have a 6 or anything else and could have a 9 or anything else.

Q. One moment. So in paragraph 5.2.2.3 of those--of that same SWGDAM guidelines document that I referenced it says--since you mentioned alleles present, it states that an example of what calculation is used for an alleles present statistic accounting for dropout--well, excuse me; 5.2.2.3 says "In a mixture--in a mixture having at a locus alleles P, Q, and R, assumed to be from two contributors, where all three alleles are below the stochastic threshold, the interpretation may be that the two contributors could be heterozygote-homozygote, pairing where all alleles were detected, a heterozygote-heterozygote paring where all alleges were detected or heterozygote-heterozygote pairing where a fourth allele might have dropped out." So is it the case in your view that the SWGDAM guidelines allow for an alleles present calculation when you have an unknown number of contributors or when you have two specific--an assumption of two contributors?

A. It's whatever your assumptions is. If you're saying it's a lower peak height, so it depends on what you're saying is your--if we get into like a stochastic threshold where you're saying that you know all the alleles are there versus if you don't know the alleles are there, so in my opinion it doesn't matter if you're saying you know the number of contributors or don't. It's just if you know that the alleles are there or if they're below your stochastic threshold where you have to say it could be something else that's dropping out.

Q. I'd like to talk a little bit about stochastic thresholds. Could you explain what a stochastic threshold is, just for----

A. Yeah, so when we develop profiles you have an amount florescence that's added to each of the alleles that you're looking at. That's detected and tells you how much DNA is there based on how much florescent is seen and observed, and to make--based on your testing, based on your testing of the cases and working it you've set a threshold of where you would see something and have the sister alleles--we talked about that there's two alleles per person, not dropout, so not possibly have a PCR effect of dropping out and not being seen, so in--our laboratory has--we have a 300 RFU, so 300 florescent units, you have to have that before you can say there's a possibility that a sister allele to that person could be below threshold or we could not be seeing it.

Q. Right, but specifically the stochastic threshold which--well, could you comment on how your lab adjusts or deals with the possibility of a stutter and how to distinguish that?

A. A stutter?

Q. Um-hum.

A. So a stutter peak is a PCR product that can occur--that does occur and is documented occurring. It's usually about a base pair ahead of the allele that's being called. Through a validation and through published data we have a percentage that you expect to see, like a max percentage of how much--or a few would be there based on the allele it's coming from, and so if it's under that max percentage, it's filtered out so we don't see it. So if, say, one's like 15 percent if something--go to specific instance, if it's like an 11, the allele is an 11, at 10 you might see like a little--something's there, but if it's below the 15 percent stutter ratio, then it's not considered an actual allele; it's considered a possible stutter.

Q. And that's by--that's with the--that's in terms of what the computer software does in terms of automatically filtering it out if it's below that range.

A. That's how we've set out our computer software, correct.

Q. However, in terms of when you do your analysis you look at it to see whether or not what has been identified as a stutter peak by the software might be an actually allelic peak, right?

A. If it's in our range we wouldn't consider it that, so if it's under our stutter range, we wouldn't consider an actual allele peak because it could be expected to be a stutter, so we wouldn't want to call something that could be just a PCR product an actual allele.

Q. Okay. The SWGDAM guidelines specifically say that if a peak is below--at 3.5 dash-- 3.5.8.3, "If a peak is at or below the expected stutter threshold it is generally designated as a stutter peak. However, it should also be considered as a possible allelic peak particularly if the peak height of the potential stutter peaks is consistent with or greater than the heights observed for any allelic peaks that are conclusively attributed." So the peaks that were conclusively attributed in this case involved peaks that were in the hundred, two-hundred range, right, even lower than that, right?

A. There are low peak heights for the minor, yes.

Q. So the stutter peak heights from potentially major profiles were about the same as the actual allelic peaks that you identified, correct?

A. And I think from what you're reading without reading it they're saying you have to take into account and make sure that

you're not calling that an allele that where it could be an actual just stutter.

Q. Okay, so it actually says "However, it should also be considered as a possible allelic peak particularly if the peak height of the potential stutter peaks is consistent with or greater than the height observed for any allelic peaks that are conclusively contributed."

A. And that would be something like if I was doing mixture notes and saying that it was one person, only one person and I was--if--and I think if the peaks were even higher is what they're talking stutter, because there are circumstances that you would want to take that into account. In this case where I'm not saying it's just one person and saying whose alleles have to be there I'm not missing any information or I'm not falsely saying that it's--um--like somebody is an 11, 11 when they could have had something that's in stutter and I'm missing, and I'm not falsely saying that. I'm just saying these are the alleles that are there and not saying it's one profile and not saying anything is homozygote, which is what they're saying why you have to take into account stutter is that you might falsely call something a homozygote versus that it could be actually a heterozygote with that allele that's in stutter.

Q. Right, but how about in this case where at the D-18 locus you have an unlabeled peak at a height of 100 RFU and it's only 8.4

percent of the labeled 15 peak that was at that locus and--an unlabeled 17 peak of the D-18 has a height of 97 RFU and is only 9.6 percent of the height of the labeled 18 peak at that locus, right, so I guess how do you account for the fact that you have this major contributor with these very high peaks and it seems like you might have been mixing the stutter from that major contributor with an allelic peak in the minor contributor. How do you differentiate those?

A. We consider those because they're in the range that they could be stutter. We're going to consider those that they are not true allelic data, that they are stutter, so it's not considered a peak. I'm not adding that as an allele that's possibly there. We're saying that that most likely is stutter and we can't say that it's not, so we're not going to consider something--it would be worse to consider something an allele when it's not an actual true allele versus saying that it's stutter and a PCR product, which this accounted for, which we've shown occurred and which we see all the time in every profile we work. You always see stutter, so we're not going to ever give something an allele, call it an allele when it falls into the range of what our stutter is and what we have seen stutter go to and that's why we have a percentage.

Q. Right, but in the case--in the case where you have something that could potentially be stutter, but also potentially be

an allele and you can't tell because the actual allelic peaks are about the same height and that potential stutter, potential allele peak would actually be exculpatory, for instance, in a case like this. Your--the position of your lab in that circumstances is to do what?

A. Again, if it fits into our stutter range it's considered stutter. Stutter is documented. We see it all the time. It happens in everything, so we're going--that is stutter. It's falling within the range, that's what it is going to be.

Q. Okay. Would you agree that there's no generally accepted means of attaching a--like a statistical weight to a mixed DNA sample with an unknown number of contributors? Is that a true statement or not?

A. A might be we--that's what I did in this case.

Q. Okay.

A. We have an alleles present statistic that's--again, whatever the statistic we did matches our assumption is generated.

Q. So you think you can do that?

A. Correct.

DC: Thank you, ma'am, I have no further questions.

MJ: Captain Wardlow, repeat again your last question. Just tell me what it was.

DC: Yes, sir. The last question was simply that I asked Miss Hanna if she would agree that there's no generally accepted means of attaching a statistical weight to a mixed DNA sample with an unknown number of contributors where there may have been allelic dropout, and she indicated that they could.

MJ: Right.

TC: Miss Hanna, I actually have a few brief questions.

MJ: Do me a favor. Just check that Dr. Krane is still listening.

TC: Dr. Krane, can you still hear us in the courtroom?

Dr. Krane: Yes, I can, thank you.

TC: Okay, thank you.

CROSS-EXAMINATION

Questions by the trial counsel:

Q. You went over in great detail sort of the science that you did, that you employed at the KCPCL in this particular case, but you kind of jumped around in a few areas, so I just want to talk about the science and what it is specifically, and if you could just take it linear for us. So when you received the sample--when you signed out the sample from the evidence lab what is the first thing that you did with respect to that particular sample?

A. So we take it through our whole DNA process, so first we take it through an extraction process where we're separating the DNA

from the subtrate, whatever it's on, and then separating the DNA out from the cells and getting rid of everything else that could be possibly--that's in cells and making it just pure DNA. Then we take it to a quantitative process where we find out how much DNA is there, how much male DNA is there. From there we determine the appropriate amount, do kind of like a normalization to find the template amount that you want to amplify so then the amplification process is where the florescent tag gets attached to the areas that we're looking at and we make--it's a copy machine. We make millions of copies of that location and how much is there. From there it goes to a detection stage, so it goes through an instrument and the alleles that were copied are detected and separated out in through the software, and then we go--we analyze it to determine mixtures and allele calls and things like that.

Q. Okay.

A. And then compare it and add a statistic behind any matches, possible matches.

Q. Okay. Now is this particular form of DNA analysis is that something that's accepted in your community?

A. Yes.

Q. Is that something that can be reviewed?

A. It is.

Q. Okay. Is it something that you document in notes?

A. It is.

Q. And did you do those things in this case?

A. I did.

Q. And to your knowledge were those notes and documents provided to the government, to myself?

A. As part of discovery, correct. Yes.

Q. And about two weeks ago I forwarded an electropherogram to your laboratory and that electropherogram was provided to me by Dr. Krane. Did you receive that electropherogram?

A. I did.

Q. And did you conduct an analysis of that electropherogram?

A. I looked at it and compared it to our project, our electronic project.

Q. Okay. And from your review of that electropherogram did it seem as though Dr. Krane and his associates were able to reanalyze your data?

A. It looked like from what the list was they had the same information that we had in our project.

Q. I want to talk about the formula that you used to generate your random match probabilities in this case. Can you just please describe it from beginning to end? Just describe what that formula is.

A. Okay. So for any formula we're looking at the locus frequency so we're finding out at each of those locations how frequent the alleles that are in there are considered. When you go to do a full profile when you put it all together you multiply that all together because they're all independent events of how you--or how DNA is inherited, so in this case what we're looking at is just if the allele is there and comparing it to the person and they have to have an allele at each of those locations. In this case, again, putting it together is just doing the statistic on how frequent that allele is with anything else in the population, any other sister or the other allele that could possibly go with it including a homozygote or a heterozygote of any other thing. Those were multiplied together for the four locations that we have and a profile frequency was developed.

Q. Okay. Now the equations that you used in this case, are those equations standard in the KCPCL?

A. Yes, they are.

Q. Did you make those up for this particular case?

A. No, I did not.

Q. Were they published in a policy guideline that----

A. They're in our procedures.

Q. Could you explain that?

A. In our procedures we have operating procedures that we use step by step for everything that we do and we go into statistical analysis of all different situations that possibly could occur in the laboratory.

Q. Okay. Now, how often is your laboratory externally audited?

A. We're--we go through an audit every year, external audits every other year from that audit, and then that's in tune with the every five years of the whole laboratory audit.

Q. Now, are these policies and equations, are they part of what's audited externally?

A. Yes, they are.

Q. To your knowledge has your laboratory ever failed an external audit?

A. Not with this kind of information, no, they've not failed.

Q. Ma'am, I'd like for you to talk a little bit about the different--in your mind the difference between the science of what you did in this particular case and the conclusions that you drew, if you could just draw a distinction, ma'am.

A. So the science is from like start to finish is what we do with every----

Q. Just generally speaking if you could draw a distinction between the science of conducting a DNA analysis and then the process by which you draw a scientific conclusion.

A. Okay, so we get--we have the results, we have information that is reviewed and everybody can replicate, and then from that information we draw conclusions based on our training, based on our validations, based on our experiences and, again, that's something that can be looked upon and people can draw their own conclusions, but in our laboratory it's also technically reviewed and the person has to agree with our conclusions and results.

Q. And so you agree with the statement that there is a difference between the science that's employed at the KCPCL and then the conclusions that are drawn based on that science?

A. There can be, yes.

Q. And the conclusions are your particular conclusions drawn based off of this particular scientific test?

A. Correct.

TC: No further questions, ma'am. Thank you.

DC: No redirect, Your Honor.

EXAMINATION BY THE COURT-MARTIAL

Questions by the military judge:

Q. Okay, so let's back up. Let's pretend I'm a 3rd grader.

A. Okay.

Q. So you have a chromosome----

A. Yes.

Q. --and it has locations on the chromosomes.

A. Yes.

Q. And there are alleles attached to those locations?

A. Alleles are part of that location, yes. So what allele is---

Q. Okay. One allele from mom and one allele from dad?

A. Correct.

Q. At each one of the locations?

A. Correct.

Q. Okay. And so you inject some sort of florescence and it tells me--tells you whether an allele is present at a particular place?

A. Yeah, there's certain florescence that are attached to tags basically and those anneal to basically just have a medium replicate in nature. It happens in this--it's basically an instrument that just changes temperature so it makes DNA unanneal and then the primers that have the present on an anneal to those certain locations, so the certain locations that we're looking at that we use with our kit that's used in a forensic world, so we basically--and the forensic world allows us to have the same genetic information for the most part so we can communicate in a way with like CODIS and

everything. So, yeah, then you're getting the florescence on there and based on how much DNA is there you get more and more florescence, so if you've started--if somebody had more DNA on a sample than somebody else, making multiple copies of that, adding more florescence to those people to when you detect it that's how you can tell the heights and who has more and who has less DNA.

Q. Okay, so for this florescence, in order to say that the allele even exists you set a certain threshold for florescence units?

A. Correct.

Q. All right, and your particular threshold is 300?

A. That is for--our threshold to say that it even exists is actually set 65 RFUs. The 300 means--that's what we call stochastics, so a stochastic effect can happen when it's lower where you could maybe lose that second one, like you're seeing one, but you're not seeing the other one or it's below our threshold, so that 300 is saying when it's above there we're not expecting the other one to possibly drop out, so-----

Q. Okay, what do you mean by "dropout"?

A. We'll go back to--so when you get one from your mom, one from your dad they could be the same, so you could both have like a--one could be an 8 and one could be an 8 because it's just the amount repeat you get or one could be an 11, one could be a 12. You could have differences or the same, so we differentiate--we're talking

about sister alleles ~~as~~ in our ~~eri~~ter minology. When you have one you're considered a homozygote. So when you're talking about if it's above 300 and you have just one allele we are comfortable, based on our validations and experiencing that that person's a homozygote there. We know they're not dropping out, their allele is not dropping out. We're not missing genetic information from them, and then if you are under that because of stochastic effects because things can happen with PCR, we're saying they have that allele, but something else could be there that we're not seeing, so we're taking into consideration that they have an 8, but they could be an 8 8 or they could be an 8 anything else that we're possibly not seeing at that location.

Q. Okay, so--I think I got it. In this particular minor profile that I think you called minor genetic information, what happened, what did you see?

A. So in this case there was a major that--well, they kind of talked about a little bit, and a minor. We separate it out by how much DNA there was. This minor was very low. The peak heights were very low so I--doing the analysis wasn't comfortable saying that it was one or more than one because there is only a little bit of genetic information with very low peaks heights, so in this case with those low peak heights we have to not say--again, I'm not saying it's one person so I'm not putting that genetic information together,

especially the one location that has two. I'm not saying that that's both from the same person, I'm saying that those alleles are there. They could be from one person. Through the math they could be from two people depending on what's going on, and so statistically that's how I based what we were doing with the alleles present. That answer your question?

Q. Yes. But go back to the stochastic threshold and what you found in that minor profile.

A. It was very low. It was under the stochastic, so that's why I'm taking into the consideration that it could be that allele with anything else because it's under our stochastic threshold, the minor is.

Q. Right. So if it was over the stochastic threshold, would you have been able to say it's one person?

A. Depending on how much genetic information they had there and what was going on possibly. If the peak heights would have been a lot higher it's easier to make conclusions when you have more DNA because you have more DNA and you can--you're not--you're not possibly losing anything below threshold just because of the stochastic effect occurring.

Q. Okay, and what is this stochastic thing?

A. So a stochastic effect is just based on the little amount of DNA possibly--things can happen during PCR where it's dropping out

where as--because we said that the tag--they have to go find the amount of DNA, well, again maybe because it's so little there it's not actually finding that DNA there, so you're not seeing it or it's below our threshold that we have to have to get it. Like there's only a little bit of DNA.

Q. Below a 65?

A. Below a 65, yes.

Q. So in this particular minor profile you found----

A. Very low peak heights.

Q. --certain alleles?

A. Yeah, in certain alleles. Yeah, so what we found was a major profile and we took those alleles out and what was left were the certain alleles. There were five alleles at four different locations.

Q. [Audio problems] So we're dealing with the two at that location?

A. Yeah, two of them-- there's two alleles at one location.

Q. And three somewhere else?

A. Yes.

Q. So three other locations?

A. Correct.

Q. And while normally if the two at one location were above the stochastic threshold they could eventually say one person here--you just said these two were at this location?

A. Correct.

Q. All right, and then--so really the conclusion is that there are-- five alleles exist, they exist at these locations and above.

A. That's why I call it genetic information and not a profile because I'm not attaching like a profile that these all went to the one person.

Q. So then, taking that, what conclusion are you able to draw from that?

A. So--yes, what we--we didn't get into the results. What we did was then compare it to different individuals and in this case Henning matched to that genetic information and then we attached--that's why we did the statistic, so any time you give a conclusion of somebody being included into any kind of genetic information, a profile or a genetic information, you have to attach a weight to it and so this is the way to conservatively attach a weight to this genetic information.

Q. Okay, so you have Major Henning's DNA?

A. Um-hum [affirmative response].

Q. And he has every one of the alleles at those specific locations in that minor genetic information that you have?

A. Correct.

Q. All right. And then how do you come up with a statistic and what does the statistic mean?

A. The statistic is based on the genetic information that you have in your assumptions that you make, so a statistic is when we're talking about the locus frequency, so the locus frequency is based on numbers of how often you see that in certain population, and then when you get that then you're giving this frequency to that genetic information at each location because that's how often you would expect to find it. The more genetic information you have, you're multiplying it together, the smaller the number the more less likely it's more people than what it is, so the more genetic information you have the more you're narrowing it down. That make sense?

Q. Um-hum [affirmative].

A. So in this case there's not as much genetic information. We have five loci. All those are--or four loci, I'm sorry, five alleles. Those four loci are multiplied of--this person's included because they have this allele and they could have anything else in the population, so we're saying they're at 12, which they could be a 12, 10, 12, 11, 12, 13, whatever has been seen in the population and then multiply those four locuses together to get--or loci together to get that allele--or the profile frequency, and in this case it's the alleles present frequency.

Q. I'm still not understanding the frequency. What is it compared against? Is it compared against the entire population on a whole?

A. So it's not necessarily compared against anything. What was done is a database was made. We use an FBI database, and they take a sampling of individuals and get their profiles, and so for each allele at each location there is a profile frequency, so what was seen in that sampling of people and statistically we apply that to our statistics. It's not compared to anything for the whole world. They didn't test everybody in the whole world. They don't take that. They do a statistically accurate--they get statisticians involved when they're doing these sample sets to find out these allele frequencies for each allele at each of those locations.

Q. So, let's see if I get this right, probably will not. Let's say the FBI has fifty people and look at fifty people's DNA and they say that out of these fifty people when you have a 12 at a particular location that you're going to have an 11 the same location 80 percent of the time?

A. It's different than that. They're actually each individual, so what they're saying is I have seen those ten in 15 percent of the population, so you would expect to see a 10 15 percent of the time. So you're using that 15 for that calculation, and then the other one is separate, so then I've seen an 11 in 20 percent of

the population, so then you're using that number for that 11. If you're saying those people go together, so you're saying that 10 and 11 is from one person, then those are then multiplied together as those are your only two samples, so what it's expected to be from those two numbers multiplied together, so that's not what we did in this scenario because, again, we didn't say that that--those went together. We're saying that those could be separate from two different people.

Q. And is it standard practice to use the FBI database?

A. Yes. That's--um--yes.

Q. Okay, then how does the frequency fit in when determining whether your known DNA sample--you didn't say anything about that though. How do you go from the unknown, you know, your minor genetic ~~equation~~ information with frequencies, and how does that tie into known genetic--

--

A. Well, the frequencies come after, so what we do is we have a known profile developed and we have an unknown profile developed. We do whatever analysis we need to do on the unknowns, like in this case separating out major and the minor, and then from there we'll compare whatever knowns we need to compare it to. If a match occurs, then we have to put a weight behind it, something that's required to do so that you know what the match is because the weight could be--if

you have the full single source, you have a huge number of weight that this person matches and nobody else, and----

Q. Right, so in this case where you've got five alleles that you would take the percentage that they received in the population based on the FBI database, so each one of those alleles somehow have a formula that multiplies into five or whatever, and say that's--you know, you would expect to see this in 30 percent of the population, this--these particular five alleles at these locations, discounting the fact that two of them were in the same location, we're just treating those as individual alleles?

A. Correct, and there's not usually a percentage. We get a number, so like in this--it's like 1 in this many people unrelated in the population--or unrelated individuals as how often we see it.

MJ: I think I've got it. All right, any questions based on mine?

TC: No, Your Honor.

DC: One follow up.

REDIRECT EXAMINATION

Questions by the defense counsel:

Q. So, Miss Hanna, this is from my understanding primarily, but since you have--since you cannot say how many people contributed to that profile, right?

A. Correct.

Q. That means that one person could have contributed to that minor genetic information?

A. Correct.

Q. Two people could have contributed to it?

A. Correct.

Q. Three people could have contributed to it?

A. They could, but what we're seeing genetically that doesn't make much sense since there's only at most two alleles there, if that is understandable.

Q. Well, actually, no. I mean I don't understand that, because couldn't each of those loci have been contributed from a different person?

A. They could.

Q. Okay, so--so----

A. It's not expected that that would happen based on the amount of DNA that's there. If somebody has some DNA there, you would expect them to have a--not a different person contributing to each different one. Scientifically that doesn't make too much sense, and, again this is minor genetic information, so you can't draw as many conclusions like saying it's one person or more than one.

Q. Okay, so it's possible that--so I mean you said you would not expect that, but it's possible to have, based on those five

alleles, one, two, three, four, five people contributing separately to that sample making up that minor genetic information?

A. It--very long realm possibility it is. It's not something that I've experienced in my working information and having more information and knowing how the DNA works and how the minor is there with the major.

Q. Okay, but you indicated that it was at least not in that remote realm of possibility to have two people?

A. And that's what the calculation is based on is that--I can't say that it's just one person. It could be two people.

Q. Okay. How would the calculation change if it was one person?

A. It would actually be less conservative, so in this case if I was saying that that minor person is just one person, it actually changes the one--the one loci, that loci that has the two alleles, so in that case instead of saying that it was a six anything and a nine anything with my statistic, which makes it a lot more people in the population, I would say that person has to have a six and a nine, that that's their profile and I would make that number a lot smaller. That would be more--you know, you're narrowing it down to a lot more than saying this person can have this and/or this with anything else. You're saying this person has to have these two things.

Q. Does your calculation account for the possibility of three people or just two?

A. It doesn't take into consideration any numbers, it's just doing the alleles, so the only difference of saying it's one is how I do the calculation at one location versus not saying a number. It's just saying if you have these--if you possibly have these alleles, then you're included in this and then giving the weight behind that. So if some--like when I do a comparison if somebody wasn't in--like if--I'm comparing those four loci. If somebody wasn't included in one of those, I wouldn't have said they match this information, so then they're excluded. So if you're trying to say other people are in there, then they might not have that genetic information there. Does that make sense? So then they'd be excluded from this genetic information.

DC: Sure. No further questions, sir.

TC: Just one set of follow-ups.

RECROSS-EXAMINATION

Questions by the trial counsel:

Q. You reviewed a case file accompanying this information, the forensic part of your analysis?

A. I'm sorry, what----

Q. The case file, you reviewed a case file that accompanied the genetic information?

A. Yes.

Q. And you're aware that there were other male individuals in the home that night?

A. Yes.

Q. And did you do testing with regards to those males?

A. We compared all three males to the profiles, yes.

Q. And were any of the other ones included as a possible match?

A. No, they were both excluded.

TC: No further questions, sir.

EXAMINATION BY THE COURT-MARTIAL

Questions by the military judge:

Q. So hypothetically if one person contributed two alleles and another person contributed three alleles in order to be included as a possible match you have to have all five despite the fact that----

A. You'd have to share--you'd have to have the same alleles just by chance.

Q. And the probability or the percentage calculation somehow accounts for this?

A. Yes, what's taking in consideration of just looking at what alleles are there.

MJ: Anything else, Counsel?

TC: No, Your Honor.

DC: No, sir.

[The witness was duly warned, temporarily excused, and she withdrew from the witness stand.]

MJ: Do you guys need to recall her today?

TC: I don't--I don't believe so, sir.

DC: I would ask that she just be temporarily excused until Dr. Krane testifies.

MJ: Okay, ma'am, just hang out a while.

WIT: Okay.

MJ: Thanks.

[The witness departs the courtroom.]

DC: Sir, I would ask for a brief recess to confer with Dr. Krane on the phone prior to calling him as a witness.

MJ: Okay. Court's in recess.

[The Article 39(a) session recessed at 0926 hours, 24 April 2015.]

[END OF PAGE]

[The Article 39(a) session reconvened at 0940 hours, 24 April 2015.]

MJ: This Article 39(a) session is called to order. All parties present when the court recessed are again present.

DC: Sir, I'm just going to get Dr. Krane on the phone again.

[The defense counsel called Dr. Krane telephonically.]

DAN E. KRANE, civilian, was called telephonically as a witness for the defense, was sworn, and testified as follows:

DIRECT EXAMINATION

Questions by the defense counsel:

Q. Dr. Krane, good morning.

A. Good morning.

Q. If at any time you can't hear me or my question's not clear, just feel free to ask me to restate it, okay?

A. I will. Thank you.

Q. And, sir, if you could just speak up so that the judge--so that we can make sure the judge can hear you, okay?

A. All right. [Making adjustments] Is that better?

Q. That's excellent, sir. Thank you.

So, sir, could you just let the court know first of all what is your current duty position or title?

A. Well, I wear a few hats. In no particular order I am a professor of Biological Sciences and--with a courtesy appointment also in Computer Science at Wright State University in Dayton, Ohio.

I am also the president and CEO of a consulting company that does business as Forensic Bioinformatics and I am also enjoying time as a fellow of the American Council on Education where my host institution for that fellowship is the University of Notre Dame in Notre Dame, Indiana.

Q. Okay, sir. And you reviewed the electronic data that was divulged as part of this case, correct?

A. Yes.

Q. And you were also--you also were able to listen to the testimony of Miss Hanna who just testified a moment ago, correct?

A. Yes, I was.

Q. Okay. Initially I would just like to ask you--I asked her the question about template DNA and she indicated that it was one--one nanogram. Do you recall that?

A. Yes, I do.

Q. From your view and your experience how do you evaluate--well, what additionally can you say about that, having reviewed the electronic data as well?

A. Well, a total amount of human DNA that was used to generate the results in this case doesn't--does in fact appear to have been one nanogram of DNA, but it seems to me that the vast majority of the discussion, if not the totality of it, is not about the major contributor to the sample of a female, but rather of the minor

contributor to the sample, a male and the laboratory also assessed how much template DNA might have originated from a male in addition to the total amount of DNA. Using just sort of a back of the envelope calculation here with the laboratory's numbers, that approach tells us that there's on the order of 45 picograms of male DNA that gave rise to the male profile, the minor profile that we see. And then the DNA profile itself gives us an indication based on the relative heights of the X allele and the Y allele at the amelogenin locus that there was on the order of 15, one-five, picograms of male DNA associated with the sample that gave rise to the minor profile that we've been talking about.

Q. Okay, now what are the implications of that? What is that--what does that mean for purposes of doing an analysis?

A. Well, I think there's some quite significant implications. The test kit that the laboratory used to generate the DNA profile information specifically recommends that one nanogram of template DNA be used. One nanogram is a thousand picograms and, again, you know, the total amount of DNA that was used was a nanogram, but the focus now seems to be on some things that originated from very much less than that recommended amount of template DNA, again, by one estimate 45 picograms, by another estimate 15 picograms on the order of, you know, I'll let you do the math. I suppose that 1/50th perhaps

of what it is that the test kit is recommended and designed to be able to generate reliable results from.

Q. Okay. Miss Hanna mentioned--well, spoke extensively about the alleles present calculation, the calculation that she indicated was used. What can you--what can you say about that, about her description of that calculation and what is required by the SWGDAM guidelines?

A. Well, let me start by saying that the SWGDAM guidelines are really very fair. They provide a set of approaches to be used for circumstances where the number of contributors is unknown. Those equations, those statistical approaches only apply if allelic dropout, and I should add allelic drop-in, are not something that needs to be considered. There's an alternative set of approaches that can be used when allelic dropout, and again drop-in, may have occurred, but those only apply when there is a known number of contributors to the sample that's being evaluated. There is nothing within the SWGDAM guidelines that provides suggestions or guidance regarding reliable or useful approaches for a sample with an unknown number of contributors where dropout may have occurred.

Q. And you mentioned that other set of calculations that could be used if there was a known number of multiple contributors. Is that CPI or CPE that you referred to?

A. That's--that--CPI and CPE are two approaches that fall within that area of approaches to use for an unknown number of contributors.

Q. Okay. Now Miss Hanna also testified that all of the--all of the alleles that were identified in that minor genetic information were inclusive with the profile, the known profile, the standard profile for Major Henning. However, can you comment on that please?

A. Well, yes. That is factually correct, but I think it bears pointing out that all--the word "all" here translates to five alleles were seen, two at one locus and one each at three additional loci, but, and I think this is a very important "but", there are two alleles that Major Henning has at those four loci that do not appear in the minor profile that the statistic was generated for, so there were seven opportunities to find--and I'm going to use air quotes here, "matching" between Major Henning and the evidence sample, and at the end he's found only to--again with the air quotes, "match" at five of those seven possible opportunities for matching.

Q. So does the statistic--is the statistic able to account for that?

A. Well, the approach that Miss Hanna has used is effectively presuming that allelic dropout has occurred, not even that it might have occurred, but really in practice to include Major Henning it's presuming that the test has failed to obtain or to show us all of the

information that was inherent to the sample. In other words, that allelic dropout has occurred. Let me put this simply. Major Henning can only be included as a possible contributor if dropout has occurred.

Q. Okay, and you're saying that she was assuming that without being able to assume it, is that what you're--

A. Well, yeah, I don't know that I would quite put it that way. I think you've got what I'm trying to convey. What she has said is that because these peaks are at such a low level and then also because there's such a small amount of template DNA that dropout might or may have occurred. Her statistic is predicated on the fact that dropout did occur. Her inclusion of Major Henning as a possible contributor is predicated on the idea that dropout must have occurred. I'm more comfortable in saying that--well, let me put it this way. If dropout had not occurred, if we could be confident that these test results reliably told us all the information associated with the sample as the tests are designed to do, then Major Henning is actually excluded as a possible contributor.

Q. And could you explain why, sir?

A. Well, again, this was a test that was based upon a sample where the recommended amount of template was being used and we failed to detect two of an individual's alleles when examining the information at just four different loci, I'm confident that every--

well, that may be hard to do, but the vast majority of laboratories would in that circumstance exclude such an individual as a possible contributor. You know, just practically speaking, if an individual is contributing--let me use a specific example. If they're contributing a 13 allele at the D-18 locus and they also have a 20 allele to contribute, those two alleles should be present in equal quantity with any cells that they might leave associated with a sample. They should be equally likely to be detected. If one is detected and the other is not, the simple conclusion at that point is that that individual is not a contributor because where the 13 goes the 20 should be there as well. In this case there are two instances where Major Henning has two alleles at a locus yet only one of those two alleles is observed.

Q. Yes, sir. Is there anything else about the testing in this case that you believe is relevant to the consideration of--well, to the consideration of what the conclusions drawn were?

A. Well, I do have additional concerns. If--let me be plain, that if we were talking here about the chance that a randomly chosen unrelated individual would be found to match or be included as a possible major contributor, I think this would be a very different conversation. That fact that we're talking here about a possible minor contributor or minor contributors is ultimately really where the issue lies. Interpretation of this type of sample is extremely

complicated. It's confounded by the fact that dropout may have occurred. When you're dealing with such small quantities of DNA a very real consideration needs to be drop-in has occurred and in addition to that there can be serious problems associated with--I'll use the word "masking" from things that are attributable to the major contributor. I heard you ask a line of questions pertaining to the possibility of confusing a stutter peak with a peak from another minor contributor. That's part of what I'm talking about here, but the major contributor's peaks could also easily be hiding peaks that have come from a minor contributor, so at the end of the day this is about the most difficult of any sample that might possibly be interpreted. We have questions about the amount of drop-in and dropout and questions about the number of minor contributors, and even questions about where minor contributor alleles are present and where they're masked by the major contributor. It's not possible to generate a scenario that is more difficult to interpret than what we have for this case.

Q. And, sir, you're familiar with a number of different laboratories and their standards for interpreting results like this, correct?

A. Yes.

Q. Could you name some of them?

A. Well, surely. Maybe it would help if I start by saying that I've--I first testified as a DNA profiling expert in the winter, January, I believe, of 1991, so I've been involved with reviewing DNA testing results for--well, pretty close to the very beginning of this methodology being used. The tests themselves have changed since those early days, but the kinds of results that were generated in this case I've been reviewing and testifying about since the mid-1990s. I've testified in over twenty different states, several different courts-martial, on the order of five different federal courts as well as courts in the United Kingdom, Northern Ireland, England, and even places like Australia, so I've reviewed test results from a very wide number of places. I've served on--as a gubernatorial appointee to Virginia's Scientific Advisory Committee which oversees the policies and practices of the Virginia Department of Forensic Science. In that capacity I chaired subcommittees regarding the review of the validation studies that the laboratory did for DNA testing protocols, and I also reviewed and ultimately approved with intimate familiarity the Department of Forensic Sciences standard operating procedures and interpretation guidelines. So I've--and I've spoken at many meetings and published a number peer reviewed papers about these types of issues.

Q. So is it fair to say, sir, that the only accurate conclusion that you think can be drawn with this minor genetic

information is that it is in fact inconclusive as regards to Major Henning?

A. I'm very comfortable saying that that is the only safe opinion that can be rendered. I think it could be said this way; we are in no better position to say if Major Henning's DNA is present with this sample after we've seen the test results than we were before the tests were performed.

Q. And--well, is there anything else that you can add, sir, or that you do believe should be added?

A. Well, let me just harken back to the questions that I heard you ask Miss Hanna about the SWGDAM guidelines regarding stutter because I think some of the other points that she's made are fairly difficult to point to how it is that they're at odds with the SWGDAM guidelines. I believe I've done that when I tell you that SWGDAM provides a set of approaches for mixtures without dropout or unmixed samples or, you know, a known number of contributors with dropout, but no hybrids of the two, so I think that alone suggests that the approach that she described has some significant issues with it, but I think unequivocally her practice with respect to stutter peaks is clearly at odds with what it is the SWGDAM guidelines recommend as well as what some peer reviewed scientific literature that speaks to that topic also recommends, so I think there's clearly a departure

there between what is generally accepted within the forensic scientific community on that regard.

Q. And is it correct, sir, that the point or the location in the SWGDAM guidelines that we're referring to are the 3.5.8 section?

A. Yes, that's correct.

Q. Okay. And could you elaborate a little bit specifically about what you feel is not being met by the approach Miss Hanna described as it relates to what SWGDAM talks about?

A. Well, with regard to that specific section I think it can be expressed pretty clearly. What she testifies to is that if a peak is below the stutter threshold for a particular locus that she considers it to be an artifact. She considers it to be stutter. She does not consider the possibility that that peak might possibly also be derived in part from a minor contributor and even in the circumstance where the height of the stutter peak is equal to or greater than the height of the peaks that are associated with the minor contributor to the sample. I'm paraphrasing some language here directly from SWGDAM 3.5.8.3.

Q. And it specifically advises that an analyst has to consider that possibility, is that correct?

A. Well, here's a direct quote. It says, "However, it should also be considered as a possible allelic peak, particularly if the peak height of the potential stutter peak(s) are consistent with (or

greater than) the heights observed for any allelic peaks that are conclusively attributed (i.e., peaks in non-stutter positions) to the minor contributor or contributors."

Q. And is that specific circumstance present in this case or is the possibility for that present in this case?

A. Yes, it is.

Q. And could you say specifically where, sir?

A. Well, both. It's the D-2 and the D-18 locus there are--at both loci there are two stutter peaks associated--well, in the stutter position, relative to peaks that could have been contributed from a major contributor and in both instances those peaks were disregarded by Miss Hanna and her statistical evaluation and in both instances the heights of those peaks exceeds fairly significantly the heights of the peaks from the minor contributor that she did consider.

Q. Thank you, sir. Is there anything else that concerns you about the testing in this case?

A. Well, if I may, just on that same point if Miss Hanna had considered those peaks, it would certainly have complicated the statistic, but unequivocally it would have resulted in a less remarkable or a less damning number for the final statistic. The number that she reports is effectively 1 in 223, very weak by-- DNA profiling standards are, you know, general experience to begin with,

but that number would have been less impressive still if those stutter peaks had been added into the calculation.

Q. Thank you, sir. And finally, is there anything else that you think is relevant to the issues that have been discussed so far?

A. No, I think that sums the--well, there's one other thing. I talked earlier now about the small quantities of DNA that are the basis of these results for the male or the minor contributor or contributors. It might help to put that in a bit of context. A single human cell has on the order of six picograms of DNA associated with it, so these test results for the minor contributor or contributors are being derived from a very small number of cells, perhaps as few as two or three and unlikely to be any more than a dozen, and to put that in perspective, a human body typically has on the order of three to four billion cells, and an average fingerprint will have on the order of one hundred cells associated with it, so we're talking here about results derived from a--an exceedingly small quantity of starting material. In those circumstances the results are--there's serious questions as to their reliability because of the problems associated with dropout and drop-in, but also we have to ask about how it is that those cells could have become associated with a sample, transfer contamination, those sorts of things can become very real considerations as well, and none of that gets captured by these

types of statistics that either SWGDAM talks about or that Miss Hanna used.

DC: Thank you, sir.

WIT: My pleasure.

DC: Your Honor, those are all the question I have.

TC: Sir, could I have a brief recess to go over the information prior to cross?

MJ: Is he going to be available?

DC: Dr. Krane, if you could just stand by for a moment. We're going to take a recess. Actually, you know what, we will call you back in a few moments since we will be in recess for a few moments while the government reviews the information. Okay?

WIT: Very good.

DC: Thank you, sir.

MJ: Court's in recess.

[The Article 39(a) session recessed at 1008 hours, 24 April 2015.]

[END OF PAGE]

[The Article 39(a) session reconvened at 1037 hours, 24 April 2015.]

MJ: This Article 39(a) session is called to order. All parties present when the court recessed are again present.

[Dr. Krane is recalled telephonically and reminded that he is still under oath.]

TC: Hello, Dr. Krane, this is Captain Morman. I just want to remind you again that you're under oath.

WIT: Thank you. I recall.

TC: Thank you, sir.

I have no questions, Your Honor.

EXAMINATION BY THE COURT-MARTIAL

Questions by the military judge:

Q. Okay, Dr. Krane, this is Lieutenant Colonel Prichard, the military judge. Let me collect my thoughts and then ask you some questions. I guess the first one is tell me a little bit about the SWGDAM guidelines. It almost sounds from the way that the defense counsel is asking the questions and the way you're answering them that they are more than guidelines, that they are mandates.

A. Well, you know, I appreciate that there's a, you know, a difference in the meaning between guidelines and recommendations versus mandates. The reality is is that they do not purport to be more than guidelines or recommendations, but in reality they do reflect the best--the consensus as to what is the best practice by

the forensic science community and I think they spell out in fair--fairly specific detail what it is that is at the present time generally accepted within the scientific community and given that that translates to a legal standard in some sense then they do act as mandates as opposed to just recommendations because crime laboratories want their work to be considered, generally accepted within the forensic science community.

Q. Okay, and I may jump around here a little bit. You testified earlier that there were seven opportunities to find "matching between Major Henning and the sample" but he was only "matched at five locations". Can you explain that?

A. Yes. So [pause]. I'm just looking at some notes here. I thinking I may be able to give you some specific examples. There are four loci that are being considered here from the perspective of a statistic. There's a locus called THO 1, T-H-O-1; another called D-13, D as in Dan; another D-2; and another D-18. At any locus, given that human beings are diploid, meaning that they have two copies of their genetic instructions, we might find either one or two alleles, so we're talking about eight loci--I'm sorry, about four loci. That means that we might find anywhere between four alleles for comparison purposes and as--but not more than eight, all right, so if an individual had--the technical term is "homozygote"-- if they had two copies. If they got the same instructions from both their mother and

father, we would only see one peak or one allele at this test, but if they were a heterozygote, meaning that they got different information from both of their parents, we might see two. So let me give you a specific example, if I may. At the THO1 locus Major Henning is described as a 6, 9. The nomenclature is usually 6 comma 9. In the evidence samples the minor contributor that the lab deduces in fact has both a 6 and a 9. In contrast at the D-13 locus Major Henning is a homozygote. He has what appeared to be two copies of the 12 alleles, so he's a 12 comma 12, and the minor profile deduced by the laboratory in fact has just a 12. So, so far Major Henning is matching at 3 out of 3 possibilities or opportunities to match, but it's at the next two loci that the discrepancy in the matching arises. At D-2 Major Henning is a heterozygote. He is a 16 comma 22 and yet the minor deduced profile has only a 16. There is no 22 and similarly at the D-18 locus Major Henning is a heterozygote. He is a 13 comma 20, and yet the deduced minor profile for that locus has only a 13. There is no 20, so there were--let's--we consider it clearly two alleles that are missing, a 22 at peak 2 and a 20 at D-18, and he's a homozygote at D-18, so that brings us from 8 down to 7, if you follow my reasoning----

Q. I'm following.

A. --and at the end of this process there were seven opportunities to match. Five of those alleles are found in the deduced minor profile, two are not.

Q. And the significance you think is?

A. Well, the significance is it in some sense boils down to this. An argument can reasonably be made that if Major Henning was the source for a contributor among others, to the minor alleles that were found in this sample, then where are his 22 and 20 alleles at the D-2 and D-18 loci respectively. It's difficult to contribute some alleles and not others, and the only explanation that could be invoked to answer that question is that dropout--and let me emphasize here, must have occurred and to some extent there's a logical fallacy that's starting to creep in. How do you know that dropout has occurred? Well, because that's the only way that we can explain the absence of the alleles. Well, why do you expect them to be absent? Well, because Major Henning has those alleles, so if you see it, it's a very short logical loop that we're going through here. It's the--the anomaly is being explained by the anomaly itself, so the possibility of dropout really throws a monkey wrench, to put it very, you know, plainly into an effort to attach a statistical weight to a sample like this, and in this circumstance--there's nothing about the statistic that captures the fact that an argument could reasonably be

made that he's actually excluded as opposed to included as a possible contributor.

Q. So if I understand correctly, if you have--let's take this case, five alleles at four loci and at one or more of those loci you only find one allele that you can draw no conclusion from that because you must be able to find a second allele?

A. Well, I would say that's not quite right. What I would prefer to say is that there are essentially three ways that one might look at such a circumstance. If an individual has two alleles and yet only one is observed at that locus in an evidence sample, one might conclude that the individual cannot be excluded because dropout had occurred. Another is that the individual--another possible conclusion is that the individual is actually excluded because dropout did not occur, and a third conclusion might be to refrain from drawing a conclusion and say that we can't say if dropout or what the likelihood that dropout has or has not occurred is, therefore, since we can't decide which of those two possibilities is most likely or how to capture that into some sort of statistic it's simply safest to walk away and say that we don't care to draw a conclusion at all.

Q. Is there a definitive way to determine whether dropout has occurred other than through this, you know, backwards determination based on a known contributor?

A. Well, the short answer is more or less, yes. There--in some instances dropout is easy to identify. If no alleles at all are detected at a locus, we can reasonably conclude and everybody should agree that occurred at that locus, so if we simply have no test results, that's easy and, in fact, that circumstance is described as locus dropout. If a sample is exhibiting locus dropout at some loci that should make it more likely that allelic dropout at other loci is in play as well. Now it doesn't necessarily--the more locus dropout there is the more allelic dropout we might expect, but the only thing that the scientific community would agree upon are some fairly unhelpful generalities like the one that I just gave you. The more locus dropout there is, the more allelic dropout there may be, and the less template DNA that you start with, the more likely locus dropout and allelic dropout there will be and those generalities don't serve us well because the statistics here would require--we could capture that, but to capture those possibilities we need specific numbers. We can't just say that it's more or less likely. We need like a it's 80 percent likely, or it is 22.7 percent likely to be able to capture it in an equation and we're nowhere near that at this stage in the history of forensic DNA profiling.

Q. So your analysis is that with this so called minor profile the only conclusion that can be drawn is that allelic dropout might have occurred?

A. That is fair, dropout may have occurred. Not that-----

Q. But not that it did occur?

A. --Major Henning. It must be asserted that dropout has in fact occurred.

Q. But, again, back to what you just said, it's not possible to make that determination in this case?

A. Not with certainty, no. "Must occur" is within the realm of may occur, but also within the realm of "may occur" is "has not occurred", and so I--since we can't discern between the two and since the statistics can't capture that, again, I would say that consensus opinion in the forensic science community would be that a result such as this is simply unreliable and inconclusive.

Q. You also talked about allelic drop-in. What is that?

A. Well, let me start by making sure we're on common ground with respect to dropout. Dropout means that an allele is associated with a sample yet fails to be detected by the test, and then drop-in is the reciprocal of that. The allele is not actually associated with the evidence sample and yet manifests itself as part of the test result, and the simplest explanation for drop-in is contamination of some kind. So all that I've been saying before with small amounts of template DNA the possibility of dropout increases. The smaller the amount, the greater the possibility of dropout. That also applies

for drop-in. The smaller amount of template, the greater the risk of observing peaks due to drop-in.

Q. But, again, in this particular case there's nothing to be said other than possibility of dropout or a possibility of drop-in?

A. Correct.

Q. All right, I want to move to the stutter peaks.

A. All right.

Q. And I am now trying to remember the question I had about this. Okay, so as I understand this, in a case where an observed stutter peak is at a height equal to or greater than the peaks--the allelic peaks that you should consider the possibility that the stutter peak is actually an allelic peak?

A. I think your understanding is correct. We might be safest if we just slipped in the word minor contributor or minor contributors allelic peak, minor would be good to slip in front of the word "allelic".

Q. Okay. So if you were to consider a stutter peak as a possible minor--

A. Minor contributor's allele.

Q. Okay. Then how could you make any calculation at all? I mean it seems that you're hypothesizing that it is--it is an allele, not a--you know, not a stutter peak, but you don't know what allele it is, so how then could you draw any conclusion, any percentages,

any likelihoods that somebody is a contributor if you don't know what that allele is?

A. But we would know the allele. So a stutter peak--I'll give you a specific example from this case for the D-2 locus. At the D-2 locus the major contributor has a 20 and a 23 allele. I'll give you the heights just for your edification, but--well, maybe I--oh, yeah, here they are. The 20 is 1,889 tall and the 23 is 2,092 tall, so these are large peaks. The stutter peaks are peaks associated with those two tall peaks. There is a 19 that's associated, but may be as stutter off of the 20. That 19 has a height of 152, and there is a 22 that may be a stutter associated with the 23. The 22 has a height of 191, so as Miss Hanna had testified, stutter is a very commonly observed artifact of these tests and it is typically recognized by the position of a peak relative to another peak as well as the height of that peak relative to the other peak, so here the 19 could easily be stutter associated with the 20 because the 19 precedes the 20 and the 19 is small relative to the height of the 20 and the same could be said of the 22 with respect to the 23, so those are peaks in stutter position and what the SWGDAM guideline does unequivocally recommend is that in a statistical calculation for a minor contributor that in addition to the 16 which the laboratory deduced as being part of the minor contributor contribution, the 19 and the

22 should also be included, and just as we have allele frequencies for the 16, they're also available for the 19 and the 22.

Q. Okay, I'm not really following how you would know that the 19 and the 22 were a particular allele such that when you, for example, took Major Henning's DNA sample you could say whether or not that particular allele existed in his DNA.

A. Let me try to help you understand. So just--you know, so everybody's clear here at the D-2 locus Major Henning is a 16,22. He doesn't have either of--well, if he does have a 22, which is one of these two peaks, but he doesn't have the 19, and yet I don't know that that necessarily has to be factored into the equation here, so just as the lab has endeavored to attach a statistic to the fact that there's a 16 it's also possible to roll into that statistic the possibility that minor contributors have a 19 and/or a 22 as well. Now, obviously we've gotta start talking here about there being more than one contributor because we expect each contributor at most to contribute 2, so now we're formally entertaining and using a statistic that would require more than one contributor, but none the less that is something that could be done. That helpful?

Q. Let me mull it over.

A. All right.

Q. Well, is there any way if you were to take this particular minor profile and factor in the stutter peaks to determine what those

stutter peaks--what alleles those would represent and therefore compare it to Major Henning and say well, he is now excluded because he doesn't have that one?

A. Well, I think we may need to talk of that here, but let me start this dialogue by just putting out--Major Henning does not have a 19, so he could not be the source of the 19 that we may observe at that locus, but he does have a 16 and a 22, and so since those are there and that's what he has, then we wouldn't exclude him on the basis of that observation. We could exclude him as a possible contributor of the 19, but not of the 16 or the 22. So it might help if I just point this out, so the statistic, the general class of statistic you would use for a circumstance like that where we have an unknown number of contributors because it could--we know that there are at least two, but there could be three, there might be four people or more who could have combined to give us the 16, the 19, and the 22. The class of statistic that would be used in a circumstance like that with an unknown number of contributors falls broadly into the category of a CPI or a CPE statistic. Those approaches cannot handle, they cannot work with the possibility of dropout. It must be explicitly assumed that dropout has categorically not occurred. So if we start to talk about this being a mixture, yeah, I can help you with that. We have an approach for an unknown number of contributors then we add that "Oh, and there's a good chance that dropout may have

occurred", then all bets are off. There is no guidance from SWGDAM for such a circumstance.

Q. So there is no way to test or I guess to come up with a statistic where there are multiple, but unknown numbers of contributors and the possibility of allelic dropout?

A. There is nothing in the SWGDAM guidelines that would assist with that and there is nothing in the peer reviewed literature that provides a generally accepted approach. Let me just--this may be an unnecessary aside, but there's a new kid on the block in some sense in this regard called probabilistic genotyping. That's not at all what the testing laboratory has used in this case and SWGDAM doesn't give very much specific guidance about it so it does allow for that possibility. There's an emerging area of research where this problem might be resolved, but I don't feel we're at the point yet where any of those probable genotyping approaches have reached general acceptance and I don't know what they would tell us about this particular evidence sample. It's possible that a probabilistic genotyping approach would look at this and say, gee, it's more likely that Major Henning is excluded because of the absence of those two alleles of his than that he is included or they may say that he is included even with that taken into consideration, so there's this emerging area of work, but I think that goes beyond what it is. I can say unequivocally it goes beyond what it is the lab has used here

and I think it may go beyond what it is that you're interested in hearing about.

Q. Okay, so next let's talk about laboratory audits. Do you know anything about laboratory audits, what they do when they audit, what they're looking at, etcetera?

A. Yes, I do.

Q. Okay. Do they look at this level of detail? So my real question is if the KCPCL survived multiple years of audits, both internal and external, and has, at least from what Miss Hanna has said, been using this particular type of analysis, that is unknown multiple contributors and possibility of allelic dropout, how do they get accredited?

A. Well, I--you know, I think you've asked a very astute question and I found myself wondering that myself. Let me tell you up front that I have not served as an auditor and I do not maintain a laboratory that is audited for the purposes of the work that I do. My understanding is is that these audits look to a large extent to determine if a laboratory is capable of doing the work that it purports to do and it's assessing things like does it have adequate personnel, are those personnel adequately trained to be able to handle general issues that might arise in the course of their work, do they have adequate equipment and resources and physical space to do the work that they are purporting that they can do, do they have

protocols and validation studies that support those protocols? Those are the types of questions that it's my understanding the auditors are looking for. Now, under that sort of umbrella an auditor could ask to look--you know, to dive in deep and look at the specifics of the protocols and I'm personally firmly of the opinion that if an auditor looked very carefully at this statistic that's being used by the laboratory in this case, that that would have raised a red flag and the questions would have--would have arisen. The fact that that hasn't occurred at the very least tells us that--well, I don't know, it tells me that nobody has looked at that level of detail. I mean the laboratory's interpretation guidelines includes formula. I think the issues arising is with the application of those formula and to really see how that works you have to get under the hood and look at the spread sheets, which the lab has very helpfully provided to us, and it's when you look at them that, again, we find a sort of mixed bag where in some circumstances they're using equations that are for unknown number as contributors where dropout hasn't occurred, and in other loci they're using a set of equations for a known number of contributors where dropout may have occurred. And, again, it's that mixed bag that's the problem here.

MJ: Okay, I think that's all I have for now. Any questions based on mine, Counsel?

TC: No, Your Honor.

DC: No, Your Honor.

MJ: All right, thank you, Dr. Krane. Temporarily I assume?

DC: Yes, sir.

[The witness was temporarily excused, duly warned, and the telephonic connection was terminated.]

TC: You don't want to keep him on the line?

MJ: I may recall Miss Hanna. Do you need him to be listening?

TC: Well--and I have a list of witnesses that I'm going to be calling as well, so I don't know if he wants to listen to their testimony. I thought that that was the point.

DC: Yeah, okay.

[The witness was again called telephonically.]

Dr. Krane: Hey, Captain Wardlow, so what's your take?

DC: Well, sir, we're actually still in the courtroom now and I actually hung up a little too soon. We're going to have the--the government is going to call some witnesses, so I needed to keep you on the line. Is that all right?

Dr. Krane: Oh, sure. I'll be happy to hang on for a while.

DC: All right, thank you.

Dr. Krane: No problem.

MJ: Any other evidence, Defense?

DC: No, Your Honor.

MJ: Government?

TC: Your Honor, the government calls Mr. Scott Hummel.

SCOTT HUMMEL, civilian, was called as a witness for the prosecution, was sworn, and testified as follows:

DIRECT EXAMINATION

Questions by the trial counsel:

Q. And you are Mr. Scott Hummel?

A. Yes, that's correct.

Q. And can you please state your city and state of residence?

A. I live in Kansas City, Missouri.

Q. Thank you. Mr. Hummel, I just want to get a little bit of background as to who you are before we jump into some of the more substantive evidence. Where do you currently work?

A. I work at the Kansas City Police Crime Laboratory and I'm the Chief Criminalist of the DNA Biology Section.

Q. And could you please give us a little bit of detail about what all is entailed in your job?

A. My primary function as Chief Criminalist is administrative. I manage the staff, oversee the personnel issues, case management, case assignment, things of that nature. Ultimately the quality assurance and technical aspects are my responsibility although we do have a technical leader in my section as well. Is that not loud enough [referring to the microphone and adjusting it]?

Q. Yeah, if you could just please, and then just--if you could just speak up just a little bit.

A. Sure.

Q. Thank you. And have you received formal civilian education in the area of biology?

A. Yes, I have a Bachelor's degree in biology and I have a Master's Degree with a concentration in Forensic Serology in DNA.

Q. Okay. And how long have you been working with the KCPCL?

A. Almost 15 years.

Q. And more specifically how long have you been in your current assignment, your current job?

A. I've been the Chief Criminalist of the section for almost 6 years.

Q. Thank you. I want to talk to you a little bit about nanograms and picograms and how that relates to testing particularly in your laboratory.

A. Okay.

Q. So how many nanograms is recommended by your particular testing materials?

A. The target template that we use is part of the kit referencing in this case is 750 picograms or .75 nanograms, the same equivalent.

Q. And in cases such as this where there's a major and a minor contributor and the minor contributor may have a lower number of picograms in and around the 50 picogram area, why might that be in a testing situation?

A. Well, again, specifically in this case what we're talking about is a mixture of DNA, so we have a component from one individual and a component from another individual, so when we go into that testing the target amount that we're looking for is from that extract from the sample, but that sample itself is a mixture. We can't go into that sample and parse out, for instance, in this case the male contributor. We're looking at the sample as a totality, so when we target that 750 picograms the hope is of course we'll have enough or sufficient information in that minor contributor to make useful interpretations, but it's quite possible that there's a small amount of DNA present in the sample and we get a small amount of genetic information, but you can't simply add more DNA to the sample to bring up the minor contributor, because what that does is overload the sample and makes the entire sample unreadable.

Q. And can you please describe a little bit more what you mean by that, it makes the sample unreadable and specifically as it relates to the major contributor?

A. Yes, so as we've said, we had a target amount of DNA that we're looking for. Now we can use less than that amount of target

because all that--what that does is simply means we may get less information from the sample. We have an idea amount we want. If we don't have that much, we may still attempt testing to try to get some useful information. However, you cannot go beyond that amount because it's a very sensitive system, and so by adding more DNA than you need, what you do is create a lot more additional artifacts. The system becomes saturated and it basically makes the genetic information, the electropherograms that we've discussed a lot in this case, it makes them difficult, if not impossible, to read depending on the amount of material that you add beyond what is the recommended or ideal amounts.

Q. So, fair to say that when you pull out a sample amount, in this case 1 nanogram, you're stuck with the genetic information in that particular sample?

A. Yes, that's correct.

Q. Okay. And so--and in your experience that lab wouldn't go in and manipulate, you know, various picograms if they're from major minor contributors in any one sample?

A. That's not possible, that's not a--that's not a real--that's not something that I could do.

Q. Okay. Thank you. I want to talk to you a little bit about SWGDAM and I want to talk about the difference between SWGDAM

guidelines and then quality assurance standards and how they relate to accreditation and how they relate to auditing.

A. Yes.

Q. Could you please tell us a little bit about the SWGDAM guidelines, what they are and how they relate to a lab?

A. So if I might back up just one step and just get a little background. SWGDAM, which is the scientific working group on DNA analysis methods is composed of a variety of personnel across the country from laboratories, from academia, research institutions, governmental bodies coming together to try to provide consistent procedures and protocols for all laboratories across the country to use and agree upon. Those standards, those recommendations are then issued--or, sorry, given over to the FBI, who issues the formal standards. Those standards are a requirement by which we can say we're--we followed those standards for accreditation purposes for accrediting bodies as well as for participation in a national DNA database. In addition to these standards that we must follow to be a DNA laboratory in this country this working group, this body of people over time, and this isn't just an isolated incidence, as the DNA technology has evolved over decades periodically issues guidelines. These guidelines are a working product, a living product for labs to try to come together and address common issues, common technologies to try to get a consensus about how these things should

be done. However, as the name implies, these guidelines are not requirements or mandates as they are in relation to the standards that we must follow. They're practices suggested for us to look at--look at our own practices, see if we're completely out of line with the community, if we're in line with the community, if there's things that we should be thinking about that we haven't thought about, and then to take these guidelines and adapt them to our own laboratory's policies and procedures as we see fit through our experimental validation studies and through our case working history and experience.

Q. Okay. Now I want to focus in on accreditation before we talk about your--the KCPCL's particular accreditation. I want to talk about what specifically is reviewed through the accreditation process. Are individual case files and particular case work reviewed in this process?

A. Yes. So, in the--the accreditation process speaks to the laboratory being accredited by a body or as it's the American Society of Crime Lab Directors, Laboratory Accreditation Board. In addition to accreditations as part of the DNA standards that we follow we're also required to undergo external audits at least once every two years. In both of those instances during the DNA audits and during the accreditation audits one of the key components is case work

review of each analyst who has produced case work in that--in any discipline.

Q. Okay, so they do case work review. Do they also review policies and procedures of the DNA section of the laboratory as well?

A. Yes. In each of those instances we provide them all of our manuals well before they ever come on site, so they'd had plenty of time to read through each of those manuals before they ever get to the laboratory.

Q. Okay, now I want to talk specifically here. In your policies and procedures in those manuals does it contain the equations that are used by the laboratory?

A. Yes. All of our statistical formulas, equations, guidelines are listed in our analytical procedures.

Q. And so all that is sent out to the accrediting body in advance of any audit?

A. Yes, it is.

Q. Okay. Now I want to talk about the case files. Now, obviously in this case and in other cases these equations are used in DNA testing at the laboratory?

A. Yes.

Q. And those particular case files have been reviewed?

A. Yes.

Q. Okay. And your lab is currently accredited?

A. Yes. We recently just passed our third--our new accreditation under international standards, but our third accreditation under ASCLD/LAB this past June.

Q. Okay, so ASCLD, can you please----

A. Yes, again, so there are a couple of different accrediting bodies that you can use in the forensic community. One of the most popular is the American Society of Crime Lab Directors Laboratory Accreditation Board. That body now currently uses what are called ISO standards. They're international standards used not in just this country, but across the world. In addition to those standards ASCLD LAB issues supplemental standards that we must follow if we want to use them as an accrediting body to the ISO standards. In addition to that being a DNA laboratory we also are audited against the quality assurance standards issued by the FBI in conjunction with SWGDAM, so the DNA laboratory gets audited under three sets of guiding standards.

Q. Thank you. I want to talk a little bit about allelic dropout and specifically the formula that was used in this particular case. My understanding is that a way we could describe it is unknown number of contributors accounting for allelic dropout.

A. Yes, that's correct.

Q. Can you explain or describe for the court why that equation, that standard doesn't violate the standard practices in the community?

A. Yes. I mean it's not a formula that we created in our laboratory. It's a formula that's used in forensic sciences and it's a--why our laboratory chooses to use this formula is it allows us to provide weight given the assumptions that we're using in the case to describe what is the likelihood that an allele is present in the community, not specifically to a person, but what is the likelihood that someone may have an allele. As I said, these guidelines explicitly state in them that not every permutation or possible calculation can be possibly listed within these guidelines.

Q. And that's stated in the SWGDAM guidelines?

A. Yes, it is.

Q. I want to talk to you a little bit about the alleles present at any particular loci and I want to run a statement by you and I want you to comment on whether or not you find that to be an accurate statement. If a contributor has a--let's just say a 16, 22 allele at any particular loci is it a fair statement to say that both the 16 and the 22 are equally likely to be present at that loci and therefore must be present in any analysis?

A. No, that's not a true statement. Specifically why I say that is in reference to small amounts of DNA present in a sample when

we're talking about partial profiles, that's the crux of what this is, a partial profile by its very name implies that you have not developed all of the genetic information at a particular locus or a particular set of loci and to break that statement down a little further it is not as equally likely that both of those alleles could be present in a result, in a profile. The term used in our community is what's called preferential amplification, and a very simplistic form the 16 allele in this example is smaller than the 22 allele, and the biochemical reaction that takes place in the process that we do it's easier and quicker to make a 16 than it is a 22 because it takes less time. It's smaller. What can happen when you have small amounts of DNA is that you get a preferential amplification of the short fragments versus the large fragments and when you don't have very much of the DNA to begin with you end up with only one of them being present in your results. That is what we've talked about, I believe it's come up before in this court, what's referred to just the stochastic threshold, meaning that it's possible that results are there, but they have not reached a detectable level and that's a very common occurrence.

Q. Thank you. And now I want to shift focus a little bit and talk about a stutter peaks vice allele peaks. And, again, I want to come back to these numbers because I think we can illustrate what a stutter peak is and how it is identified.

A. Yes.

Q. So if you could please describe for the court, number one, how is a stutter peak identified; and, number two, what identifies the stutter peak?

A. Okay, I believe it's been discussed, so I'll state briefly the stutter peaks are merely an artifact of the process. It's a well-known highly documented occurrence in this type of testing that we do where a small percentage of the main peak is amplified at a repeat smaller than that main peak and that occurs at very specific percentages. These percentages are determined in not only the manufacturer's developmental validation of these kits, but also within the internal validations of the laboratories when they bring those kits on line and choose to adopt those kits. They're most specifically identified because, as I said, they're--they fall exactly one repeat below the peaks--the main peaks that you see. By repeats what I'm--the type of testing we do is based upon repeating DNA. There are a very specific number of base pairs. Typically what we're looking at is four, so four base pair smaller than the--a large peak, we see a small peak. We look at that peak and see what the percentage or the ratio is of that large peak to the small peak and that's how we identify stutter peak. A stutter peak will never be outside-again, if we go back to your example of a 16 and a 22, if we had a very small 16 peak and a very large 22 peak I would never

assume that that 16 is a stutter peak from the 22. That's not how this phenomenon occurs.

Q. Okay, so to use an example, if you had a 20, 23 at a particular locus and a 19, 22 it is within the range of a stutter of the 20, 23 at that particular locus?

A. Yes. The 19 would be within range of the 20. The 22 would be--excuse me, be within range of the 23, and, again, we look at the peak heights of those associated peaks. I would look at the peak height of the 20, the peak height of the 23 and gage whether it's expected that I would have stutter present in that sample and evaluate the--you know, the data as it's presented.

Q. Okay. So now I want to bring in a minor contributor at that same locus.

A. Yes.

Q. If a minor contributor, say a 16 is present at that locus, it's conceivable that that 16 would be smaller than the stutter 19?

A. Yes, it is conceivable.

Q. Can you explain that?

A. Yes. Again, as I said, stutter is an artifact of the process and the larger the peaks are, the higher the propensity for stutter to occur, so if we keep it very simple math, if our stutter percentage is 10 percent and we had a peak with a height of 1,000, we expect that the stutter peak is 100--can be up to 100 what we call

RFUs. If you have a stutter peak--or, I'm sorry. If you have a large peak that's 3,000, you have the propensity to have a stutter peak upwards of 300 RFUs, so the higher that peak gets, the higher the stutter peaks get. Well, obviously as you're probably following along, you're going to cross at the stochastic threshold where these minor contributors are residing. That does not discount the fact, though, that a minor contributor is present in addition to stutter peaks.

TC: Thank you. I have no further questions. Thank you.

WIT: Thank you.

CDC: Sir, may we take a brief recess to confer prior to cross-examination?

[The witness was duly warned.]

[The telephonic connection with Dr. Krane was terminated for the recess.]

MJ: Court's in recess.

[The Article 39(a) session recessed at 1130 hours, 24 April 2015.]

[END OF PAGE]

[The Article 39(a) session reconvened at 1143 hours, 24 April 2015.]

MJ: This Article 39(a) session is called order. All parties present when the court recessed are again present.

[The witness is back on the witness stand.]

TC: And, Mr. Hummel, I just want to remind you that you're still under oath.

WIT: Yes.

[Dr. Krane is called telephonically and he continues his observation of the testimony at hand.]

CROSS-EXAMINATION

Questions by the defense counsel:

Q. Mr. Hummel, just a couple questions. Regarding the issue of stutter, which you spoke about with Captain Morman, are you familiar with what the SWGDAM guidelines say in terms of accounting for stutter and determining whether you have stutter or an allelic peak?

A. I am familiar with it. I've read through the guidelines before, yes.

Q. So in this particular case is it your view that those guidelines were followed in terms of accounting for whether or considering the possibility of whether an observed peak is a stutter peak or an allelic peak?

A. Yes. As you've just described the guidelines discussed considering whether those peaks may be allelic or stutter and those peaks, as I have said, I believe, yes, those guidelines have been followed. That profile was looked at. We always consider whether peaks are allelic or not, but the mere presence of a peak in stutter position does not mean you should automatically call it allelic. That's not scientifically valid.

Q. And so what are the considerations that allow you to say whether it's an allelic peak or a stutter peak?

A. Well, again as I described earlier, we're looking at the ratios of those peaks together. We're looking at the profile as in a totality. You know, you would be less likely to assume that it's stutter at that level if that's the only stutter peak present in that range across the totality of the profile. I can't speak directly about specifics in a lot of those because I did not do the testing on these samples, so I'm not as familiar as Miss Hanna is with the sample, but, again, we're looking at not just a particular stutter peak at one particular allele and one particular locus. We look at the data as a whole and we look at the ratio of those peaks to each other and we look at the height of the major contributor. As I testified earlier, you know, the higher that major contributor becomes the more likely it is that it's stutter, and, again, if

there's any doubt, one wouldn't conclusively just say that that's an allelic peak because that wouldn't be scientifically valid.

Q. So in this--did you review this particular case?

A. Did I do the technical review? Not to split hairs with you, I'm familiar with the circumstances of the case. I did not technically review the data in this case as I remember.

Q. So maybe you could, for my edification can you describe what the difference in those are?

A. Yes, in the DNA--in the forensic community we undergo what's commonly referred to as technical review peer review where a second qualified analyst looks at all the data's--data, the conclusions, the reports, the notes and assures that they come to the same conclusions and that they analyze the data the same way versus are you asking me if I have just read the reports before. I'm not sure what distinction you're making.

Q. Well, sir, well then what review did you do in this case?

A. I have not technically reviewed this case. I had read the reports and consultation with Captain Morman and with Miss Hanna, but I was not responsible for the technical work in this case.

DC: Thank you. No further questions.

[END OF PAGE]

TC: Sir, I just have one redirect based on that cross, just one question--well, it might be a couple, one topic.

REDIRECT EXAMINATION

Questions by the trial counsel:

Q. I want to talk a little bit about the process that your lab employs, not necessarily specific to this case, but the process.

A. Yes.

Q. And I want you to, if you could break this particular phase down for the judge.

A. Yes.

Q. When is the determination made whether a peak is an allele peak or a stutter peak vice the actual comparing to a sample?

A. All determinations on the quality of the profile whether a peak is allelic, artifactual, stutter, what have you, all those determinations are made on the front end, so the unknown samples are generated, the data is analyzed, those allelic calls are made, determinations are made if we have major minor components, if they can be mathematically discerned or separated, all that is done on the front end. Once that has been completed then the analyst ~~is~~ will look at the request made in that case and see, okay, do we have a known suspect? We do. Do we have an elimination standard? Do we have a victim standard? What are the known components that we've been asked to compare to the genetic information developed in a case? At that

point then they will look at the unknown samples, the profiles generated--generated from those, and make determinations on, you know, if it's a single source profile, does it match. If it's a partial profile, can someone--is there a match? Can someone be included? Are they included as a contributor to a mixture? I mean there's different variations upon that comparison, but all that happens after those unknown profiles have been completely analyzed.

Q. So is it even possible that a peak that's been identified as a stutter peak might later on--the analyst ~~is~~ might say later on, "Hey, this also matches the profile of the particular subject in this case; I'm going to switch this over to an allele"?

A. No, that would be and un--that would be unethical.

Q. So in a case where a peak has been identified as a stutter peak that happens before any analysis is conducted?

A. Yes, that's correct.

TC: Thank you. No further questions, sir.

EXAMINATION BY THE COURT-MARTIAL

Questions by the military judge:

Q. And so if the guidelines say that a stutter peak of a certain size in comparison to allelic peaks should be considered with the possibility that it's an allelic peak and that doesn't happen before it gets to the analyst, then what's the impact on the end result?

A. Well, the impact that I believe you're getting to if you're saying if they made those determinations or evaluations upon comparisons to the known standards, that's a violation of our protocols, our procedures. Our process is to look at that data, and this all goes to bias. We want to look at that data with a clean slate, with a fresh pair of eyes so that we aren't biased by knowing, hey, the defendant has a 16 20 at D-2. Oh, well, look, when I look at the D-2 locus there's some stutter peaks there and if I call this one stutter, it makes my match a lot more stronger. That's not how the process works.

Q. No, no, I understand.

A. Okay. I might have misunderstood-----

Q. I may have ~~raised~~ phrased it poorly. There's been some discussion about the SWGDAM guidelines that's--I can't remember it off the top of my head. If somebody can refresh my memory, but let's say if a stutter peak is at a certain height in comparison to known allelic peaks, then you should consider the possibility that the stutter peak is actually an allelic peak.

A. Yes, and I believe the key word that you've just said is there's--a consideration should be made.

Q. Okay, so you consider and then say, no, stutter peak or yes, allelic peak?

A. Yes. I mean in the vast array of samples and cases we deal with there are certain circumstances where it could go in different directions, again looking at the totality of the data, and that I believe is the crux of the guidelines and why the guidelines are written as such. You cannot explicitly delineate step one, two, three, four, five that would encompass every type of scenario that we encounter in our work.

Q. So why would--assuming my hypothetical is still correct, that you have the stutter peak that's of the same or greater height than an allelic peak, why would you decide not to consider that an allelic peak such that you can get a better--I don't know, does it give you a better or worse statistic in the end?

A. If--if you called something a--if something was a stutter peak that you called an allelic peak and it so happens to match the defendant, yes, it would give the prosecution a much higher statistical weight to the evidence. Conversely, you could call something that's a stutter peak an allelic peak when in fact it is not and now having excluded the true contributor to the peak, you know, there's a variety of scenarios that you could create by misappropriating a stutter peak or any artifactual peak as allelic. Making something allelic is a very definitive, a very serious point that you've made that you're saying this is genetic material that is present in a sample and it is from this material that I am going to

make all of my comparisons and decisions and bring to a court and testify to.

Q. The guidelines talk about random match probability, likelihood ratio, and combined probability of exclusion and inclusion and they associate random match probability with ~~no~~ known contributors and CPE CPI with an unknown number of contributors, but when I heard Dr. or Miss Hanna testify she didn't use any of those terms, so is what you are doing at the lab something completely different than those?

A. No. What we specifically do--let me back up one step. Those are a set of terms that are sometimes interchangeable in the community as, you know, you can find that in any discipline. If we want to specifically reference the terms and the guidelines, what our laboratory uses is a modification of an unrestricted random match probability.

Q. And is it modified because you're applying it to unknown numbers of contributors?

A. Yes, that's correct.

Q. Very good.

A. And it allows for dropout.

Q. And in the audit/accreditation procedure I understand that they are different things. Have those auditors or accreditors looked at this particular formula? That is, unknown number of contributors and the possibility of allelic dropout?

A. Yes. We've been using the same statistical calculations since we started PCR STR testing 15 years ago. In that time we've been audited and inspected about ten different times, off the top of my head.

MJ: Any based on mine, Counsel?

TC: No, Your Honor.

DC: No, Your Honor.

MJ: Temporary I assume?

TC: Temporarily, sir.

[The witness was duly warned, temporarily excused, and he withdrew from the courtroom.]

TC: Your Honor, if I could have a brief moment before calling my next witness. [Pause. Reviewing notes]

Your Honor, there's no further evidence from the government.

MJ: All right, anything else for the defense?

DC: Yes, Your Honor. The defense would like to recall Dr. Krane.

MJ: Okay, go ahead.

DC: Dr. Krane, you still there?

Dr. Krane: Yes, I am.

DC: All right, I'm just reminding you that you're still under oath.

Dr. Krane: All right, thank you.

DAN E. KRANE, civilian, was recalled telephonically as a witness for the defense, and testified as follows:

DIRECT EXAMINATION

Questions by the defense counsel:

Q. I just want to cover a couple things because I think there might have been some misinterpretation in the translation from your testimony to Dr. Hummel's testimony. You had originally testified that the--concerning the template amount and the issues with an amount of male DNA that was extremely less than the one nanogram or in this case the 750 picogram targeting value. Could you clarify that, sir? So what were you saying with regards to the fact that the amount of male DNA used in this case was between 15 and 45 picograms?

A. Right. Yeah, I'd be very happy to--[coughing], excuse me, clarify that. Let me say what I was not saying. I wasn't saying that the testing laboratory should have used more template DNA. I agree that using more than the recommended amounts for the test kit leads to its own set of problems. What I was trying to convey is that the testing lab through, no fault of their own, used too little of the minor contributors' DNA to be able to get a reliable result in regards to that minor contributor's profile and if I could just expound on that a bit. You know, Mr. Hummel points out that the target based on their laboratory's validation, their internal

validation is 750 picograms. The manufacturer of the test kit actually recommends 1,000 picograms or a nanogram, but I have no issue with them, you know, targeting less if their validation supports that, but the thing though is is that in the lab's own bench notes with respect to the quantities of DNA for this sample there's a notation that says, and this is in regards to the volume of DNA that they used, this is a quote from their bench notes. "Increased template due to ratio", and so the lab chose in this case to use one nanogram as opposed to their normal target of 750 because they had performed a test to determine the relative amount of male and female DNA and determined that there was a very small amount of DNA and in the hopes of being able to get a better look at that small amount of male DNA they increased the amount of template that they used. Despite that best effort and, you know, well intentioned and I think a reasonable effort on their part, the reality is that the amount of templates DNA that comes from the minor contributor or contributors in this case is exceedingly small. Again, on the range of 15 to 45 picograms, far lower than the lab's target and far lower than laboratories which deliberately set out use.

Q. Yes, sir, and finally with regards to the statistics I would like to be clear again about what you are saying. What--are you saying that the formulas included in their manuals are somehow not following the SWGDAM guidelines or are you saying something else?

A. I think it would be best to say I'm saying something a little bit different. I'm saying that they're not being applied appropriately. The formulas in their operating procedures and their interpretation guidelines are clearly consistent with and derived from the SWGDAM guidelines. However, the SWGDAM guidelines provide two different kinds of statistical approaches; one set of approaches for a mixed sample with an unknown number of contributors where allelic dropout has not occurred, and another set for a sample with a known number of contributors where allelic dropout may have occurred. The laboratory's protocols have those same formulas, but they have misapplied them. They have used formulations here for a--well, they are statistically evaluating a sample that falls into neither of those two different kinds of buckets. This is a mixed sample with an unknown number of contributors where dropout may have occurred.

DC: Yes, sir. Thank you. Sir, those are all the questions I have.

TC: No questions from the government, Your Honor.

MJ: I don't have any others either.

[The witness was temporarily excused.]

DC: Sir, I'm going to-- do you have anything else?

TC: No.

MJ: Let me just review something for a second.

DC: Dr. Krane, hold just one moment.

Dr. Krane: All right.

[The military judge reviews his notes]

MJ: Okay, I don't think I need to recall anyone.

DC: Sir, the defense has no further evidence on the motion.

TC: And the government has no further motions--no further evidence on the motion, Your Honor.

[Dr. Krane was excused and the telephonic connection was terminated.]

DC: So, sir, for argument, sir, the defense in this case, sir, under the *Daubert* standard really what we're looking for is reliability and even though those words have been used in court today the defense concedes that we are not operating under the general acceptance standard. However, the issue here that the defense would point the court to is some of the case law cited in the defense motion, namely the persuasive case law of the *In Re Paoli Railroad Litigation* where it specifically talks about the fact that it is not only the general approach of a scientific field, but that the proponent of scientific evidence under *Daubert* has to show that every step along the way in their analysis is reliable, meets that reliability standard and one of the places where the defense would contend that the government fails to show that reliability is particularly in regard to the statistics. The government can talk all day about how the lab has passed its accreditation studies, how many times it has gone through that process, the general guidelines

that it follows in all of these cases, it can do all of that, but ultimately in this particular case, maybe not in another case that the lab has worked on, but in this particular case the lab fails to meet that reliability standard in calculating the statistics that they have used to say that Major Henning's DNA has a random match probability of 1 in 223. That is the primary point where it fails in that reliability standard. Now, the defense would also say--would point to Dr. Krane's testimony in that regarding the way--under the circumstances that they calculated that statistic when you have an unknown number of contributors with a possibility of allelic dropout, in terms of statistics, all bets are off, right, there isn't a reliable way to do that. The SWGDAM guidelines, they are combining and re-- they're basically combining the SWGDAM guidelines in a way that those guidelines do not contemplate and I would point to the language in the government's motion itself where it says the government concurs that SWGDAM is the definitive authority on reliable procedures and methods. Right, and SWGDAM specifically says you can do this with CPE or CPI, you can do this with RMP and it never says that you can do both, but that's exactly what the lab did. The lab put those two together.

Even if in the alternative, Your Honor, the defense would ask that you not admit this evidence under 403 grounds because as Dr. Krane said, when you're talking about this degraded of a sample where

it is at 1 percent in terms of the amount of data, 1 percent, 15 to 45 picograms, 1 to 5 percent of the target amount for that sample, and when you're talking about that low RMP you have to measure that against the effect that it's going to have on the panel. If this were a judge alone case, this argument would have much less effect, but especially in these circumstances where the disagreements and the arguments about that data are so complicated such to the fact that all of the attorneys in the room and all the lay people in the room are struggling often to follow what the actual disagreements are. The defense submits that the effect on the panel is simply going to be, oh, well, DNA evidence and they're not going to take the appropriate measure of skepticism that is warranted by the actual evidence. That would have a prejudicial effect far beyond its probative value on the panel and for that reason in this particular circumstance, again, DNA most of the time absolutely appropriate, absolutely probative, absolutely admissible under 403, under *Daubert*, under 702, but in this circumstance both because of that point in this lab's analysis where it broke down when they decided--when they had a situation that didn't meet SWGDAM guidelines for either CPE or RMP, so they put them together, both because of that and even if that's okay, which the defense contends it is not, even if that's okay given the fact of the limited probative value of the information, given its incredibly degrade--the incredibly degraded

sample and the low amount of weight that can be given to it and the likely prejudicial effect that it will have on a panel, the defense asks that you disallow the government from entering in expert testimony on this issue. Thank you, Your Honor.

TC: Your Honor, experts disagree. Experts disagree. There's science and then there's conclusions based on science and what we've heard today is for the most part we've got good science and we've got experts disagreeing on how to interpret, disagreeing on what conclusions to be drawn from that good science.

MJ: What part was not good science?

TC: No, I----

MJ: You said for the most part it was good science.

TC: Oh, Roger, sir. We talked about good science today and before I continue, Your Honor, I'd like to read from page 1 of the SWGDAM guidelines almost to the bottom of the page. "Due to the multiplicity of forensic sample types and the potential complexity of DNA typing results it is impractical and infeasible to cover every aspect of DNA interpretation by present rule." And it goes on to talk about the lab must then identify and then sort of promulgate their own rules and procedures on how they're going to conduct testing, specifically, according to the rules, so that it can be peer reviewed, which is exactly what happened in this case. The KCPCL came in here today and they identified exactly how their testing was

conducted, a modified version of an equation that's contained in the SWGDAM guidelines, and again, Your Honor, the government stresses that these are not--these aren't rules. These aren't set in stone equations that must be followed. They are recommendations from an accrediting body. And over the last 14 years the KCPCL case work and their equations and their policies and procedures have gone through rigorous auditing, external auditing; internal auditing. In fact, you've even heard testimony today where Mr. Hummel outlined a technical review that's conducted within their own laboratory where a separate scientist who has no part in the original testing then does his own internal peer review of that testing, so in this case these results have been tested three times; once by the original scientist, once by the technical reviewer within the KCPCL, and then once by Dr. Krane and his associates, so the peer review aspect of this case is satisfied under the rule. The defense points out reliability and refers to calculating statistics and, again, Your Honor, this reliability does not go towards the science. These are weight arguments, not admissibility arguments. The defense is properly positioned with an expert to come into court and argue, just as they did today, that this is less reliable, that this should be given less weight, that there are holes here and here. They have every tool available to them to highlight where the defense believes there are weaknesses in this particular scientific evidence, and so the

reliability aspect I think is being blurred here. What I believe to be the case is that the defense under the umbrella of *Daubert* has taken what is a standard that bars evidence from court because it's unreliable bad science and they've applied that to an analysis and they've said "My expert disagrees with your expert", and points to reliability issues, now I'm going to lump that disagreement under the umbrella of a federal standard and then ask the court to preclude this evidence at trial and that's a misapplication of the rule. And to that point, we didn't do much *Daubert* stuff today. We didn't go through the various--the four part test outlined by *Daubert*. What we did in painstaking detail was talk about the random match probability and the conclusions that were drawn and at the end of the day what this comes down to is two experts disagreeing as to how to draw conclusions based on good science.

So the 403 issue, Your Honor, I don't know what case law we have or what authority I can argue either for or against that proper science DNA should be excluded because it's prejudicial. It's prejudicial, Your Honor, because that's why the government is putting it in its case. The key here is is it unduly prejudicial, does the prejudice outweigh the probative value, and the answer is no. We've got good science. The government is going to introduce as evidence in a trial and then allow the defense to invoke 403 to get the evidence if Set aside, and so I don't know how else to stress that

other than I don't know of any case precedent out there that shows when a random match probability is a little low that it should be excluded because it's unduly prejudicial, and for those reasons, Your Honor, the government rests on the fact that these arguments go to weight, not to admissibility. Thank you, Your Honor.

[The trial counsel returns to his table.]

MJ: All right, I'll take the motion under advisement and issue a written ruling in due course.

Court's in recess until the trial date.

[The Article 39(a) session recessed at 1220 hours, 24 April 2015.

[END OF PAGE]

IN A GENERAL COURT-MARTIAL OF THE UNITED STATES
US ARMY TRIAL JUDICIARY, THIRD JUDICIAL CIRCUIT

UNITED STATES	)	
	)	**GOVERNMENT RESPONSE TO DEFENSE MOTION FOR APPROPRIATE RELIEF: TO EXCLUDE EVIDENCE**
v.	)	
HENNING, Antiwan M. MAJ, U.S. Army Headquarters and Headquarters Company, Combined Arms Center, Fort Leavenworth, Kansas 66027	)	12 March 2015

RELIEF SOUGHT

COMES NOW through undersigned counsel, the Government of the United States, in the above-captioned case and moves the Court to wholly deny the Defense Motion for Appropriate Relief: To Exclude Evidence, dated 9 March 2015. As grounds therefore, the Government submits that evidence and expert testimony concerning MAJ Henning being a possible contributor of genetic material recovered from the underwear of Ms. Sarah Nightengale is admissible under MRE 403 and 702.

I. BURDEN

As the moving party, the Defense bears the burden of persuasion. See Manual for Courts-Martial, R.C.M. 905(c)(2). Additionally, as the moving party the Defense bears the burden of proof by a preponderance of the evidence. See Manual for Courts-Martial, R.C.M. 905(c)(1).

II. FACTS

1. The Government stipulates to the statements contained in the "Forensic DNA Standards" section of the Defense's fact proffer and adds the following statements to that section:

a. The most recent publication from Scientific Working Group for DNA Analysis Methods (SWGDAM) concerning quality assurance standards for forensic laboratories was published on 1 September 2011, entitled, "Quality Assurance Standards for Forensic DNA Testing Laboratories," (Forensic Standards) states as its scope, "These standards describe the quality assurance requirements that laboratories performing forensic DNA testing or utilizing the Combined DNA Index System (CODIS) ***shall follow*** to ensure the quality and integrity of the data generated by the laboratory." Forensic Standards, page 1 (emphasis added).

APPELLATE EXHIBIT IX

b. Concerning the standard for maintenance of DNA analysis and reports, the Forensic Standards state, "The laboratory shall maintain all analytical documentation generated by analysts related to case analyses. The laboratory shall retain, ***in hard or electronic format***, sufficient documentation for each technical analysis to support the report conclusions such that another qualified individual could evaluate and interpret the data." Forensic Standards, Paragraph 11.1, page 22 (emphasis added).

c. Concerning the standard for technical review of DNA analysis, the Forensic Standards state, "Completion of the technical review shall be documented and the technical review of forensic casework shall include the following elements: (1) A review of all case notes, all worksheets, and the ***electronic data*** (or printed electropherograms or images) supporting the conclusions. (2) A review of all DNA types to verify that they are supported by the ***raw or analyzed data*** (electropherograms or images)." QA Standards, Paragraph 12.2, page 23 (emphasis added).

d. The Government concurs that SWGDAM is the definitive authority on reliable procedures and methods for forensic DNA testing and analysis. Additionally, SWGDAM also provides recommendations to the FBI Director on quality assurance standards for forensic DNA analysis. The Kansas City Police Crime Lab (KCPCL) undergoes a yearly audit performed by SWGDAM in which their quality assurance standards undergo intense scrutiny. To date, the KCPCL has never failed an audit performed by SWGDAM.

2. The Government stipulates to the statements contained in the "MAJ Henning Case Initiation and Investigation" section of the Defense's fact proffer for the limited purposes of this motion.

3. The Government stipulates to the statements contained in the "KCPCL Testing and Analysis" section of the Defense's fact proffer for the limited purpose of this motion with the following exceptions:

a. The statements contained in Paragraph 16 of the Defense proffer of facts is simply incorrect. Paragraph 2.2.6 of the KCPCL DNA Analytical Procedure Manual clearly states that the stochastic threshold used for forensic DNA testing is 300RFU. Said threshold was used in the testing conducted in MAJ Henning's case.

b. The statements contained in Paragraph 19 of the Defense proffer of facts concerning the restricted RMP formula used by KCPCL when conducting statistical calculations in MAJ Henning's case are also totally false. The KCPCL did not employ a restricted RMP formula; rather, the laboratory used a modified calculation that allows for drop-out AND an unknown number of contributors, neither of which are precluded by the SWGDAM guidelines. Furthermore, the calculation listed in Paragraph 5.2.2.3 of the Guidelines is an example of what calculation is used for an "alleles present" statistic, accounting for drop-out similar to the calculation used in the Henning case.

c. The Government does not stipulate to paragraph 20 of the Defense fact proffer. The Government expressly rejects any Defense claim seeking to explain the charging decision in this case. MAJ Henning's commander based his decision to prefer charges against MAJ Henning after a complete and thorough review of the entire case file. To suggest otherwise is a misleading statement and has no basis in fact.

4. Electropherogram Discovery and Expert Assistance

a. The Government disclosed all laboratory reports in its possession to the Defense at the time of preferral. Those reports included all forensic DNA testing concerning MAJ Henning. These reports summarized the conclusions of the forensic analysts for performed the serological and DNA testing in the MAJ Henning case.

b. Prior to convening the Article 32b investigation in this case, the Government coordinate with KCPCL for production of what the lab refers to as a discovery and litigation packet. This packet in included everything that the lab is accustomed to providing in the discovery phase of criminal proceedings for the state of Missouri. Included in this packet was all of the electronic data pertaining to this case. Specifically, the electronic data disclosed was all of the electronic data in the possession of the KCPCL and which their forensic analysts used to reach their scientific conclusions. Additionally, there were ten (10) total phases of scientific testing which the lab generated reports for. These reports ranged from 22 to 36 pages in length and contained all notes taken by any forensic analysts who performed DNA and serological testing in the Henning case.

c. On 1 September 2014, the Defense improperly submitted a request for expert assistance to Commanding General, LTG Robert B. Brown. At the time this request was submitted, the convening authority for the case was COL Timothy R. Wulff, the SPCMCA. The Defense was promptly notified of the error by CPT Joseph Morman, Trial Counsel.

d. On 9 September 2014, the Defense resubmitted its request for expert assistance to COL Wulff. This request was denied.

e. On 15 September 2014, the Defense submitted a supplemental discovery request in advance of the Article 32 Investigation requesting, among other items, production of paper copies of the electropherograms (EPGs) used by KCPCL in all of their analysis concerning MAJ Henning's case. After receiving this request, the Government coordinated with KCPCL to produce the requested EPGs, but was informed, for the first time, that KCPCL is a paperless lab and the requested EPGs did not exist. Mr. Scott Hummel, Director of the KCPCL DNA Branch, further informed the Government that the requested EPGs never existed as his forensic analysts do not use two dimensional or paper EPGs when reaching their scientific conclusions. He informed the Government that production of paper EPGs is in violation of lab policy but also improper as the defense request specifically cited the paper EPGs "used by the lab" in

reaching their conclusions. As previously stated, such EPGs were never used by the KCPCL.

f. The Government expressly rejects the Defense assertion that paper EPGs are the *lingua franca* for DNA analysis. This statement is an oversimplification of the scientific process employed by KCPCL. The KCPCL is a paperless lab which means more than simply providing electronic data in discovery. The KCPCL policy dictates that forensic analysts record all notes in electronic format, sign for all DNA and testing materials through a digital scanner maintained in every testing room in order to establish chain of custody, and use the pan and zoom function in the Genetic Analyzer to rely on a more complete view of the DNA data in reaching scientific conclusions. The KCPCL has moved beyond paper functions in its lab as it relates to all phases of the genetic testing and forensic analysis. Therefore, when the Government turned over all of the electronic data to the Defense, the Defense was in possession of everything that the KCPCL forensic analysts used to reach their scientific conclusions, as well as the means to conduct testing through the defense expert.

5. The Government stipulates to the statements contained in the "Dr. Crane Appointment and Reanalysis" section of the Defense's fact proffer for the limited purpose of this motion with the following exceptions:

a. The Government rejects the contention that Dr. Crane and his associates cannot complete their analysis of the raw and electronic data without paper EPGs used by KCPCL. First, if KCPCL did not use paper EPGs in their original analysis, how is it possible that Dr. Crane and his associates cannot conduct a reanalysis of the electronic data and reach their own conclusions without them? Second, as indicated in the defense motion, it took two weeks for Dr. Crane and his associates to conduct an independent analysis of the electronic DNA data and one week to prepare a report. This is evidence on its face that indicates Dr. Crane and his associates were in fact able to conduct their own examination of the data.

III. WITNESSES / EVIDENCE

1. Witness – Ms. Jessica Hanna
2. Witness – Mr. Scott Hummel
3. American Society of Crime Laboratory Directors / Laboratory Accreditation Board (ASCLD/LAB), Scope of Accreditation Certificate, dated 3 September 2014
4. ASCLD/LAB Certificate of Accreditation, Kansas City Police Crime Lab, dated 3 September 2014
5. ASCLD/LAB Certificate of Accreditation, Kansas City Police Crime Lab, dated 3 August 2009.
6. ASCLD/LAB Certificate of Accreditation, Kansas City Police Crime Lab, dated 3 August 2004

7. ASCLD/LAB Certificate of Accreditation, Kansas City Police Crime Lab, dated 27 September 1983
8. Curriculum Vitae, Ms. Jessica Hanna
9. Curriculum Vitae, Ms. Marsena Craig
10. Curriculum Vitae, Mr. Scott Hummel
11. SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories, dated 14 January 2010
12. SWGDAM Quality Assurance Standards for Forensic DNA Testing Laboratories, dated 1 September 2011

IV. LAW AND ARGUMENT

Expert testimony concerning MAJ Henning being a possible contributor of genetic material recovered from the underwear of Ms. Sarah Nightengale is admissible under MRE 702. The Defense relied on factually incorrect assumptions in making the claim that the DNA analysis and Random Match Probability (RMP) calculations conducted by KCPCL in this case fails to follow the basic scientific procedures required to ensure reliability. These factually incorrect assumptions have resulted from the Defense's own unwillingness to conduct proper interviews and basic investigative work in this case. First, the Defense asserts in its motion that the KCPCL used a "restricted RMP calculation" in case of MAJ Henning which is simply not true. The KCPCL employed a modified calculation that allows for drop-out AND an unknown number of contributors. Second, the Defense asserts that the RMP calculations in the case of MAJ Henning are less reliable because of the "high degree of deference" given to forensic analysts as evidenced by the lack of any stochastic thresholds. Again, this is simply factually incorrect. The KCPCL stochastic threshold used in the case of MAJ Henning was 300RFU. Third, the Defense asserts that the KCPCL policy of refusing to print out two-dimensional hard copy EPGs violates the basic scientific principle of peer review. While said statement is factually correct as it pertains to the KCPCL refusal to release paper copy EPGs, the assertion is wholly incorrect as it argues the scientific work conducted at the KCPCL is incapable of peer review.

Additionally, in light of the factual errors contained in the defense brief, the primary thrust of the remaining defense arguments as it pertains to admissibility of the scientific evidence in this case stems from an apparent disagreement that defense experts have with the conclusions drawn by KCPCL experts. As such, this dispute should go towards the weight of the Government evidence and not towards its admissibility.

I. Expert Testimony concerning MAJ Henning as a possible contributor to genetic information contained in Mrs. Nightengale's underwear is admissible under MRE 702

In accordance with MRE 702, expert testimony is admissible on a relevant matter if: (1) the experts scientific, technical, or other specialized knowledge will assist the trier

of fact to understand the evidence or to determine a fact in issue; (2) the testimony is based upon sufficient facts or data; (3) the testimony is the product of reliable principles and methods; and (4) the witness has applied the principles and methods reliably to the facts of the case. M.R.E. 702. Expert Testimony concerning DNA evidence has a long history of admissibility under MRE 702. In 1995, the United States Court of Appeals for the Armed Forces (CAAF) took up the issue of the admissibility of DNA evidence for the first time in United States v. Youngberg, 43 MJ 379, (C.A.A.F. 1995). In *Youngberg*, CAAF held that evidence of DNA testing is admissible at courts-martial if a proper foundation is laid. *Id* at 385. The well-established case law regarding the admissibility of DNA evidence was expanded upon in *United States v. Allison*, 63 MJ 365 (C.A.A.F. 2006) when the court took up issues concerning the defense allegation that government experts were not qualified to interpret the statistical probabilities basic to DNA analysis. In *Allison*, CAAF reasoned that evidence of statistical probabilities is not only basic to DNA analysis but also essential to the admissibility of that analysis. *Id* at 369. Like the underlying DNA analysis, statistical evidence is also admissible at court-martial so long as proper foundation is laid. *Id.*

Controlling case law establishes that DNA analysis and the statistical evidence associated with said analysis meet the requirements set for in *Daubert v. Dow Merrell*, 509 US 579, (1993). That evidence of DNA analysis and statistical probabilities is accepted scientific evidence and admissible at courts-martial is not in dispute. In dispute in the present case are the procedures and policies of the KCPCL and whether those practices violate *Daubert* and MRE 702. As referenced above, the Defense has structured their argument around three factually incorrect assumptions which the Government will now address:

First, the KCPCL did not employ a restricted RMP calculation in the case of MAJ Henning. The lab employed a modified RMP calculation that allows for drop-out AND an unknown number of contributors, neither of which methods are precluded by the SWGDAM guidelines. In addition to not precluding the aforementioned calculations, the SWGDAM Guidelines account for such a calculation and provide a sample equation for that type of RMP interpretation. Guidelines, page 16, Paragraph 5.2.2.3. The crux of the issue in this case is that certain key factual assumptions relied upon by the Defense are simply incorrect. As such, the legal analysis misses the mark as the Defense cites to inapplicable SWGDAM guidelines because they did not properly ascertain which type of RMP equation the KCPCL employed in the case of MAJ Henning.

Additionally, it is important to draw a distinction between what SWGDAM publishes as a guideline and what is published as a requirement under the standards for practice in the forensic DNA testing community. The SWGDAM Guidelines address this issue in a critical area of this case in Paragraph 3.6.5 as it states, "because assumptions regarding the origin of evidence or the number of contributors to a mixture can impact comparisons, the laboratory should establish guidelines for documenting any assumptions that are made when formulating conclusions." Guidelines at page 12. Assumptions made in the case of MAJ Henning, such as those envisioned by

Paragraph 3.6.5, are clearly indicated in the case notes and detail how comparisons were made to the sample including minimum number of contributors, alleles used for comparison, and the possibility of drop-out. Furthermore, the statistical formula applied in this case used identical assumptions regarding the sample and was likewise documented in the case notes.

As further evidence that the KCPCL policies and procedures fall within not only the SWGDAM standards, but also the standards for forensic DNA testing in the scientific community, the Government submits that the KCPCL undergoes yearly audits conducted by SWGDAM. These audits are documented on a 99 page form and covers all lab policies and procedures, to include forensic DNA testing. The KCPCL is also an accredited lab and has operated as an accredited lab certified by the American Society of Crime Laboratory Directors uninterrupted since 3 August 2004.

Second, the KCPCL RMP calculations in the case of MAJ Henning are reliable and do not deviate from acceptable scientific standards because the used standardized stochastic thresholds set at 300RFU. The Defense in large part relied on the argument that the lack of a stochastic threshold in the case of MAJ Henning made the forensic work conducted by KCPCL less reliable and that, in conjunction with the labs failure to produce paper copy EPGs, renders their work incapable of peer review. As the first part of the defense analysis is not applicable once the correct facts are brought into the analysis, the Government will address the KCPCL's failure to produce EPGs.

Third, as previously stated *ad nauseam* in the fact section of this motion and in previous court filings in this case, the KCPCL crime lab is a paperless lab. More important to the discussion at hand, the paperless moniker does not refer solely to discovery and two dimensional paper copy EPGs, the KCPCL conducts all of its operations paperless. This ranges from the digital bar code scanner located in the evidence room that employees use to scan evidence in and out in order to maintain chain of custody to the computers located at every work station that employees used whenever they are handling evidence to record their notes. It may seem like a radically idea to an attorney used to dealing with Army CID and USACIL where hand written notes and paper EPGs are common place, but in the KCPCL those same notes and EPGs are maintained in digital format. All notes are recorded on a computer and saved under a particular forensic analysts profile and all electronic data is maintained in a program on Gene Mapper. To be clear, there have never been paper copy EPGs nor did any KCPCL analyst rely on such paper copy EPGs when reaching scientific conclusions. The defense assertion that the lab has structured itself to destroy EPGs in order to shield itself from peer review is patently false and completely without any basis in fact.

Everything, including all of the notes and electronic data used by Ms. Jessica Hanna and Ms. Marsena Craig to reach scientific conclusions in this case, was turned over to the Defense more than five months prior to the filing of this motion and just before the Article 32b Investigation which was conducted on 1 October 2014. With

respect to the ability to peer review the KCPCL's DNA analysis, the Defense has already provided an answer to this court in its motion. Dr. Krane and his associates conducted a reanalysis of the electronic data on provided a report to the Defense on 16 February 2015. This report can be compared to the analysis and statistical probabilities provided by KCPCL and satisfies the requirement that the DNA analysis be subject to peer review. There is no difference in providing the electronic data and a paper copy provided the Defense expert has the requisite programs and scientific equipment to interpret and analyze the data. That is clearly the case here.

II. As admissible evidence under MRE 702, this court should allow for inclusion of DNA evidence in the present case because its probative value far outweighs minimal prejudice, if any, to the Accused

Striking a balance between the probative value and prejudicial effect of particular evidence is left to the trial judge and that balance "should be struck in favor of admission." *United States v. Teeter*, 12 MJ 716, 725 (A.C.M.R. 1981). The Defense primarily relies on *United States v. Graves*, 465 F. Supp. 2d 450 (E.D. Penn. 2006) in making the argument that the potential for unfair prejudice in the present case is sufficiently high to warrant exclusion of the DNA evidence when taken in consideration with the other concerns raised in the Defense brief including the contested issues outlined under MRE 702. First, as outlined in the Government brief, the majority of the defense contentions under MRE 702 are without merit as they rely on wholly incorrect facts. Second, the case holding in *Graves* is not applicable here as the RMP in *Graves* was statistically less significant than the RMP in the present case, where in *Graves* the RMP probability was 1 in 2 the RMP in the present case is 1 in 220. See *Graves* at 460. The statistical probability in Graves was sufficiently low that the court reasoned the minimal probative value was substantially outweighed by the danger of unfair prejudice and confusion of the issues. *Id.* The concerns in Graves are not present in this case.

VI. CONCLUSION

For the reasons stated above, the Government respectfully requests that this court wholly deny the defense motion to exclude DNA evidence under MRE 702 and *Daubert v. Dow Merrell*, 509 US 579, (1993).

JOSEPH A. MORMAN
CPT, JA
Trial Counsel

CERTIFICATE OF SERVICE

I certify that a copy of this response was served on the Defense on 12 March 2015, via email.

JOSEPH A. MORMAN
CPT, JA
Trial Counsel

American Society of Crime Laboratory Directors / Laboratory Accreditation Board

ASCLD/LAB-*International* Program

SCOPE of ACCREDITATION

Corresponds to Certificate Number
ALI-358-T

Name and Address of Accredited Laboratory

Kansas City Police Department
Crime Laboratory
6633 Troost Ave.
Kansas City, Missouri 64131

Laboratory Contact Information

Linda Netzel, Laboratory Director
Phone: 816-349-3210
Fax: 816-349-3240
E-Mail: linda.netzel@kcpd.org

The management and technical operations of this laboratory were assessed and found to conform with **ISO/IEC 17025:2005**, the **ASCLD/LAB-*International* Supplemental Requirements for Testing Laboratories (2011)** and all other requirements of the ASCLD/LAB-*International* program. The laboratory was found to be competent and was accredited in the following area (s):

Field of Accreditation

Forensic Science Testing

Discipline (s)

1.0 Drug Chemistry
2.0 Toxicology
3.0 Biology
4.0 Trace Evidence
5.0 Firearms/Toolmarks
6.0 Latent Prints
8.0 Crime Scene
9.0 Digital & Multimedia Evidence
10.0 Other

Categories of Testing:

1.1 Controlled Substances
1.2 Quantitative Analysis
1.3 General Chemical Testing
1.4 Clandestine Laboratory Analysis
2.1 Human Performance Forensic Toxicology Screening only (urine alcohol/drug)
3.1 DNA - Nuclear
3.3 Body Fluid Identification
3.4 Individual Characteristic Database
3.5 Bloodstain Pattern Analysis
4.1 Paint
4.3 Fiber and Textiles
4.6 Glass
4.7 Hair
4.10 Fire Debris
4.15 General Physical and Chemical Analysis
5.1 Firearms
5.2 Toolmarks
6.1 Latent Print Processing
6.2 Latent Print Comparisons
8.1 Crime Scene Investigation
8.4 Bloodstain Pattern Analysis
9.2 Video Analysis
9.4 Image Analysis
10.1 Impression Evidence (footwear/tires)
10.2 Serial Number Restoration

Note 1: In this laboratory, testing category 10.1 is considered part of the Latent Prints discipline and 10.2 is considered part of the Firearms/Toolmarks discipline.

Customers Served: The Kansas City Police Department - Crime Laboratory is a local government laboratory that provides forensic services and assistance to law enforcement agencies in and around Kansas City, Missouri.

Accreditation Dates

Date Granted: September 3, 2014
Date Expires: September 2, 2018
Date Last Updated: No Updates

Troy Hamlin
Accreditation Program Manager-Testing
ASCLD/LAB

American Society of Crime Laboratory Directors
Laboratory Accreditation Board

declares to all Advocates of Truth, Justice and the Law that the management and technical operations of the

Kansas City Police Department
Crime Laboratory

6633 Troost Ave.
Kansas City, Missouri 64131

have been found through assessment to meet the requirements of ISO/IEC 17025:2005 "General Requirements for the Competence of Testing and Calibration Laboratories" the ASCLD/LAB-International Supplemental Requirements for Testing Laboratories: 2011 and all other requirements of the

ASCLD/LAB-*International*

program, and is granted this

Certificate of Accreditation

in the field of

Forensic Science Testing

for the categories of testing listed on the corresponding Scope of Accreditation

Renee Romero, ASCLD/LAB Chair

John K. Neuner, Executive Director

Pamela L. Bordner, Senior Accreditation Program Manager

Troy Hamlin, Accreditation Program Manager-Testing

Certificate Number

ALI-358-T

granted this

3rd day of September, 2014

which expires on the

2nd day of September, 2018

The American Society of Crime Laboratory Directors

Laboratory Accreditation Board

declares to all Advocates of Truth, Justice and the Law
that the management, personnel, procedures, and facilities of the

Kansas City Police Crime Laboratory

6633 Troost Avenue
Kansas City, Missouri

have been found to meet or exceed the standards and requirements of the 2008 version of the ASCLD/LAB Accreditation Manual, and therefore the Board of Directors grants this

CERTIFICATE OF ACCREDITATION

in the disciplines of

Controlled Substances, Trace Evidence, Biology, Firearms/Toolmarks, Latent Prints, Crime Scene, and Digital & Multimedia Evidence (video analysis only)

Michael Grabb, Chair

Ralph M. Keaton, Executive Director

Tracy Cheung-Plummer, Legacy Program Manager

Certificate number
19
effective date
3rd day of August, 2009
expires on the
2nd day of August, 2014

The American Society of Crime Laboratory Directors

Laboratory Accreditation Board

declares to all Advocates of Truth, Justice and the Law
that the management, personnel, and facilities of the

Kansas City Police Department
Crime Laboratory

have been found satisfactory and that the other requirements of this Board have been fulfilled, and therefore grants this

CERTIFICATE OF ACCREDITATION

in the disciplines of

Controlled Substances, Toxicology (blood alcohol only), Biology, Trace Evidence, Firearms/Toolmarks, Latent Prints and Crime Scene

ASCLD/LAB CHAIR

Ralph M. Keaton
EXECUTIVE DIRECTOR

Certificate number
19
effective date
3rd day of August, 2004
expires on the
2nd day of August, 2009

The American Society of Crime Laboratory Directors

Laboratory Accreditation Board

declares to all Advocates of Truth, Justice, and the Law
that the management, personnel, and facilities of

Kansas City Regional Crime Laboratory

have been found satisfactory and that the other requirements of
this Board have been fulfilled, and therefore grants this

CERTIFICATE OF ACCREDITATION

granted this
27 September 1983

CERTIFICATE NO.
19

EXPIRES
26 September 1988

Carlton L. Rahm
CHAIRMAN

Travis E. Owen
EXECUTIVE SECRETARY

CURRICULUM VITAE

NAME: Jessica L. Hanna

TITLE: Forensic Specialist IV

ADDRESS: 6633 Troost
Kansas City, MO 64131

TELEPHONE: (816) 349-6467

EDUCATION:

2005	Oklahoma State University- Center for Health Sciences- Tulsa, OK MS Forensic Science concentration in DNA Analysis
2003	University of Kansas – Lawrence, KS BS Genetics

EXPERIENCE:

2006-Present	Kansas City Missouri Police Department Kansas City Police Crime Laboratory-DNA Section Forensic Specialist III and IV (Sept 2011)
2001-2003	Quintiles, Inc. Pharmaceutical Dissolution Laboratory Laboratory Intern
2002-2003	University of Kansas Biology Department – Lawrence, KS Undergraduate Teaching Assistant Introduction to Genetics Lab and Introduction to Biology Lab

PROFESSIONAL AFFILIATIONS:

American Academy of Forensic Science	Member
Midwestern Association of Forensic Scientist	Member

CERTIFICATIONS:

American Board of Criminalistics Achieved 03/12/2010	Molecular Biology Fellow

CONTINUING EDUCATION:

June 2006 (3 week course)	Crime Scene Investigation School – Kansas City Police Department Kansas City, MO
July 2006 (1 week training)	President's DNA Initiative Training; 3130, 7500, and GeneMapper ID Marshal University Forensic Science Center - Huntington, WV
November 2006 (2 day class)	Forensic Statistics: The Calculations Behind PopStats and Beyond - Dr. John Planz, UNT Health Science Center – O'Fallen, MO
April 2007 (1 day)	Y Chromosome Workshop- Ruth Montgomery and Jason Wyckoff – PTC Laboratories in Columbia, MO
April 2007	Mid-America 2001 Forensic DNA Conference –Columbia, MO

(2 day)

May 2007 (2 day)	Courtroom Testimony Techniques "Success Instead of Survival" – Ron Smith and Associates, Dwame Hilderbrand – Largo, FL
July 2007 (3 day)	7 Habits for Law Enforcement Training – KC, MO PD
Oct 2007 (3 day)	National CODIS Conference – San Francisco, CA
Nov 2007 (2 day)	Auditor Training - Heather Seubert– San Francisco, CA
May 2008 (1 day)	Alert/Mules/NCIC Training, KC, MO PD
July 2008 (2 day)	International Association of Forensic Science Conference, New Orleans, LA
Nov 2008 (3 day)	National CODIS Conference – Washington D.C
Feb 2009 (5 day)	CODIS User Software Training by SAIC – Vienna, VA
July 2009 (5 day)	NIJ Sponsored Population Genetics Workshop – Florida International University, Miami, FL
Oct 2009 (1 day)	Y-STRs: Science and Statistics – Joint Meeting, Orlando, FL Presented by Dr. Martin Tracey, FIU
Oct 2009 (2 day)	Joint Meeting of Forensic Organizations (SAFS, MAFS, MAAFS, SWAFS) – Orlando, FL
Nov 2009 (3 day)	National CODIS Conference – Reston, VA
Feb 2010 (3 day)	Annual AAFS Conference – Seattle, WA
May 2010 (5 day)	Forensic Y-STR Training – Marshall University Forensic Science Center, Sarah Bowen
July 2010 (1 hr)	Offender Profiling: Psychology Contributions to Crime Scene Analysis On-line Dr. Gabrielle Salfati
Jan 2011 (3 day)	Choice Training – Leadership – KCPD
Feb 2011 (4 day)	Kinship Statistical Workshop – California Department of Criminal Justice, Steve Meyer and Brian Harmon
May 2011 (4 day)	Forensic Relationship Training – Marshall University Forensic Science Center, Kelly Beatty

Sept 2011 (2 day)	Access 2007 – Level 1 Training – New Horizons Computer Learning Center – Overland Park, KS
Nov 2011 (2.5 days)	National CODIS Convention – Jacksonville, FL
April 2012 (4 hours)	KC-MORG Mobile Morgue Training – Olathe, Kansas
June 2012 (2.5 days)	CODIS 7.0 Training – Austin, TX
Aug 2012 (1 day)	KC-MORG Family Assistance Center Training – Lee's Summit, MO
Sept. 2012 (5 days)	Comprehensive Training Program in Forensic DNA Interpretation and Statistics – online through NIJ and University of North Texas Health Science Center (occurred between Aug 13th and Oct 5th)
Nov 2012 (2 days)	National CODIS Convention – Norman, OK
May 2013 (5 hours)	KC-MORG Mass Fatalities Tabletop Exercise – Overland Park, KS
May 2013 (1 hour)	Internal Validation of QIAcube for Differential Separation – online presentation presented by Josh Stewart of Marshall University
Nov 2013 (1 day)	National CODIS Convention – Norman, OK
Nov 2013 (2 days)	DNA Technical Leader Summit – Norman, OK
Feb 2014 (5 hrs)	KCRMORG Mass Fatality Operations Classroom Training – Blue Springs, MO
March 2014 (2 days)	Mid-America Forensic DNA Conference – Columbia, MO
May 2014 (2 days)	Crucial Conversations Training – Kansas City, MO, Sgt. Luster

TESTIMONY:

State Courts-

Jackson County, Missouri
Cass County, Missouri

Federal Courts-

Western District Missouri – Kansas City, Missouri

SCIENTIFIC PRESENTATIONS AND PUBLICATIONS:

2005	*Forensic Use of RAPD Analysis in the Investigation of Bioterrorism.* Unpublished masters thesis, Oklahoma State University Center for Health Sciences, Tulsa, Oklahoma.
June 2005	Invited Novice Speaker, Variability in Chromosomal DNA in Isolates of *Bacillus*. Annual Meeting of Association of Genetic Technologists, Inc. (AGT) Kansas City, MO.

CURRICULUM VITAE

Name: Marsena D. Craig

Title: Forensic Specialist III

Address: 6633 Troost Avenue
Kansas City, MO 64131

Telephone: (816) 349-3258

Education:

2007	University of Central Oklahoma – Edmond, OK MS Forensic Science
2005	Jackson State University – Jackson, MS BS Biology

Experience:

2010-present	Kansas City Missouri Police Department Kansas City Police Crime Laboratory-Biology Section Forensic Specialist III
2008-2010	Viracor/IBT Laboratories Immunology Reference Laboratory Clinical Laboratory Scientist
2007-2008	Silliker Laboratories Food Quality Microbiology Laboratory Microbiology Technician
2004	Rocky Mountain Biological Laboratory Undergraduate Research Student (summer internship)

Continuing Education:

May 7-8, 2014 (2 day course)	Crucial Conversations Training Sgt. Paul Luster Police Academy KC, MO
April 9, 2014 (2 day seminar)	Mid-America 2014 Forensic DNA Conference Columbia, MO
April 7, 2014 (8hr course)	Death Investigation and Violent Crime Scene Response Sergeant Everett C. Babcock, KCPD Police Academy, KC, MO

October 8, 2013 (3 Hour Lecture)	Investigating and Collecting Evidence in Non-stranger Sexual Assault Cases Presenter Dr. David Lisak, Ph.D. Johnson County Community College – Overland Park, KS
April 2013 (2 day seminar)	Mid-America 2013 Forensic DNA Conference Columbia, MO
April 2012 (2 day seminar)	Mid-America 2012 Forensic DNA Conference Columbia, MO

Testimony:

Federal Court-
8th District Court- Kansas City, Missouri

Public speaking:

July 15, 2013	Guest speaker- 1 hour presentation Black Family Technology Awareness Association Boys and Girls clubs of Greater Kansas City 6th-8th grade students

CURRICULUM VITAE

NAME: Gregory Scott Hummel

TITLE: Chief Criminalist – DNA Section
-appointed Acting Supervisor 1/21/09
-appointed Acting Technical Leader 4/9/09
-promoted to Supervisor / Technical Leader 8/23/09

ADDRESS: 6633 Troost
Kansas City, MO 64131

TELEPHONE: (816) 349-3263

EDUCATION:

1995	William Jewell College - Liberty, Missouri BA Biology Magna Cum Laude
2006	University of Florida – Gainesville, Florida MS Pharmacy – Concentration in Forensic Serology and DNA

EXPERIENCE:

2000-present	Kansas City Missouri Police Department Kansas City Police Crime Laboratory - DNA Section
2008	William Jewell College – Liberty, MO Adjunct Professor, Bio 234 – Genetics
1995-2000	Children's Mercy Hospital - Kansas City, Missouri Genetics Dept. Senior Molecular Genetics Technologist

PROFESSIONAL AFFILIATIONS:

American Academy of Forensic Sciences	Member
-Criminalistics Section Ad Hoc Membership Committee	*2009-2010*
Midwestern Association of Forensic Scientists	Member
-Awards Committee	*2009-2012*
-Biology Section Coordinator	*2011-2012*
National DNA Index System Procedures Board	Board Member (2004-2006)

CERTIFICATIONS:

American Board of Criminalistics
Fellow – Molecular Biology (2007-present)

CONTINUING EDUCATION:

December 1997	American Society of Hematology National Meeting
(5 day seminar)	San Diego, California

December 1998 (5 day seminar)	American Society of Hematology National Meeting Miami, Florida
December 1999 (5 day seminar)	American Society of Hematology National Meeting New Orleans, Louisiana
November 2000 (1 day seminar)	Missouri-Kansas Regional Forensic Meeting - ABI Columbia, Missouri
April 2001 (14 day course) August 2001 (1 week course)	Crime Scene Investigation School Kansas City, Missouri Analysis of Short Tandem Repeats by Capillary Electrophoresis School Quantico, Virginia
September 2001 (2 day course)	Population Statistics and Forensic DNA Analysis Workshop Minneapolis, Minnesota
September 2001 (2 day seminar)	Midwestern Association of Forensic Scientists Minneapolis, Minnesota
June 2002 (3 day seminar)	NIJ DNA Grantee's Workshop Washington, D.C.
March 2003 (2 day seminar)	MO-KS 2003 Forensic DNA Conference Columbia, Missouri
March 2003 (2 hour course)	Paternity Statistics Workshop- Michelle Beckwith (PTC) Columbia, Missouri
May 2003 (3 day seminar)	Advanced Homicide Investigation Training Kansas City, Missouri
June 2003 (1 day seminar)	CODIS Administrator's Meeting Jefferson City, Missouri
November 2003 (4 day seminar)	National CODIS Conference Lansdowne, Virginia
March 2004 (2 day seminar)	MO-KS 2004 Forensic DNA Conference Columbia, Missouri
March 2004 (2.5 hour workshop)	Forensic Statistics Workshop Columbia, Missouri
May 2004 (2day seminar)	CODIS State Administrator's Meeting Quantico, Virginia
August 2004 (5 day course)	CODIS v5.7 Training McLean, Virginia
September 2004 (3 day seminar)	Bloodstain and Bullet Pattern Analysis for Crime Scene Reconstruction North Kansas City, Missouri
November 2004 (4 day seminar)	National CODIS Conference Arlington, Virginia

March 20005 (2 day seminar)	Mid-America 2005 Forensic DNA Conference Columbia, Missouri
March 2005 (5day workshop)	Bloodstain Pattern Interpretation Workshop Kansas City, Missouri
November 2005 (4 day seminar)	National CODIS Conference Arlington, Virginia
April 2006 (1 day workshop)	ISO 17025 Workshop Columbia, Missouri
April 2006 (2 day seminar)	Mid-America 2006 Forensic DNA Conference Columbia, Missouri
July 2006 (2 day seminar)	CODIS State Administrator's Meeting Dallas, Texas
September 2006 (1 day seminar)	CODIS Administrator's Meeting Scottsdale, Arizona
September 2006 (2 day workshop)	DNA Auditor's Training Scottsdale, Arizona
October 2006 (4 day workshop)	Advanced Bloodstain Pattern Interpretation Workshop Independence, Missouri
October 2006 (4 day seminar)	National CODIS Conference Arlington, Virginia
February 2007 (4 day seminar)	American Academy of Forensic Sciences San Antonio, Texas
March 2007 (0.5 day seminar)	Continuing Education for Forensic Professionals Program – Expert Testimony Orlando, Florida
March 2007 (2 day workshop)	Continuing Education for Forensic Professionals Program – Forensic Entomology Orlando, Florida
April 2007 (1 day workshop)	Mitochondrial DNA Workshop Columbia, Missouri
April 2007 (2 day seminar)	Mid-America 2007 Forensic DNA Conference Columbia, Missouri
November 2007 (3 day seminar)	National CODIS Conference San Francisco, California
August 2008 (3 day seminar) October 2008 (1 day workshop)	Forensic Medical Investigation Seminar North Kansas City, Missouri Forensic Population Genetics Workshop Los Angeles, California
October 2008	19th International Symposium on Human Identification

(3day seminar)	Los Angeles, California
October 2008 (0.5 day workshop)	Troubleshooting Common Laboratory Problems Workshop Los Angeles, California
November 2008 (3 day seminar)	National CODIS Conference Arlington, Virginia
April 2009 (2 day seminar)	Mid-America 2009 Forensic DNA Conference Columbia, Missouri
April 2009 (2.5 day seminar)	NIJ Applied Technology Conference Kansas City, Missouri
June 2009 (2.5 day seminar)	NIJ Conference Arlington, Virginia
October 2008 (3day seminar)	20th International Symposium on Human Identification Las Vegas, Nevada
October 2009 (0.5 day workshop)	Technical Leader Workshop Las Vegas, Nevada
April 2010 (1 day workshop)	Y-STR Workshop Columbia, Missouri
April 2010 (2 day seminar)	Mid-America 2010 Forensic DNA Conference Columbia, Missouri
June 2010 (2.5 day seminar)	NIJ Conference Arlington, Virginia
November 2010 (3 day seminar)	National CODIS Conference Salt Lake City, Utah
November 2010 (8 day seminar)	Supervisor School Kansas City, Missouri (Kansas City Police Academy)
February 2011 (1/2 day workshop)	Method Validation and Estimating the Uncertainty of Measurements in the Modern Forensic Laboratory - AAFS Chicago, Illinois
February 2011 (1/2 day workshop)	Veterinary Forensic Sciences: Animals as Evidence - AAFS Chicago, Illinois
February 2011 (4 day seminar)	American Academy of Forensic Sciences Chicago, Illinois
April 2011 (1 day workshop)	Relationship Testing Statistics Workshop Columbia, Missouri
April 2011 (2 day seminar)	Mid-America 2011 Forensic DNA Conference Columbia, Missouri
June 2011 (2.5 day seminar)	MFRC – DNA Symposium (Facilitator) Ames, Iowa

June 2011 (2.5 day seminar)	NIJ Conference Arlington, Virginia
September 2011 (2 day seminar)	40th Annual MAFS Meeting Lombard, Illinois
October 2011 (5 day workshop)	ASCLD/LAB-International Assessor Training Course El Segundo, California
April 2012 (1 day workshop)	Introduction to CODIS 7 & Paternity Testing for Crime Laboratories Columbia, Missouri
April 2012 (2 day seminar)	Mid-America 2012 Forensic DNA Conference Columbia, Missouri
April 2013 (1 day workshop)	6-Dye Evolution: Prepare Your Lab for the Future of CE Fragment Analysis and beyond, presented by Life Technologies Columbia, Missouri
April 2013 (2 day seminar)	Mid-America 2013 Forensic DNA Conference Columbia, Missouri
June 2013 (5 day seminar)	International Society for Applied Biological Sciences Conference Split, Croatia
October 8, 2013 (0.5 day seminar)	Investigating and Collecting Evidence in Non-stranger Sexual Assault Cases, present by Dr. David Lisak, Ph.D. Johnson County Community College – Overland Park, KS
April 2014 (1 day workshop)	Top 10 Non-Conformances and Root cause Analysis Workshop presented by Anna Yoder, ASCLD/LAB Columbia, Missouri
April 2014 (2 day seminar)	Mid-America 2014 Forensic DNA Conference Columbia, Missouri
September 2014 (2 day workshop)	Cognitive Factors in Making Forensic Comparisons – Dr. Itiel Dror Johnson County Crime Laboratory – Johnson County, Kansas

PUBLICATIONS:

Manuscripts:

White, R.A., Dowler, L.L., Hummel, G.S., Adkison, L.R. 1995. Exclusion of Epb4.2 as a candidate for the mouse mutant pallid. Mouse Genome 959(2): 492-494.

Boon-Leong, L., White, R.A., Hummel, G.S., Schwaeble, W.N.J., Peerschke, E., Reid, K., Ghebrehiwet, B. 1998. Characterization of the murine gene of gC1qBP, a novel cell protein that binds the globular heads of C1q, vitronectin, high molecular weight kininogen and factor XII. Gene 209: 229-237.

Dai, G., Wang, D., Liu, B., Kasik, J.W., Muller, H., White, R.A., Hummel, G.S., Soares, M.J. 2000. Three novel paralogs of the rodent prolactin gene family. J. Endocrinology 166: 63-75.

Abstracts:

Hummel, G.S., Gaedigk, R., Reddig, R., Copple, A., Watanabe, M., White, R.A. 1998. cDNA isolation, sequence, tissue expression, genomic structure, and chromosomal mapping of mouse Glycophorin C. American Society of Hematology. Miami, FL.

White, R.A., Hummel, G.S., Copple, A., Shimizu, K., Kolbrecher, D., Pinson, D., Garg, U., Watanabe, M. 1998. Characterization and chromosomal mapping of hereditary erythroblastic anemia (hea). American Society of Hematology. Miami, FL.

Hummel, G.S., Examination of DNA Recovery Potential from Fired Shell Casings. International Society for Applied Biological Sciences Conference. Split, Croatia

TESTIMONY:

State Courts-

Cass County, Missouri
Clay County, Missouri
Clinton County, Missouri
Jackson County, Missouri
Platte County, Missouri

Adams County, Colorado
Douglas County, Kansas

Federal Courts-

Western District Missouri - Kansas City, Missouri

SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories

Scientific Working Group on DNA Analysis Methods (SWGDAM)

The Scientific Working Group on DNA Analysis Methods, better known by its acronym of SWGDAM, is a group of approximately 50 scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada. During meetings, which are held twice a year, subcommittees discuss topics of interest to the forensic DNA community and often develop documents to provide direction and guidance for the community. A mixture interpretation subcommittee was formed in January 2007 and worked for several years to provide a guidance document on autosomal short tandem repeat (STR). This document was presented to the full SWGDAM group and received approval in January 2010.

This document provides guidelines for the interpretation of DNA typing results from short tandem repeats (STR) and supersedes the Scientific Working Group on DNA Analysis Methods (SWGDAM) Short Tandem Repeat (STR) Interpretation Guidelines (2000). The revised guidelines are not intended to be applied retroactively. Guidance is provided for forensic casework analyses on the identification and application of thresholds for allele detection and interpretation, and appropriate statistical approaches to the interpretation of autosomal STRs with further guidance on mixture interpretation. Laboratories are encouraged to review their standard operating procedures and validation data in light of these guidelines and to update their procedures as needed. It is anticipated that these guidelines will evolve further as future technologies emerge. Some aspects of these guidelines may be applicable to low level DNA samples. However, this document is not intended to address the interpretation of analytical results from enhanced low template DNA techniques.

Introduction

The interpretation of DNA typing results for human identification purposes requires professional judgment and expertise. Additionally, laboratories that analyze DNA samples for forensic casework purposes are required by the Quality Assurance Standards for Forensic DNA Testing Laboratories (effective July 1, 2009) to establish and follow documented procedures for the interpretation of DNA typing results and reporting. Due to the multiplicity of forensic sample types and the potential complexity of DNA typing results, it is impractical and infeasible to cover every aspect of DNA interpretation by a preset rule. However, the laboratory should utilize written procedures for interpretation of analytical results with the understanding that specificity in the standard operating protocols will enable greater consistency and accuracy among analysts within a laboratory. It is recommended that standard operating procedures for the interpretation of DNA typing results be sufficiently detailed that other forensic

DNA analysts can review, understand in full, and assess the laboratory's policies and practices. The laboratory's interpretation guidelines should be based upon validation studies, scientific literature, and experience.

Background

Upon completion of the technical aspects of DNA analysis, DNA typing results must be verified and interpreted. The verification of the accuracy of the DNA typing results involves a review of peak designations and other software-generated information, as well as an evaluation of quality controls. Based on this assessment, the DNA analyst performs interpretations, makes comparisons among samples (where appropriate) and draws conclusions. These data and conclusions are technically reviewed and the conclusions are typically captured for documentation and communication purposes within a laboratory report.

Using current technologies for human identification, DNA typing results are derived through application of analytical software during and after electrophoresis of fluorescently-labeled amplification products that are generated for each sample using an amplification kit. For each sample, the software translates fluorescence intensity data into electropherograms and then labels any detected peaks with such descriptors as size (in base-pairs, or bp) and peak height (in relative fluorescence units, or RFU). Using allelic ladders for reference, the software then labels peaks that meet certain criteria with allelic designations.

To ensure the accuracy of these computer-generated allele designations, the DNA analyst must verify that appropriate genotyping parameters (i.e., internal size standard and allelic ladder) were used and that the correct genotyping results were obtained for a known positive control. Additionally, if a sample is amplified using multiple kits that contain redundant loci, the DNA analyst must address the concordance of the genotyping results at the loci that are common to both kits. As an example, a given sample amplified using both the Profiler Plus™ and COfiler™ Amplification Kits exhibits concordance when identical alleles for the genetic loci amelogenin, D3S1358, and D7S820 are obtained. After verification of the allelic designations, the alleles are classified based on their peak height relative to an established minimum peak height threshold for comparison purposes.

The results of the analysis controls [i.e., reagent blank(s), positive amplification control(s), and negative amplification control(s)] are evaluated. If the reagent blank(s), positive amplification control(s), and negative amplification control(s) yield results that are within their prescribed specifications, the DNA analyst interprets the DNA typing results from each sample to determine if the DNA typing results originated from a single donor or multiple donors. If the expected results are not obtained from a control sample(s), the DNA analyst must determine if the control(s) and/or sample(s) should be re-processed or proceed within the prescribed limitations of interpretation.

Based on the interpretation of the forensic samples and a comparison of the DNA typing results obtained from the questioned sample(s) to those of any known sample(s), or a comparison between multiple questioned samples, a DNA analyst can reach one of three primary conclusions: cannot exclude, can exclude, or inconclusive/uninterpretable.

Statistical interpretation for reported inclusionary results provides weight to the inclusionary statement. Statistical analysis is not required for exclusionary conclusions, comparisons between multiple questioned samples without a comparison to a known sample, nor applicable to inconclusive/uninterpretable results. The conclusions reached as part of the DNA interpretation process are compiled into a written draft by the DNA analyst and are subjected to technical and administrative reviews prior to issuing a final case report.

This document addresses definitions, data evaluation, interpretation of results and conclusions/reporting for autosomal STR typing, including guidance on mixture interpretation. Approaches to statistical interpretation are presented. A list of relevant literature is also included to provide further source material.

1. Preliminary Evaluation of Data

The laboratory should develop criteria to determine whether an instrumental response represents the detection of DNA fragment(s) rather than instrument noise. An analytical threshold defines the minimum height requirement at and above which detected peaks can be reliably distinguished from background noise. Because the analytical threshold is based upon a distribution of noise values, it is expected that occasional, non-reproducible noise peaks may be detected above the analytical threshold. An analytical threshold should be sufficiently high to filter out noise peaks. Usage of an exceedingly high analytical threshold increases the risk of allelic data loss which is of potential exclusionary value.

1.1. Analytical threshold: The Laboratory should establish an analytical threshold based on signal-to-noise analyses of internally derived empirical data. As an example, an analytical threshold may be based on two times the intensity difference between the highest peak and lowest trough within the instrumental noise data. Other scientific methods may be used. The usage of an analytical threshold value that differs substantially from manufacturer's recommendations should be supported by internal signal-to-noise assessments.

1.2. The laboratory must develop criteria to evaluate internal standards and/or allelic ladders.

1.3. Controls are required to assess analytical procedures.

1.3.1. The laboratory must establish criteria for evaluation of the following controls, including but not limited to: reagent blank and positive and negative amplification controls.

1.3.2. The laboratory must develop criteria for the interpretation and documentation of results in the event that the controls do not perform as expected.

1.4. A laboratory using STR multiplexes that contain redundant loci must establish criteria regarding the concordance of such data.

2. Allele Designation

2.1. The laboratory establishes criteria to assign allele designations to appropriate peaks.

2.1.1. Locus Designation: The laboratory establishes criteria to address locus assignment for alleles. The criteria should address alleles that fall above the largest or below the smallest allele (or virtual bin) of the allelic ladder.

2.1.2. Allele Designation: The laboratory designates alleles as numerical values in accordance with recommendations of the International Society of Forensic Genetics.

2.1.2.1. Allele designation is based operationally on the number of repeat sequences contained within the allele and by comparison to an allelic ladder.

2.1.2.2. The laboratory establishes guidelines for the designation of alleles containing an incomplete repeat motif (i.e., an off-ladder allele falling within the range spanned by the ladder alleles). This designation includes the number of complete repeats and, separated by a decimal point, the number of base pairs in the incomplete repeat (e.g., FGA 18.2 allele).

2.1.2.3. The laboratory establishes criteria for designating alleles that fall above the largest or below the smallest allele of the allelic ladder (or virtual bin). Extrapolation of an above/below ladder allele to a specific designation (e.g., generally to no more than one repeat unit) should also be supported by precision studies, validation and determination of measurement variance. Above/below ladder alleles should be designated as either greater than (>) or less than (<) the respective ladder allele (or virtual bin), or designated numerically when appropriate extrapolation can be used. When the ">" or "<" designation is used, the laboratory should establish criteria, based on relative sizes, for the comparison of such alleles among samples.

3. Interpretation of DNA Typing Results

3.1. Non-Allelic Peaks

Because forensic DNA typing characterizes STR loci using PCR and electrophoretic technologies, some data that result from this analytical scheme may not represent actual alleles that originate in the sample. It is therefore necessary, before the STR typing results can be used for comparison purposes, to identify any potential non-allelic peaks. Non-allelic peaks may be PCR products (e.g., stutter, non-template dependent nucleotide addition, and non-specific amplification product), analytical artifacts (e.g., spikes and raised baseline), instrumental limitations (e.g., incomplete spectral separation resulting in pull-up or bleed-through), or may be introduced into the process (e.g., disassociated primer dye). Generally, non-allelic data such as stutter, non-template dependent nucleotide addition, disassociated dye, and incomplete spectral separation are reproducible; spikes and raised baseline are generally non-reproducible.

3.1.1. The laboratory establishes criteria based on empirical data (obtained internally or externally), and specific to the amplification and detection systems used, to address the interpretation of non-allelic peaks. The guidelines address identification of non-allelic peaks and the uniform application, across all loci of a DNA profile, of the criteria used to identify non-allelic peaks.

3.1.1.1. In general, the empirical criteria are based on qualitative and/or quantitative characteristics of peaks. As an example, dye artifacts and spikes may be distinguished from allelic peaks based on morphology and/or reproducibility. Stutter and non-template dependent nucleotide addition peaks may be characterized based on size relative to an allelic peak and amplitude.

3.1.1.2. While the application of an analytical threshold may serve to filter out some non-allelic peaks, the analytical threshold should be established based on signal-to-noise considerations (i.e., distinguishing potential allelic peaks from background). The analytical threshold should not be established for purposes of avoiding artifact labeling as such may result in the potential loss of allelic data.

3.1.1.3. The laboratory establishes guidelines addressing off-scale data. Fluorescence detection instruments have a limited linear range of detection, and signal saturation can result in off-scale peaks. Following peak detection, such peaks in the analyzed data are assigned an artificial height value which is not representative of the true amplitude. Peak

height values for off-scale peaks should not be used in quantitative aspects of interpretation (e.g., stutter and peak height ratio assessments).

3.2. Application of Peak Height Thresholds to Allelic Peaks

Amplification of low-level DNA samples may be subject to stochastic effects, where two alleles at a heterozygous locus exhibit considerably different peak heights (i.e., peak height ratio generally <60%) or an allele fails to amplify to a detectable level (i.e., allelic dropout). Stochastic effects within an amplification may affect one or more loci irrespective of allele size. Such low-level samples exhibit peak heights within a given range which is dependent on quantitation system, amplification kit and detection instrumentation. A threshold value can be applied to alert the DNA analyst that all of the DNA typing information may not have been detected for a given sample. This threshold, referred to as a stochastic threshold, is defined as the value above which it is reasonable to assume that allelic dropout has not occurred within a single-source sample. The application of a stochastic threshold to the interpretation of mixtures should take into account the additive effects of potential allele sharing.

3.2.1. The laboratory establishes a stochastic threshold based on empirical data derived within the laboratory and specific to the quantitation and amplification systems (e.g., kits) and the detection instrumentation used. It is noted that a stochastic threshold may be established by assessing peak height ratios across multiple loci in dilution series of DNA amplified in replicate. The RFU value above which it is reasonable to assume that, at a given locus, allelic dropout of a sister allele has not occurred constitutes a stochastic threshold.

3.2.1.1. If measures are used to enhance detection sensitivity (i.e., allelic height), the laboratory should perform additional studies to establish independent criteria for application of a separate stochastic threshold(s). Such measures may include but not be limited to increased amplification cycle number, increased injection time, and post-amplification purification/concentration of amplified products.

3.2.1.2. For samples for which an assumption can be made as to the number of contributors, the laboratory should establish criteria for comparison of allelic peaks which fall below the stochastic threshold. As an example, if a locus in an assumed single-source sample exhibits two peaks, one or both of which are below the stochastic threshold, the laboratory may use that locus for comparison purposes. Also, the presence of male DNA may be established based on a Y-allele at amelogenin that is below the stochastic threshold.

3.2.2. If a stochastic threshold based on peak height is not used in the evaluation of DNA typing results, the laboratory must establish alternative

criteria (e.g., quantitation values or use of a probabilistic genotype approach) for addressing potential stochastic amplification. The criteria must be supported by empirical data and internal validation and must be documented in the standard operating procedures.

3.3. Peak Height Ratio

Intra-locus peak height ratios (PHR) are calculated for a given locus by dividing the peak height of an allele with a lower RFU value by the peak height of an allele with a higher RFU value, and then multiplying this value by 100 to express the PHR as a percentage.

3.3.1. The laboratory should establish PHR requirements based on empirical data for interpretation of DNA typing results from single-source samples. Different PHR expectations can be applied to individual loci (e.g., 70% for D3S1358, 65% for vWA, etc.); alternatively, a single PHR expectation can be applied to multiple loci (e.g., 60%).

3.3.1.1. The laboratory may evaluate PHRs at various DNA template levels (e.g., dilution series of DNA). It is noted that different PHR expectations at different peak height ranges may be established.

3.3.2. PHR requirements are only applicable to allelic peaks that meet or exceed the stochastic threshold.

3.4. Number of Contributors to a DNA Profile

Generally, a sample is considered to have originated from a single individual if one or two alleles are present at all loci for which typing results were obtained (although tri-allelic loci may occur), and the peak height ratios for all heterozygous loci are within the empirically determined values. It is noted that peak height imbalances may be seen in the typing results from, for example, a primer binding site variant that results in attenuated amplification of one allele of a heterozygous pair.

A sample is generally considered to have originated from more than one individual if three or more alleles are present at one or more loci (excepting tri-allelic loci) and/or the peak height ratios between a single pair of allelic peaks for one or more loci are below the empirically determined heterozygous peak height ratio expectation. Generally, the minimum number of contributors to a mixed sample can be determined based on the locus that exhibits the greatest number of allelic peaks. As an example, if at most five alleles are detected per locus, then the DNA typing results are consistent with having arisen from at least three individuals.

3.4.1. For DNA mixtures, the laboratory should establish guidelines for determination of the minimum number of contributors to a sample. Alleles need not meet the stochastic threshold to be used in this assessment.

3.4.2. The laboratory should define the number of alleles per locus and the relative intra-locus peak height requirements for assessing whether a DNA typing result is consistent with originating from one or more sources. The minimum number of loci should be defined for determination of whether a sample is a mixture.

3.4.3. Where multiple amplifications and/or injections are generated for a given sample extract, the laboratory should establish guidelines for determining which results are used for comparisons and statistical calculations.

3.4.3.1. If composite profiles (i.e., generated by combining typing results obtained from multiple amplifications and/or injections) are used, the laboratory should establish guidelines for the generation of the composite result. When separate extracts from different locations on a given evidentiary item are combined prior to amplification, the resultant DNA profile is not considered a composite profile. Unless there is a reasonable expectation of sample(s) originating from a common source (e.g., duplicate vaginal swabs or a bone), allelic data from separate extractions from different locations on a given evidentiary item should not be combined into a composite profile. The laboratory should establish guidelines for determining the suitability of developing composite profiles from such samples.

3.5. Interpretation of DNA Typing Results for Mixed Samples

An individual's contribution to a mixed biological sample is generally proportional to their quantitative representation within the DNA typing results. Accordingly, depending on the relative contribution of the various contributors to a mixture, the DNA typing results may potentially be further refined.

As an example, if a sample contains a predominance of one individual's DNA, that individual's DNA profile may be determined. This state results in a distinguishable mixture, whereby there is a distinct contrast in signal intensities (e.g., peak heights) among the different contributors' alleles. In such instances, major and/or minor contributors may be determined. Discernment of the STR typing results for the major or minor contributors to a mixture may be limited to only some loci (with the remaining loci yielding multiple potential genotypes for the major or minor contributor). The major (and possibly the minor) contributor may effectively constitute a deduced single-source profile.

Alternatively, if the amounts of biological material from multiple donors are similar, it may not be possible to further refine the mixture profile. When major or minor contributors cannot be distinguished because of similarity in signal intensities, the sample is considered to be an indistinguishable mixture. The classification as indistinguishable may be limited to some, not all, of the loci for which DNA typing results are obtained and does not imply that the profile is uninterpretable. Individuals may still be included or excluded as possible contributors to an indistinguishable mixture.

Evidence items taken directly from an intimate sample, as determined by the laboratory, are generally expected to yield DNA from the individual from whom the sample was taken. If another source of DNA is present in sufficient quantity in such a sample, a mixture of DNA is likely to be detected. Based on this expectation, any DNA typing results from such a mixture that match a conditional known sample (e.g., from the victim) may be separated from the other mixture results to facilitate identification of the foreign alleles. The obligate alleles may effectively constitute a single-source profile (i.e., if there is one DNA contributor in addition to the individual from whom the sample was taken) or a mixture profile (i.e., if there are multiple additional DNA contributors). A similar state can exist when another known individual (i.e., consensual partner) is expected to have contributed biological material to the mixed sample.

3.5.1. The laboratory should establish guidelines based on peak height ratio assessments for evaluating potential sharing of allelic peaks among contributors and for determining whether contributors to a mixed DNA typing result are distinguishable. When assessing peak height ratios, pair-wise comparison of all potential genotypic combinations should be evaluated.

3.5.2. The laboratory should define and document what, if any, assumptions are used in a particular mixture deconvolution.

3.5.2.1. If no assumptions are made as to the number of contributors, at a minimum, the laboratory should assign to a major contributor an allele (e.g., homozygous) or pair of alleles (e.g., heterozygous) of greater amplitude at a given locus that do not meet peak height ratio expectations with any other allelic peak(s).

3.5.2.2. If assumptions are made as to the number of contributors, additional information such as the number of alleles at a given locus and the relative peak heights can be used to distinguish major and minor contributors.

3.5.3. A laboratory may define other quantitative characteristics of mixtures (e.g., mixture ratios) to aid in further refining the contributors.

3.5.3.1. Differential degradation of the contributors to a mixture may impact the mixture ratio across the entire profile.

3.5.4. Mixtures with a Single Major Contributor and One or More Minor Contributors:

3.5.4.1. In general, heterozygous alleles attributed to a major contributor should meet the laboratory's established peak height ratio expectations for single-source samples. Due to the potential for overlapping peaks to cause imbalance of major heterozygous alleles, the laboratory may establish a quantitative means of evaluating the distinction in peak heights of the major and minor contributors (i.e., mixture ratio).

3.5.4.2. After deconvolution, the DNA typing results attributed to an individual minor contributor should also meet PHR expectations. The PHR expectations of a minor contributor may be reduced due to stochastic peak height variation and the additive effects of peak sharing (e.g., minor peak and stutter peaks).

3.5.4.3. Due to the possibility that the minor contributor's alleles may be shared by the major contributor (and thus masked), determination of a single genotype for a minor contributor may be possible at only some loci (while multiple allelic combinations, or allelic drop out, are possible at other loci).

3.5.5. Mixtures with Multiple Major Contributors and One or More Minor Contributors: The laboratory should establish guidelines based on peak height ratio assessments and/or mixture ratios for determining whether multiple major contributors are present in a mixed sample.

3.5.6. Mixtures with Indistinguishable Contributors: The laboratory should establish guidelines based on peak height ratio assessments for identifying mixtures for which no major or minor contributors can be discerned.

3.5.7. Mixtures with a Known Contributor(s): The laboratory should establish guidelines for determining whether separation of a known contributor's profile is applicable (e.g., based on the types of evidentiary items).

3.5.7.1. At a minimum, where there is no indication of sharing of the known and obligate alleles, the laboratory should separate out those alleles attributable to the known sample (e.g., victim, consensual partner, etc.).

3.5.7.2. To further refine the obligate alleles in a profile, the laboratory may establish guidelines for addressing potential sharing of alleles among

the individual known to have contributed to a sample and the additional contributor(s).

3.5.8. Interpretation of Potential Stutter Peaks in a Mixed Sample

3.5.8.1. For mixtures in which minor contributors are determined to be present, a peak in stutter position (generally n-4) may be determined to be 1) a stutter peak, 2) an allelic peak, or 3) indistinguishable as being either an allelic or stutter peak. This determination is based principally on the height of the peak in the stutter position and its relationship to the stutter percentage expectations established by the laboratory.

3.5.8.2. Generally, when the height of a peak in the stutter position exceeds the laboratory's stutter expectation for a given locus, that peak is consistent with being of allelic origin and should be designated as an allele.

3.5.8.3. If a peak is at or below this expectation, it is generally designated as a stutter peak. However, it should also be considered as a possible allelic peak, particularly if the peak height of the potential stutter peak(s) is consistent with (or greater than) the heights observed for any allelic peaks that are conclusively attributed (i.e., peaks in non-stutter positions) to the minor contributor(s).

3.6 Comparison of DNA Typing Results

The following determinations can be made upon comparison of evidentiary and known DNA typing results (and between evidentiary samples):

- The known individual cannot be excluded (i.e., is included) as a possible contributor to the DNA obtained from an evidentiary item.
- The known individual is excluded as a possible contributor.
- The DNA typing results are inconclusive/uninterpretable.
- The DNA typing results from multiple evidentiary items are consistent or inconsistent with originating from a common source(s).

3.6.1. The laboratory must establish guidelines to ensure that, to the extent possible, DNA typing results from evidentiary samples are interpreted before comparison with any known samples, other than those of assumed contributors.

3.6.2. DNA typing results may not be obtained at all loci for a given evidentiary sample (e.g., due to DNA degradation, inhibition of amplification and/or low-template quantity); a partial profile thus results.

3.6.2.1. For partial profiles, the determination of which alleles/loci are suitable for comparison and statistical analysis should be made prior to comparison to the known profiles.

3.6.2.2. The laboratory should establish guidelines for inclusions and exclusions when a known individual's DNA profile is not fully observed in the evidentiary profile.

3.6.3. The laboratory must establish guidelines for inclusionary, exclusionary and inconclusive/uninterpretable conclusions based on comparisons of DNA typing results from known samples and both single-source and mixed evidentiary samples.

3.6.4. For mixtures for which two or more individuals cannot be excluded as potential contributors, the laboratory may establish guidelines for assessing whether all of the DNA typing results obtained from the mixed sample are accounted for by the multiple known samples.

3.6.5. Because assumptions regarding the origin of evidence or the number of contributors to a mixture can impact comparisons, the laboratory should establish guidelines for documenting any assumptions that are made when formulating conclusions.

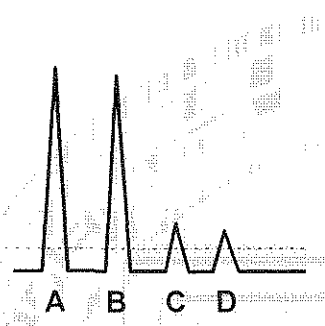
3.6.6. The laboratory should establish guidelines for identifying DNA typing results for which comparisons of evidentiary and known samples are not made (at a minimum, to include inconclusive/uninterpretable results).

4. Statistical Analysis of DNA Typing Results

In forensic DNA testing, calculations are performed on evidentiary DNA profiles that are established as relevant in the context of the case to aid in the assessment of the significance of an inclusion. These calculations are based on the random match probability (RMP), the likelihood ratio (LR), or the combined probability of exclusion/inclusion (CPE/CPI).

While the RMP is commonly thought of in terms of single-source profiles, the application of this formula to evidentiary profiles inherently includes an assumption of the number of contributors to the DNA sample. As such, this document also applies the term RMP to mixture calculations where the number of contributors is assumed (this has sometimes been referred to as a "modified RMP"). By using the RMP nomenclature, these calculations are distinguished from the CPI nomenclature which is commonly thought of in terms of a mixture calculation that makes no assumption as to the number of contributors.

In addition to assumptions of the number of contributors, quantitative peak height information and mixture ratio assessments may or may not be included in the interpretation of an evidentiary profile. Calculations performed using interpretations incorporating this information are termed "restricted." When this quantitative peak height information is not included, the resultant calculation is termed "unrestricted" (Figure 1).



Unrestricted

All combinations of alleles are deemed possible (relative peak height differences are not utilized)

AB + AC + AD + BC + BD + CD

Restricted

Based on relative peak heights, alleles are paired only where specific combinations of alleles are deemed possible

AB + AC + AD + BC + BD + CD

Figure 1. Illustration of "restricted" versus "unrestricted" approaches based on relative peak heights (using an assumption of two donors with all peaks above the stochastic threshold).

The genetic loci and assumptions used for statistical calculations must be documented, at a minimum, in the case notes.

4.1. The laboratory must perform statistical analysis in support of any inclusion that is determined to be relevant in the context of a case, irrespective of the number of alleles detected and the quantitative value of the statistical analysis.

4.1.1. The laboratory should establish guidelines where multiple stains from the same or separate items have provided genetic information that is consistent with originating from a common source(s) but having various levels of discrimination. In general, the statistics for the typing results that provide the most genetic information and/or the highest discrimination potential are reported.

4.2. For calculating the CPE or RMP, any DNA typing results used for statistical analysis must be derived from evidentiary items and not known samples. This precludes combining multiple CPE or RMP results for the same mixture component of an evidentiary sample. However, different calculations may be made for the same mixture component if different assumptions as to the number of contributors are made and clearly stated in the case notes and/or report.

4.3. The laboratory must not use inconclusive/uninterpretable data (e.g., at individual loci or an entire multi-locus profile) in statistical analysis.

4.3.1. For a distinguishable mixture, a major contributor(s) profile may be suitable for statistical analysis even in the presence of inconclusive minor contributor results.

4.4. Exclusionary conclusions do not require statistical analysis.

4.5. The laboratory must document the source of the population database(s) used in any statistical analysis.

4.6. The formulae used in any statistical analysis must be documented and must address both homozygous and heterozygous typing results, multiple locus profiles, mixtures, minimum allele frequencies, and, where appropriate, biological relationships.

4.6.1. Given a profile for which multiple formulae are applicable, the laboratory must have guidelines for the selection of the formula(e) suitable for statistical application (see Table 1).

4.6.2. It is not appropriate to calculate a composite statistic using multiple formulae for a multi-locus profile. For example, the CPI and RMP cannot be multiplied across loci in the statistical analysis of an individual DNA profile because they rely upon different fundamental assumptions about the number of contributors to the mixture.

4.6.3. When using CPE/CPI (with no assumptions of number of contributors) to calculate the probability that a randomly selected person would be excluded/included as a contributor to the mixture, loci with alleles below the stochastic threshold may not be used for statistical purposes to support an inclusion. In these instances, the potential for allelic dropout raises the possibility of contributors having genotypes not encompassed by the interpreted alleles.

4.6.3.1. Alleles below the stochastic threshold may be used for comparisons and/or to establish the presence of a mixture or male DNA (e.g., Y allele at amelogenin).

4.6.3.2. A restricted CPE/CPI may be applied to multiple major contributors despite the presence of minor contributor(s) alleles below the stochastic threshold; a description of how to calculate can be found in Section 5.3.5.

4.7. If a laboratory uses source attribution statements, then it must establish guidelines for the criteria on which such a declaration is based.

5. Statistical Formulae

5.1. Whenever the statistical analysis at a locus is meant to represent all possible contributors to a mixture, if there is a reasonable possibility that locus dropout could have led to the loss of an entire genotype, then a statistical calculation should not be performed for that locus. Similarly, the product rule should not be applied when the resultant set of combined profiles would not include all individuals who would not be excluded as possible contributors to the mixture.

5.2. Random Match Probability (RMP)

5.2.1. When the interpretation is based upon the assumption of a single contributor (or a single major contributor to a mixture), the RMP formulae are those described in NRCII recommendations 4.1, 4.2, 4.3, and 4.4. The most commonly used formulae are listed below:

5.2.1.1. For heterozygote genotypes, the formula is 2pq. This is NRCII formula 4.1b.

5.2.1.2. For homozygote genotypes, the formula is $p^2 + p(1-p)\theta$, where $\theta = 0.01$ or 0.03 in accordance with NRCII. This is NRCII formula 4.4a.

5.2.1.3. For single-allele profiles where the zygosity is in question (e.g., it falls below the stochastic threshold):

5.2.1.3.1. The formula 2p, as described in recommendation 4.1 of NRCII, may be applied to this result.

5.2.1.3.2. Instead of using 2p, the algebraically identical formulae $2p - p^2$ and $p^2 + 2p(1-p)$ may be used to address this situation without double-counting the proportion of homozygotes in the population.

5.2.1.3.3. Laboratories may choose to assign the value of 1 to the scenario described in 5.2.1.3., i.e. not use the locus for statistical weight.

5.2.1.4. Conditional subpopulation calculations may also be performed in accordance with NRCII formulae 4.10a and 4.10b.

5.2.2. When the interpretation is conditioned upon the assumption of a particular number of contributors greater than one, the RMP is the sum of the individual frequencies for the genotypes included following a mixture deconvolution. Examples are provided below.

5.2.2.1. In a sperm fraction mixture (at a locus having alleles P, Q, and R) assumed to be from two contributors, one of whom is the victim (having genotype QR), the sperm contributor genotypes included post-deconvolution might be PP, PQ, and PR. In this case, the RMP for the sperm DNA contributor could be calculated as $[p^2 + p(1-p)\theta] + 2pq + 2pr$.

5.2.2.2. In a sperm fraction mixture (at a locus having alleles P, Q, and R) assumed to be from two contributors, where the major contributor is the victim (having genotype QR), there remains an obligate minor contributor P allele above the stochastic threshold. Also present in the results are two peaks filtered as possible stutter (S* and T*). If both filtered peaks are within an RFU range that could reasonably be paired with the P allele as heterozygous genotypes, the sperm contributor genotypes included post-deconvolution might be PP, PQ, PR, PS* and PT*. In this case, the RMP for the sperm DNA contributor could be calculated as $[p^2 + p(1-p)\theta] + 2pq + 2pr + 2ps + 2pt$. Some laboratories might instead choose to apply a single-allele formula as discussed in section 5.2.1.3, e.g., 2p.

5.2.2.3. In a mixture having at a locus alleles P, Q, and R, assumed to be from two contributors, where all three alleles are below the stochastic threshold, the interpretation may be that the two contributors could be a heterozygote-homozygote pairing where all alleles were detected, a heterozygote-heterozygote pairing where all alleles were detected, or a heterozygote-heterozygote pairing where a fourth allele might have dropped out. In this case, the RMP must account for all heterozygotes and homozygotes represented by these three alleles, but also all heterozygotes that include one of the detected alleles. The RMP for this interpretation could be calculated as $(2p - p^2) + (2q - q^2) + (2r - r^2) - 2pq - 2pr - 2qr$.

5.2.2.3.1. Since 2p includes 2pq and 2pr, 2q includes 2pq and 2qr, and 2r includes 2pr and 2rq, the formula in 5.2.2.3 subtracts 2pq, 2pr, and 2qr to avoid double-counting these genotype frequencies.

5.2.2.3.2. Laboratories may choose to use the formula 2p + 2q + 2r for the scenario described in 5.2.2.3.

5.2.2.3.3. Laboratories may choose to assign the value of 1 to the scenario described in 5.2.2.3, i.e. not use the locus for statistical weight.

5.2.2.4. Care should be taken to not report a calculated RMP greater than 1.0. This can occur when using the calculations discussed in 5.2.2.1 and 5.2.2.2 (due to the application of θ in the standard homozygote formula but not in the heterozygote formula) and in 5.2.2.3.1 (due to the double counting of the PP, QQ, RR, PQ, PR, and QR genotype frequencies).

5.2.2.5. In a sperm fraction assumed to be from two contributors, one of whom is the victim, the sperm contributor genotypes included post-deconvolution might include only a single genotype (PQ) at locus 1, but multiple possible genotypes (UU or UV) at locus 2. In this case, the two-locus RMP for the sperm DNA contributor could be calculated as $2pq * [u^2 + u(1-u)\theta + 2uv]$.

5.2.2.6. The unrestricted RMP might be calculated for mixtures that display no indications of allelic dropout. The formulae include an assumption of the number of contributors, but relative peak height information is not utilized. For two-person mixtures, the formulae for loci displaying one, two, or three alleles are identical to the CPI calculation discussed in section 5.3. For loci displaying four alleles (P, Q, R, and S), homozygous genotypes would not typically be included. The unrestricted RMP in this case would require the subtraction for homozygote genotype frequencies, e.g., $(p + q + r + s)^2 - p^2 - q^2 - r^2 - s^2$.

5.2.3. When a suspect's profile has been determined to match the unknown profile, if the alternate hypothesis is that a relative of the suspect is in fact the source of the unknown profile, then all efforts should be undertaken to obtain a sample directly from the relative in question so that there is no need to rely on a probability-based estimate of a coincidental match.

In the absence of a direct comparison, conditional match probabilities for various relatives can be calculated in accordance with NRCII formulae 4.8 and 4.9.

5.2.3.1. Full Siblings (NRCII formulae 4.9a and 4.9b)

Genotype of suspect	Probability of the same genotype in a sibling
PP	$(1 + 2p + p^2) / 4$
PQ	$(1 + p + q + 2pq) / 4$

5.2.3.2. Other Relatives (NRCII formulae 4.8a and 4.8b)

Genotype of suspect	Probability of the same genotype in a relative
PP	$p^2 + 4p(1 - p)F$
PQ	$2pq + 2(p + q - 4pq)F$

where F = 1/4 for parent and offspring
1/8 for half-siblings
1/8 for uncle and nephew
1/8 for grandparent and grandchild
1/16 for first cousins

5.2.3.3. Conditional subpopulation corrections could also be applied to these formulae following the methods of Ayres (2000) as described in Fung and Hu (2008).

5.3. Combined Probability of Inclusion (CPI) and Exclusion (CPE)

5.3.1. PI is calculated as (sum of allele frequencies)^2 for each locus.

5.3.2. The CPI is the product of the individual locus PIs:
$CPI = PI_1 * PI_2 * ... * PI_N$

5.3.3. The PE has been commonly presented two ways

5.3.3.1. $PE = 1 - PI$

5.3.3.2. $PE = q^2 + 2pq$, where p is the sum of allele frequencies and q represents all other alleles $(1 - p)$. This is analogous to the single allele formula described in 5.2.1.3.2.

5.3.3.3. Population substructure corrections can also be applied using $PE = 1 - [p^2 - p(1 - p)\theta]$, where p is the sum of allele frequencies observed at that locus.

5.3.4. The CPE has been commonly presented two ways

5.3.4.1. $CPE = 1 - CPI$

5.3.4.2. $CPE = 1 - [(1 - PE_1) * [(1 - PE_2) * ... * (1 - PE_N)]$

5.3.5. The CPI and CPE are typically applied to all alleles detected in a mixture, subject to the limitations described in section 4.6.3. This section also allowed for a restricted CPI and CPE. Examples of both scenarios are provided below.

5.3.5.1. Unrestricted CPI and CPE. In a mixture at a locus having alleles P, Q, and R, all above the laboratory's stochastic threshold, the interpretation might be that all potential contributors to this mixture have genotypes consisting of some combination of the detected alleles (PP, QQ, RR, PQ, PR, and QR). In this case, the probability of inclusion for the mixture could be calculated as $(p + q + r)^2$.

5.3.5.2. Unrestricted CPI and CPE. In a mixture at a locus having alleles P, Q, R, and S where alleles P, Q, and R are above the stochastic threshold, but allele S is below that threshold, in the standard application of the CPI and CPE, no calculation would be performed at this locus.

5.3.5.3. Restricted CPI and CPE. Given (a) a mixture at a locus having alleles P, Q, R, and S, (b) alleles P, Q, and R significantly (as defined by the laboratory) above the stochastic threshold, and (c) allele S is below the stochastic threshold, the interpretation might be that the higher RFU alleles are a distinct group, separate from the contributor(s) of the low-RFU S allele. The lab might choose to calculate a restricted probability of inclusion utilizing just the P, Q, and R alleles, $(p + q + r)^2$.

5.3.5.3.1. Based on the above example, had the S allele been greater than the stochastic threshold, but still identified as distinct from the higher-RFU alleles, a second general CPI or CPE could have been calculated using all four alleles.

5.4. Likelihood Ratio (LR)

5.4.1. When the evidence profile is determined to be single source, and the reference and evidence profiles are identical at all loci, LR = 1/RMP.

5.4.1.1. The numerator of the LR calculation would assume the suspect's contribution, meaning that the probability of observing results consistent with his profile would be 1.0.

5.4.1.2. The denominator would assume that the suspect is not the contributor. The probability of a randomly selected person having the evidence profile is represented by the RMP.

5.4.2. The calculation of the LR in a mixture is dependent upon the evidence profile, the comparison reference profile(s), and the individual hypotheses. Given the myriad possible combinations, any list would be necessarily incomplete. A limited set of examples is provided below.

5.4.2.1. An "unrestricted" LR is the LR calculated without taking peak heights into consideration, especially in the denominator.

5.4.2.1.1. At a locus, a mixture with alleles P and Q, is assumed to be from two contributors, and displays no indications of allelic dropout. No further considerations of peak heights are undertaken. The suspect in question is PP, and no other reference standards are being considered for inclusion.

The numerator of the LR calculation would assume the suspect's contribution, meaning that the probability of observing results consistent with his genotype would be 1.0. The second, unknown contributor must complete the mixture by having allele Q and nothing other than P or Q. Therefore the numerator to the calculation would be the sum of the frequencies for the second contributor's possible genotypes (QQ and PQ)

LR numerator = $[q^2 + q(1-q)\theta] + 2pq$

The denominator of the LR calculation might assume that the mixture is a combination of two unknown contributors. (Alternate hypotheses are possible as long as the numerator and denominator hypotheses are mutually exclusive.) The unknown contributors must have no alleles other than P or Q, and the combination of their genotypes must complete the detected mixture of P and Q.

Contrib. # 1	Contrib. # 2	Combined Probability
PP	QQ	$[p^2 + p(1-p)\theta] * [q^2 + q(1-q)\theta]$
QQ	PP	$[q^2 + q(1-q)\theta] * [p^2 + p(1-p)\theta]$
PQ	PP	$2pq * [p^2 + p(1-p)\theta]$
PP	PQ	$[p^2 + p(1-p)\theta] * 2pq$
PQ	QQ	$2pq * [q^2 + q(1-q)\theta]$
QQ	PQ	$[q^2 + q(1-q)\theta] * 2pq$
PQ	PQ	$2pq * 2pq$

LR denominator = the sum of the possible combinations of genotypes (i.e., summing the seven combined probabilities).

5.4.2.2. A "restricted" LR is the LR calculated once relative peak heights are taken into consideration. Note: Within an STR profile, some loci may have results that give identical restricted and unrestricted LRs.

5.4.2.2.1. At a locus, a mixture with alleles P and Q, is assumed to be from two contributors, and displays no indications of allelic dropout. The peak height ratio is 50% (P allele taller). Across the entire profile, the mixture appears to be 2:1. The suspect in question is PP, and no other reference standards are being considered for inclusion.

The numerator of the LR calculation would assume the suspect's contribution, meaning that the probability of observing results consistent with his genotype would be 1.0.

The second, unknown contributor must complete the mixture by having allele Q and nothing other than P or Q. If the assumed contributor (the suspect) is the minor contributor to the mixture, the possible second contributor genotypes included post-deconvolution might be PQ.

LR numerator = 2pq

Conversely, if the second contributor is the minor contributor, the possible second contributor genotypes included post-deconvolution might be QQ.

LR numerator = $q^2 + q(1-q)\theta$

The denominator of the LR calculation might assume that the mixture is a combination of two unknown contributors. The unknown contributors must have no alleles other than P or Q, and the combination of their genotypes must complete the detected mixture of P and Q. Based upon the relative peak height ratios and the overall mixture ratio, the restricted LR denominator might be limited to the following pairs of genotypes:

Major Contrib.	Minor Contrib.	Combined Probability
PP	QQ	$[p^2 + p(1-p)\theta] * [q^2 + q(1-q)\theta]$
PQ	PP	$2pq * [p^2 + p(1-p)\theta]$

LR denominator = the sum of the possible combinations of genotypes (i.e., summing the two combined probabilities).

5.4.2.3 Additional formulae for restricted and unrestricted LRs can be found in Fung and Hu (2008).

Table 1 – Suitable Statistical Analyses for DNA Typing Results
The statistical methods listed in the table cannot be combined into one calculation. For example, combining RMP at one locus with a CPI calculation at a second locus is not appropriate. However, an RMP may be calculated for the major component of a mixture and a CPE/CPI for the entire mixture (as referred to in section 4.6.2).

Category of DNA Typing Result	RMP	CPE/CPI	LR (1)
Single Source	✔		✔
Single Major Contributor to a Mixture	✔		✔
Multiple Major Contributors to a Mixture	✔ (2)	✔ (2)	✔
Single Minor Contributor to a Mixture	✔	✔ (3)	✔
Multiple Minor Contributors to a Mixture	✔ (2)	✔ (3)	✔
Indistinguishable Mixture	✔ (1)	✔	✔

(1) Restricted or unrestricted
(2) Restricted
(3) All potential alleles identified during interpretation are included in the statistical calculation

6. References and Literature Cited

Ayres, K.L. (2000) Relatedness testing in subdivided populations. *Forensic Sci. Int.* 114:107-115.

Bär, W., Brinkmann, B., Lincoln, P., Mayr, W. R., and Rossi, U. (1994) DNA recommendations – 1994 report concerning further recommendations of the DNA Commission of the ISFH regarding PCR-based polymorphisms in STR (short tandem repeat) systems. *Int. J. Legal Med.* 107: 159-160.

Bär, W., Brinkmann, B., Budowle, B., Carracedo, A., Gill, P., Lincoln, P., Mayr, W. R., and Olaisen, B. (1997) DNA recommendations – further report of the DNA Commission of the ISFH regarding the use of short tandem repeat systems. *Int. J. Legal Med.* 110: 175-176.

Committee on DNA Forensic Science, National Research Council. *An Update: The Evaluation of Forensic DNA Evidence*. National Academy Press, Washington, DC, 1996.

DNA Advisory Board. Quality Assurance Standards for Forensic DNA Typing Laboratories, *Forensic Sci. Comm.* 2 (3). See www.fbi.gov/programs/lab/fsc/backissu/july2000/codispre.htm

DNA Advisory Board (2000) Statistical and population genetic issues affecting the evaluation of the frequency of occurrence of DNA profiles calculated from pertinent population database(s). *Forensic Sci. Comm.* 2(3). See http://www.fbi.gov/programs/lab/fsc/backissu/july2000/dnastat.htm.

FBI Director (2009) Quality Assurance Standards for Forensic DNA Testing Laboratories. See http://www.fbi.gov/hq/lab/html/codis1.htm

Fung, W.K. and Hu, Y.-Q. (2008) *Statistical DNA Forensics: Theory, Methods and Computation.* Wiley: Hoboken, NJ.

Scientific Working Group on DNA Analysis Methods (SWGDAM). Short Tandem Repeat (STR) Interpretation Guidelines, *Forensic Science Communications* 2 (July 2000). See http://www.fbi.gov/hq/lab/fsc/backissu/july2000/strig.htm

7. Additional Suggested Readings

Bill, M., Gill, P., Curran, J., Clayton, T., Pinchin, R., Healy, M., and Buckleton, J. (2005) PENDULUM-a guideline-based approach to the interpretation of STR mixtures. *Forensic Sci. Int.* 148: 181-189.

Buckleton, J.S., Evett, I.W., Weir, B.S. (1998) Setting bounds for the likelihood ratio when multiple hypotheses are postulated. *Sci. Justice.* 38: 23-26.

Buckleton, J.S., Curran, J.M., Gill, P. (2007) Towards understanding the effect of uncertainty in the number of contributors to DNA stains. *Forensic Sci. Int. Genet.* 1:20-28.

Buckleton, J.S. and Curran, J.M. (2008) A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Sci. Int. Genet.* 2: 343-348.

Budowle, B., Chakraborty, R., Carmody, G., Monson, K.L. (2000) Source attribution of a forensic DNA profile. *Forensic Sci. Commun.* 2(3). See http://www.fbi.gov/hq/lab/fsc/backissu/july2000/source.htm.

Budowle, B., Onorato, A.J., Callaghan, T.F., Della Manna, A., Gross, A.M., Guerrieri, R.A., Luttman, J.C., 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.* 54: 810-821.

Clayton, T.M., Whitaker, J.P., Sparkes, R., Gill, P. (1998) Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci. Int.* 91: 55-70.

Devlin, B. (1993) Forensic inference from genetic markers. *Stat. Methods Med. Res.* 2: 241-262.

Evett, I.W. Buffery, C., Willott, G., Stoney, D. (1991) A guide to interpreting single locus profiles of DNA mixtures in forensic cases. *J. Forensic Sci. Soc.* 31: 41–47.

Evett, I.W., Weir, B.S. (1998) *Interpreting DNA Evidence*. Sinauer: Sunderland, MA.

Gill, P., Sparkes, R., Kimpton, C. (1997) Development of guidelines to designate alleles using an STR multiplex system. *Forensic Sci. Int.* 89: 185-197.

Gill, P. (2002) Role of short tandem repeat DNA in forensic casework in the UK--past, present, and future perspectives. *BioTechniques* 32(2): 366-385.

Gill, P., Brenner, C.H., Buckleton, J.S., Carracedo, A., Krawczak, M., Mayr, W.R., Morling, N., Prinz, M., Schneider, P.M., Weir, B.S. (2006) DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Sci. Int.* 160: 90-101.

Gill, P., Brown, R.M., Fairley, M., Lee, L., Smyth, M., Simpson, N., Irwin, B., Dunlop, J., Greenhalgh, M., Way, K., Westacott, E.J., Ferguson, S.J., Ford, L.V., Clayton, T., Guiness, J. (2008) National recommendations of the technical UK DNA working group on mixture interpretation for the NDNAD and for court going purposes. *FSI Genetics* 2(1): 76–82.

Gill, P., Puch-Solis, R., Curran, J. (2009) The low-template DNA (stochastic) threshold-its determination relative to risk analysis for national DNA databases. *Forensic Sci. Int. Genet.* 3: 104-111.

Gill, P. and Buckleton, J. (2009) A universal strategy to interpret DNA profiles that does not require a definition of *low-copy-number*. *Forensic Sci. Int. Genet.* (in press).

Graham, E.A.M. and Rutty, G.N. (2008) Investigation into "normal" background DNA on adult necks: implications for DNA profiling of manual strangulation victims. *J. Forensic Sci.* 53: 1074-1082.

Ladd, C., Lee, H.C., Yang, N., Bieber, F.R. (2001) Interpretation of complex forensic DNA mixtures. *Croatian Med. J.* 42(3): 244-246.

Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Budowle, B. (2001) Validation of short tandem repeats (STRs) for forensic usage: performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. *J. Forensic Sci.* 46: 647-660.

Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Budowle, B. (2001) Validation of STR typing by capillary electrophoresis. *J. Forensic Sci.* 46: 661-676.

Morling N., Bastisch, I., Gill, P., Schneider, P.M. (2007) Interpretation of DNA mixtures – European consensus on principles. *Forensic Sci. Int. Genet.* 1(3): 291–292.

Perlin, M. W. and Szabady, B. (2001) Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *J. Forensic Sci.* 46(6): 1372-1378.

Perlin, M.W., Kadane, J.B., Cotton, R.W. (2009) Match likelihood ratio for uncertain genotypes. *Law, Probability and Risk* 8(3):289-302.

Schneider, P.M., Gill, P., Carracedo, A. (2006) Editorial on the recommendations of the DNA commission of the ISFG on the interpretation of mixtures. *Forensic Sci. Int.* 160: 89.

Schneider, P.M., Fimmers, R., Keil, W., Molsberger, G., Patzelt, D., Pflug, W., Rothämel, T., Schmitter, H., Schneider, H., Brinkman, B. (2009) The German Stain Commission: recommendations for the interpretation of mixed stains. *Int. J. Legal Med.* 123: 1-5; originally published in German in 2006 *Rechtsmedizin* 16:401-404.

Stringer, P., Scheffer, J.W., Scott, P., Lee, J., Goetz, R., Ientile, V., Eckhoff, C., Turbett, G., Carroll, D., Harbison, S. (2009) Interpretation of DNA mixtures—Australian and New Zealand consensus on principles. *Forensic Sci. Int. Genet.* 3: 144-145.

Tomsey, C.S., Kurtz, M., Flowers, B., Fumea, J., Giles, B., Kucherer, S. (2001) Case work guidelines and interpretation of short tandem repeat complex mixture analysis. *Croatian Med. J.* 42(3): 276-280.

Torres, Y., Flores, I., Prieto, V., Lopez-Soto, M., Farfan, M.J., Carracedo, A., Sanz, P. (2003) DNA mixtures in forensic casework: a 4-year retrospective study. *Forensic Sci. Int.* 134: 180-186.

Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N. (2009) Estimating the probability of allelic drop-out of STR alleles in forensic genetics. *FSI Genetics* 3: 222-226.

Van Nieuwerburgh, F., Goetghebeur, E., Vandewoestyne, M., Deforce, D. (2009) Impact of allelic dropout on evidential value of forensic DNA profiles using RMNE. *Bioinformatics* 25: 225-229.

Wang, T., Xue, N., Birdwell, J.D. (2006) Least-squares deconvolution: a framework for interpreting short tandem repeat mixtures. *J. Forensic Sci.* 51(6): 1284-1297.

Weir, B.S., Triggs, C.M., Starling, L., Stowell, L.I., Walsh, K.A.J., Buckleton, J.S. (1997) Interpreting DNA mixtures. *J. Forensic Sci.* 42(2): 213-222.

Whitaker, J.P., Cotton, E.A., Gill, P. (2001) A comparison of the characteristics of profiles produced with the AmpFISTR SGM Plus multiplex system for both standard and low copy number (LCN) STR DNA analysis. *Forensic Sci. Int.* 123: 215-223.

Wickenheiser, R.A. (2006) General guidelines for categorization and interpretation of mixed STR DNA profiles. *Canadian Society of Forensic Science Journal* 39(4): 179-216.

Glossary for this document

Allelic dropout: failure to detect an allele within a sample or failure to amplify an allele during PCR.

Analytical threshold: the minimum height requirement at and above which detected peaks can be reliably distinguished from background noise; peaks above this threshold are generally not considered noise and are either artifacts or true alleles.

Artifact: a non-allelic product of the amplification process (e.g., stutter, non-templated nucleotide addition, or other non-specific product), an anomaly of the detection process (e.g., pull-up or spike), or a by-product of primer synthesis (e.g., "dye blob").

Coincidental match: a match which occurs by chance.

Composite profile: a DNA profile generated by combining typing results from different loci obtained from multiple injections of the same amplified sample and/or multiple amplifications of the same DNA extract. When separate extracts from different locations on a given evidentiary item are combined prior to amplification, the resultant DNA profile is not considered a composite profile.

Conditional: an interpretation category that incorporates assumption(s) as to the number of contributors.

CPE: combined probability of exclusion; produced by multiplying the probabilities of inclusion from each locus and subtract the product from 1; (i.e., 1-CPI).

CPI: combined probability of inclusion; produced by multiplying the probabilities of inclusion from each locus; (i.e., 1-CPE).

Deconvolution: separation of contributors to a mixed DNA profile based on quantitative peak height information and any underlying assumptions.

Deduced: inference of an unknown contributor's DNA profile after taking into consideration the contribution of a known/assumed contributor's DNA profile based on quantitative peak height information.

Differential Degradation: a DNA typing result in which contributors to a DNA mixture are subject to different levels of degradation (e.g., due to time of deposition), thereby impacting the mixture ratios across the entire profile.

Distinguishable Mixture: a DNA mixture in which relative peak height ratios allow deconvolution of the profiles of major/minor contributor(s).

Evidence sample: also known as Questioned sample.

Exclusion: a conclusion that eliminates an individual as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other).

Guidelines: a set of general principles used to provide directions and parameters for decision making.

Heterozygote: an individual having different alleles at a particular locus; usually manifested as two distinct peaks for a locus in an electropherogram.

Homozygote: an individual having the same (or indistinguishable) alleles at a particular locus; manifested as a single peak for a locus in an electropherogram.

Inclusion: a conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other).

Inconclusive/uninterpretable: an interpretation or conclusion in which the DNA typing results are insufficient, as defined by the laboratory, for comparison purposes.

Indistinguishable mixture: a DNA mixture in which relative peak height ratios are insufficient to attribute alleles to individual contributor(s).

Intimate sample: a biological sample from an evidence item that is obtained directly from an individual's body; it is not unexpected to detect that individual's allele(s) in the DNA typing results.

Known sample: biological material for which the identity of the donor is established and used for comparison purposes (referred to as a "K").

Likelihood ratio (LR): the ratio of two probabilities of the same event under different hypotheses; typically the numerator contains the prosecution's hypothesis and the denominator the defense's hypothesis.

Major contributor(s): an individual(s) who can account for the predominance of the DNA in a mixed profile.

Masked allele: an allele of the minor contributor that may not be readily distinguishable from the alleles of the major contributor or an artifact.

Minor contributor(s): an individual(s) who can account for the lesser portion of the DNA in a mixed profile.

Mixture: a DNA typing result originating from two or more individuals.

Mixture ratio: the relative ratio of the DNA contributions of multiple individuals to a mixed DNA typing result, as determined by the use of quantitative peak height information; may also be expressed as a percentage.

Noise: background signal detected by a data collection instrument.

No results: no allelic peaks detected above the analytical threshold.

Obligate allele: an allele in a mixed DNA typing result that is (a) foreign to an assumed contributor, or (b) based on quantitative peak height information, determined to be shared with the assumed contributor.

Partial profile: a DNA profile for which typing results are not obtained at all tested loci due, for example, to DNA degradation, inhibition of amplification and/or low- quantity template.

Peak height ratio (PHR): the relative ratio of two alleles at a given locus, as determined by dividing the peak height of an allele with a lower relative fluorescence unit (RFU) value by the peak height of an allele with a higher RFU value, and then multiplying this value by 100 to express the PHR as a percentage; used as an indication of which alleles may be heterozygous pairs and also in mixture deconvolution.

Probability of exclusion (PE): the percentage of the population that can be excluded as potential contributors to a DNA mixture.

Probability of inclusion (PI): the percentage of the population that can be included as potential contributors to a DNA mixture; also known as Random Man Not Excluded.

Questioned sample: biological sample recovered from a crime scene or collected from persons or objects associated with a crime (referred to as a "Q").

Random Match Probability (RMP): the probability of randomly selecting an unrelated individual from the population who could be a potential contributor to an evidentiary profile.

Reference sample: also known as Known sample.

Restricted: referring to a statistical approach conditioned on the number of contributors and with consideration of quantitative peak height information and inference of contributor mixture ratios; used to limit the genotypic combinations of possible contributors.

Signal-to-noise ratio: an assessment used to establish an analytical threshold to distinguish allelic peaks (signal) from background/instrumental noise.

Single-source profile: DNA typing results determined to originate from one individual based on peak height ratio assessments and the number of alleles at given loci.

Source attribution: a declaration which identifies an individual as the source of an evidentiary profile to a reasonable degree of scientific certainty based on a single-source or major contributor profile.

Stochastic effects: the observation of intra-locus peak imbalance and/or allele drop-out resulting from random, disproportionate amplification of alleles in low-quantity template samples.

Stochastic threshold: the peak height value above which it is reasonable to assume that, at a given locus, allelic dropout of a sister allele has not occurred.

Stutter: a minor peak typically observed one repeat unit smaller than a primary STR allele resulting from strand slippage during amplification.

Unrestricted: referring to a statistical approach performed without consideration of quantitative peak height information and inference of contributor mixture ratios; for CPE/CPI this may or may not be conditioned on the number of contributors.

QUALITY ASSURANCE STANDARDS FOR FORENSIC DNA TESTING LABORATORIES

This document consists of definitions and standards. The standards are quality assurance measures that place specific requirements on the laboratory. Equivalent measures not outlined in this document may also meet the standard if determined sufficient through an accreditation process.

EFFECTIVE DATE:

These standards shall take effect September 1, 2011.

REFERENCES: Federal Bureau of Investigation, "Quality Assurance Standards for Forensic DNA Testing Laboratories" and "Quality Assurance Standards for Convicted Offender DNA Databasing Laboratories," Forensic Science Communications, July 2000, Volume 2, Number 3.

1. SCOPE

The standards describe the quality assurance requirements that laboratories performing forensic DNA testing or utilizing the Combined DNA Index System (CODIS) shall follow to ensure the quality and integrity of the data generated by the laboratory. These standards also apply to vendor laboratories that perform forensic DNA testing in accordance with Standard 17. These standards do not preclude the participation of a laboratory, by itself or in collaboration with others, in research and development, on procedures that have not yet been validated.

2. DEFINITIONS

As used in these standards, the following terms shall have the meanings specified:

Accredited laboratory is a DNA laboratory that has received formal recognition that it meets or exceeds a list of standards, including the FBI Director's Quality Assurance Standards, to perform specific tests, by a nonprofit professional association of persons actively involved in forensic science that is nationally recognized within the forensic community in accordance with the provisions of the Federal DNA Identification Act (42 U.S.C. § 14132) or subsequent laws.

Accuracy is the degree of conformity of a measured quantity to its actual (true) value.

Administrative review is an evaluation of the report and supporting documentation for consistency with laboratory policies and for editorial correctness.

Analyst (or equivalent role, position, or title as designated by the Laboratory Director) is an employee or contract employee, that has successfully completed the laboratory's training requirements for casework sample analysis, passed a competency test, and has entered into a proficiency testing program according to these Standards. This individual conducts and/or directs the analysis of forensic samples, interprets data and reaches conclusions.

Analytical documentation is the documentation of procedures, standards, controls and instruments used, observations made, results of tests performed, charts, graphs, photos and other documentation generated which are used to support the analyst's conclusions.

Analytical procedure is an orderly step-by-step process designed to ensure operational uniformity and to minimize analytical drift.

Annual is once per calendar year.

Audit is an inspection used to evaluate, confirm, or verify activity related to quality.

Biochemistry is the study of the nature of biologically important molecules in living systems, DNA replication and protein synthesis, and the quantitative and qualitative aspects of cellular metabolism.

Calibration is the set of operations which establish, under specified conditions, the relationship between values indicated by a measuring instrument or measuring system, or values represented by a material, and the corresponding known values of a measurement.

Casework CODIS Administrator (or equivalent role, position, or title as designated by the Laboratory Director) is an employee of the laboratory responsible for administration and security of the laboratory's CODIS at a laboratory performing DNA analysis on forensic and casework reference samples.

Casework reference sample is biological material obtained from a known individual and collected for purposes of comparison to forensic samples.

CODIS is the Combined DNA Index System administered by the FBI. CODIS links DNA evidence obtained from crime scenes, thereby identifying serial criminals. CODIS also compares crime scene evidence to DNA profiles from offenders, thereby providing investigators with the identity of the putative perpetrator. In addition, CODIS contains profiles from missing persons, unidentified human remains and relatives of missing persons. There are three levels of CODIS: the Local DNA Index System (LDIS), used by individual laboratories; the State DNA Index System (SDIS), used at the state level to serve as a state's DNA database containing DNA profiles from LDIS laboratories; and the National DNA Index System (NDIS), managed by the FBI as the nation's DNA database containing all DNA profiles uploaded by participating states.

Competency test(s) is a written, oral and/or practical test or series of tests, designed to establish that an individual has demonstrated achievement of technical skills and met minimum standards of knowledge necessary to perform forensic DNA analysis.

Competency is the demonstration of technical skills and knowledge necessary to perform forensic DNA analysis successfully.

Contamination is the unintentional introduction of exogenous DNA into a DNA sample or PCR reaction.

Continuing education is an educational activity (such as a class, lecture series, conference, seminar, or short course) that is offered by a recognized organization or individual that brings participants up to date in their relevant area of knowledge.

Contract employee is an individual that provides DNA typing and/or analytical support services to the NDIS participating laboratory. The person performing these services must meet the relevant qualifications for the equivalent position in the NDIS participating laboratory. A contract employee cannot serve as a casework CODIS Administrator or technical leader and cannot be counted as a full-time qualified DNA analyst for purposes of satisfying the definition of a laboratory. Employment of a contract employee by multiple NDIS participating and/or vendor laboratories shall be disclosed and shall only be permitted subject to approval by the technical leader of the NDIS participating laboratory for which the contract employee is performing DNA typing and/or analytical services.

Coursework is an academic class officially recognized and taught through a college or university program in which the participating student successfully completed and received one or more credit hours for the class.

Critical equipment or instruments are those requiring calibration or a performance check prior to use and periodically thereafter.

Critical reagents are determined by empirical studies or routine practice to require testing on established samples before use on evidentiary or casework reference samples.

Developmental validation is the acquisition of test data and determination of conditions and limitations of a new or novel DNA methodology for use on forensic and/or casework reference samples.

Differential amplification is the selection of one target region or locus over another during the polymerase chain reaction. Differential amplification can also arise between two alleles within a single locus if one of the alleles has a mutation within a PCR primer binding site causing this allele to be copied less efficiently because of the primer-template mismatch.

DNA record is a database record that includes the DNA profile as well as data required to manage and operate NDIS, i.e., the Originating Agency Identifier which serves to identify the submitting agency; the Specimen Identification Number; and DNA personnel associated with the DNA profile analyses.

DNA type **(also known as a DNA profile)** is the genetic constitution of an individual at defined locations (also known as loci) in the DNA. A DNA type derived from nuclear DNA typically consists of one or two alleles at several loci (e.g., short tandem repeat loci). The DNA type derived from mitochondrial DNA is described in relation to the revised Cambridge Reference Sequence (Nature Genetics 1999, 23, 147).

Employee is a person: (1) in the service of the applicable federal, state or local government, subject to the terms, conditions and rules of federal/state/local employment and eligible for the federal/state/local benefits of service; or (2) formerly in the service of a federal, state, or local government who returns to service in the agency on a part time or temporary basis. For purposes of a vendor laboratory, an employee is a person in the service of a vendor laboratory and subject to the applicable terms, conditions and rules of employment of the vendor laboratory.

FBI is the Federal Bureau of Investigation, the Federal agency authorized by the DNA Identification Act of 1994 to issue quality assurance standards governing forensic DNA testing laboratories and to establish and administer the National DNA Index System (NDIS).

Forensic DNA analysis is the process of identification and evaluation of biological evidence in criminal matters using DNA technologies.

Forensic sample is a biological sample originating from and associated with a crime scene. For example, a sample associated with a crime scene may include a sample that has been carried away from the crime scene.

Genetics is the study of inherited traits, genotype/phenotype relationships, and population/species differences in allele and genotype frequencies.

Guidelines are a set of general principles used to provide direction and parameters for decision making.

Integral component is that portion of an academic course that is so significant and necessary to the understanding of the subject matter as a whole, that the course would be considered incomplete without it.

Internal validation is the accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory.

Known samples are biological material whose identity or type is established.

Laboratory is a facility: (1) employing at least two full time employees who are qualified DNA analysts; and (2) having and maintaining the capability to perform the DNA analysis of forensic and/or casework reference samples at that facility.

Laboratory support personnel (or equivalent role, position, or title as designated by the laboratory director) are employees or contract employees who perform laboratory duties exclusive of analytical techniques on forensic or database samples.

Methodology is used to describe the analytical processes and procedures used to support a DNA typing technology: for example, extraction methods (manual vs. automated), quantitation methods (slot blot, fluorometry, real time), typing test kit and platform (capillary electrophoresis, real-time gel and end-point gel systems).

Molecular biology is the study of the theories, methods, and techniques used in the study and analysis of gene structure, organization, and function.

Multi-laboratory system is used to describe an organization that has more than one laboratory performing forensic DNA analysis.

Multiplex system is a test providing for simultaneous amplification of multiple loci that is either prepared commercially or by a laboratory.

Negative amplification control is used to detect DNA contamination of the amplification reagents. This control consists of only amplification reagents without the addition of template DNA.

NIST is the National Institute of Standards and Technology.

On-site visit is a scheduled or unscheduled visit to the vendor laboratory work site by one or more representatives of an NDIS participating laboratory who is(are) a qualified or previously qualified DNA analyst(s) in the technology, platform and typing amplification test kit used to generate the DNA data, or designated FBI employee(s), to assess and document the vendor laboratory's ability to perform analysis on outsourced casework.

Outsourcing is the utilization of a vendor laboratory to provide DNA services in which the NDIS participating laboratory takes or retains ownership of the DNA data for entry into CODIS, when applicable. Outsourcing does not require the existence of a contractual agreement or the exchange of funds.

Ownership occurs when any of the following criteria are applicable:

(1) the originating laboratory will use any samples, extracts or any materials from the vendor laboratory for the purposes of forensic testing (i.e. a vendor laboratory prepares an extract that will be analyzed by the originating laboratory);
(2) the originating laboratory will interpret the data generated by the vendor laboratory;
(3) the originating laboratory will issue a report on the results of the analysis; or

(4) the originating laboratory will enter or search a DNA profile in CODIS from data generated by the vendor laboratory.

Performance check is a quality assurance measure to assess the functionality of laboratory instruments and equipment that affect the accuracy and/or validity of forensic sample analysis.

Platform is the type of analytical system utilized to generate DNA profiles such as capillary electrophoresis, real-time gel, and end-point gel instruments or systems.

Polymerase Chain Reaction (PCR) is an enzymatic process by which a specific region of DNA is replicated during repetitive cycles which consist of the following:

(1) denaturation of the template;
(2) annealing of primers to complementary sequences at an empirically determined temperature; and
(3) extension of the bound primers by a DNA polymerase.

Positive amplification control is an analytical control sample that is used to determine if the PCR performed properly. This control consists of the amplification reagents and a known DNA sample.

Precision characterizes the degree of mutual agreement among a series of individual measurements, values, and/or results.

Preferential amplification is the unequal sampling of the two alleles present in a heterozygous locus primarily due to stochastic (random) fluctuation arising when only a few DNA molecules are used to initiate the polymerase chain reaction.

Procedure (protocol, SOP or other equivalent) is an established practice to be followed in performing a specified task or under specific circumstances.

Proficiency testing is a quality assurance measure used to monitor performance and identify areas in which improvement may be needed. Proficiency tests may be classified as:

(1) An internal proficiency test, which is produced by the agency undergoing the test.
(2) An external proficiency test, which may be open or blind, is a test obtained from an approved proficiency test provider.

Qualified auditor is a current or previously qualified DNA analyst who has successfully completed the FBI DNA Auditor's training course.

Quality system is the organizational structure, responsibilities, procedures, processes and resources for implementing quality management.

Quantitative PCR is a method of determining the concentration of DNA in a sample by use of the polymerase chain reaction.

Reagent blank control is an analytical control sample that contains no template DNA and is used to monitor contamination from extraction to final fragment or sequence analysis. This control is treated the same as, and parallel to, the forensic and or casework reference samples being analyzed.

Reference material (certified or standard) is a material for which values are certified by a technically valid procedure and accompanied by, or traceable to, a certificate or other documentation which is issued by a certifying body.

Reproducibility is the ability to obtain the same result when the test or experiment is repeated.

Review is an evaluation of documentation to check for consistency, accuracy, and completeness.

Second agency is an entity or organization external to and independent of the laboratory.

Semi-annual is used to describe an event that takes place two times during one calendar year, with the first event taking place in the first six months of that year and the second event taking place in the second six months of that year and where the interval between the two events is at least four months and not more than eight months.

Service is the performance of those adjustments or procedures specified which are to be performed by the user, manufacturer or other service personnel in order to ensure the intended performance of instruments and equipment.

Technical Leader (or equivalent role, position, or title as designated by the laboratory director) is an employee who is accountable for the technical operations of the laboratory and who is authorized to stop or suspend laboratory operations.

Technical review is an evaluation of reports, notes, data, and other documents to ensure there is an appropriate and sufficient basis for the scientific conclusions.

Technical reviewer is an employee or contract employee who is a current or previously qualified analyst in the methodology being reviewed that performs a technical review of, and is not an author of, the applicable report or its contents.

Technician (or equivalent role, position, or title as designated by the laboratory director) is an employee or contract employee who performs analytical techniques on forensic samples under the supervision of a qualified analyst. Technicians do not interpret data, reach conclusions on typing results, or prepare final reports.

Technology is used to describe the type of forensic DNA analysis performed in the laboratory, such as RFLP, STR, YSTR, or mitochondrial DNA.

Test kit is a pre-assembled set of reagents that allows the user to conduct a specific DNA extraction, quantitation or amplification.

Traceability is the property of a result of a measurement whereby it can be related to appropriate standards, generally international or national standards, through an unbroken chain of comparisons.

Underlying scientific principle is a rule concerning a natural phenomenon or function that is a part of the basis used to proceed to more detailed scientific functions.

Validation is a process by which a procedure is evaluated to determine its efficacy and reliability for forensic casework analysis and includes the following:

> (1) Developmental validation is the acquisition of test data and determination of conditions and limitations of a new or novel DNA methodology for use on forensic samples.
> (2) Internal validation is an accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory.

Vendor laboratory is a governmental or private laboratory that provides DNA analysis services to another laboratory or agency and does not take ownership of the DNA data for purposes of entry into CODIS.

Work product is the material that is generated as a function of analysis, which may include extracts, amplified product and amplification tubes or plates as defined by the laboratory.

3. QUALITY ASSURANCE PROGRAM

STANDARD 3.1 The laboratory shall establish, follow and maintain a documented quality system that is appropriate to the testing activities and is equivalent to or more stringent than what is required by these Standards.

3.1.1 The quality system shall be documented in a manual that includes or references the following elements:

3.1.1.1 Goals and objectives

3.1.1.2 Organization and management

3.1.1.3 Personnel

3.1.1.4 Facilities

3.1.1.5 Evidence control

3.1.1.6 Validation

3.1.1.7 Analytical procedures

3.1.1.8 Equipment calibration and maintenance

3.1.1.9 Reports

3.1.1.10 Review

3.1.1.11 Proficiency testing

3.1.1.12 Corrective action

3.1.1.13 Audits

3.1.1.14 Safety

3.1.1.15 Outsourcing

STANDARD 3.2 The laboratory shall maintain and follow a procedure regarding document retention that specifically addresses proficiency tests, corrective action, audits, training records, continuing education, case files and court testimony monitoring.

STANDARD 3.3 The quality system as applicable to DNA shall be reviewed annually independent of the audit required by Standard 15. The review of the quality system shall be completed under the direction of the technical leader and the approval by the technical leader shall be documented.

4. ORGANIZATION AND MANAGEMENT

STANDARD 4.1 The laboratory shall:

4.1.1 Have a managerial staff with the authority and resources needed to discharge their duties and meet the requirements of the Standards in this document.

4.1.2 Have a technical leader who is accountable for the technical operations. Multi-laboratory systems shall have at least one technical leader.

4.1.3 Have a casework CODIS administrator who is accountable for CODIS on-site at each individual laboratory facility utilizing CODIS.

4.1.4 Have at least two full time employees who are qualified DNA analysts.

4.1.5 Specify and document the responsibility, authority, and interrelation of all personnel who manage, perform or verify work affecting the validity of the DNA analysis.

4.1.6 Have a documented contingency plan that is approved by laboratory management if the technical leader position is vacated.

5. PERSONNEL

STANDARD 5.1 Laboratory personnel shall have the education, training and experience commensurate with the examination and testimony provided. The laboratory shall:

5.1.1 Have a written job description for personnel, that may be augmented by additional documentation, that defines responsibilities, duties and skills.

5.1.2 Have a documented training program for qualifying all analyst/technician(s).

5.1.2.1 The laboratory's training program shall include a training manual covering all DNA analytical procedures that the analyst/technician will perform. Practical exercises shall include the examination of a range of samples routinely encountered in casework.

5.1.2.2 The training program shall teach and assess the technical skills and knowledge required to perform DNA analysis.

5.1.2.2.1 The training program shall require an individual's demonstration of competency. The laboratory shall maintain documentation of the successful completion of such competency test(s).

5.1.2.2.2 When hiring experienced analyst/technician(s), the technical leader shall be responsible for assessing their previous training and ensuring it is adequate and documented. Modification to the training program may be appropriate and shall be documented by the technical leader.

5.1.2.2.3 All analyst/technician(s), regardless of previous experience, shall successfully complete a competency test(s) covering the routine DNA methodologies to be used prior to participating in independent casework analysis.

5.1.3 Have a documented program to ensure technical qualifications are maintained through participation in continuing education.

5.1.3.1 Continuing education: The technical leader, casework CODIS administrator, and analyst(s) shall stay abreast of developments within the

field of DNA typing by attending seminars, courses, professional meetings or documented training sessions/classes in relevant subject areas at least once each calendar year. A minimum of eight cumulative hours of continuing education are required annually and shall be documented.

5.1.3.1.1 If continuing education is conducted internally, the title of the program, a record of the presentation, date of the training, attendance list, and the curriculum vitae of the presentor(s) shall be documented and retained by the laboratory.

5.1.3.1.2 If the continuing education is conducted externally, the laboratory shall maintain documentation of attendance through a mechanism such as certificates, program agenda/syllabus, or travel documentation. Attendance at a regional, national or international conference shall be deemed to provide a minimum of 8 hours of continuing education.

5.1.3.1.3 Programs based on multimedia or internet delivery shall be subject to the approval of the technical leader. Participation in such programs shall be formally recorded and its completion shall be submitted to the technical leader for review and approval. The documentation shall include the time required to complete the program.

5.1.3.2 The laboratory shall have a program approved by the technical leader for the annual review of scientific literature that documents the analysts' ongoing reading of scientific literature. The laboratory shall maintain or have physical or electronic access to a collection of current books, reviewed journals, or other literature applicable to DNA analysis.

5.1.4 Maintain records on the relevant qualifications, training, skills and experience of the technical personnel.

STANDARD 5.2 The technical leader shall meet the following qualifications:

5.2.1 Minimum educational requirements: The technical leader of a laboratory shall have, at a minimum, a Master's degree in a biology-, chemistry- or forensic science- related area and successfully completed 12 semester or equivalent credit hours from a combination of undergraduate and graduate course work covering the following subject areas: biochemistry, genetics, molecular biology, and statistics or population genetics.

5.2.1.1 The 12 semester or equivalent credit hours shall include at least one graduate level course registering three (3) or more semester or equivalent credit hours.

5.2.1.2 The specific subject areas listed in 5.2.1 shall constitute an integral component of any course work used to demonstrate compliance with this Standard.

5.2.1.3 Individuals who have completed course work with titles other than those listed in 5.2.1 shall demonstrate compliance with this Standard through a combination of pertinent materials such as a transcript, syllabus, letter from the instructor or other document that supports the course content.

5.2.1.4 If the degree requirements of section 5.2.1 were waived by the American Society of Crime Laboratory Directors (ASCLD) in accordance with criteria approved by the Director of the Federal Bureau of Investigation (FBI), such a documented waiver shall be permanent and portable.

5.2.2 Minimum experience requirements: A technical leader of a laboratory shall have three years of forensic DNA laboratory experience obtained at a laboratory where forensic DNA testing was conducted for the identification and evaluation of biological evidence in criminal matters. As of the effective date of this revision, any newly appointed technical leader shall have a minimum of three years of human DNA (current or previous) experience as a qualified analyst on forensic samples. The technical leader shall have previously completed or successfully complete the FBI sponsored auditor training within one year of appointment.

5.2.3 The technical leader shall be responsible for the following:

5.2.3.1 General duties and authority:

5.2.3.1.1 Oversee the technical operations of the laboratory.

5.2.3.1.2 Authority to initiate, suspend and resume DNA analytical operations for the laboratory or an individual.

5.2.3.2 The minimum specific responsibilities to be performed by the technical leader include the following:

5.2.3.2.1 To evaluate and document approval of all validations and methods used by the laboratory and to propose new or modified analytical procedures to be used by analysts.

5.2.3.2.2 To review the academic transcripts and training records for newly qualified analysts and approve their qualifications prior to independent casework analysis and document such review.

5.2.3.2.3 To approve the technical specifications for outsourcing agreements.

5.2.3.2.4 To review internal and external DNA Audit documents and, if applicable, approve corrective action(s), and document such review.

5.2.3.2.5 To review, on an annual basis, the procedures of the laboratory and document such review.

5.2.3.2.6 To review and approve the training, quality assurance and proficiency testing programs in the laboratory.

5.2.3.2.7 To review requests by contract employees for employment by multiple NDIS participating and/or vendor laboratories and, if no potential conflict of interests exist, may approve such requests.

5.2.4. Accessibility: The technical leader shall be accessible to the laboratory to provide onsite, telephone or electronic consultation as needed. A multi-laboratory system may have one technical leader over a system of separate laboratory facilities. For multi-laboratory systems the technical leader shall conduct a site visit to each laboratory at least semi-annually.

5.2.4.1 The technical leader shall be a full time employee of the laboratory or multi-laboratory system.

5.2.4.1.1 In the event that the technical leader position of a laboratory is vacated and there is no individual in the laboratory or multi-laboratory system who meets the requirements of this standard and serve as a technical leader, the laboratory shall immediately contact the FBI and submit their contingency plan within14 days to the FBI for its approval. Work in progress by the laboratory may be completed during this 14 day period but new casework shall not be started until the plan is approved by the FBI.

5.2.5 Newly appointed technical leaders shall be responsible for the documented review of the following:

5.2.5.1 Validation studies and methodologies currently used by the laboratory; and

5.2.5.2 Educational qualifications and training records of currently qualified analysts.

STANDARD 5.3 The casework CODIS administrator shall be an employee of the laboratory and meet the following qualifications:

5.3.1 Minimum educational requirements: The casework CODIS Administrator shall meet the education requirements for an analyst as defined in Standard 5.4. A casework CODIS Administrator appointed prior to the effective date of this revision shall be deemed to have satisfied the minimum educational requirements; satisfaction of these minimum educational requirements shall be applicable to the specific laboratory the casework CODIS Administrator is employed by prior to the effective date of this revision and shall not be portable.

5.3.2 Minimum experience requirements: A casework CODIS administrator shall be or have been a current or previously qualified DNA analyst as defined in Standard 5.4 with documented mixture interpretation training. A casework CODIS administrator appointed prior to the effective date of this revision who is not or has never been a qualified analyst (with documented training in mixture interpretation) shall be deemed to have satisfied the minimum experience requirements upon completion of FBI sponsored CODIS training; satisfaction of these minimum requirements shall be applicable to the specific laboratory the casework CODIS administrator is employed by prior to the effective date of this revision and shall not be portable.

5.3.3 Minimum CODIS training requirements. The casework CODIS Administrator shall participate in the FBI sponsored training in CODIS software within six months of assuming CODIS casework administrator duties if the Administrator had not previously attended such training. The casework CODIS Administrator shall successfully complete the FBI sponsored auditor training within one year of assuming their Administrator duties if the Administrator had not previously attended such training.

5.3.4 The casework CODIS Administrator shall be responsible for the following:

5.3.4.1 Administration of the laboratory's local CODIS network.

5.3.4.2. Scheduling and documentation of the CODIS computer training of casework analysts.

5.3.4.3 Assurance that the security of data stored in CODIS is in accordance with state and/or federal law and NDIS operational procedures.

5.3.4.4 Assurance that the quality of data stored in CODIS is in accordance with state and/or federal law and NDIS operational procedures.

5.3.4.5 Assurance that matches are dispositioned in accordance with NDIS operational procedures.

5.3.5 The casework CODIS Administrator shall be authorized to terminate an analyst's or laboratory's participation in CODIS until the reliability and security of the computer data can be assured in the event an issue with the data is identified.

5.3.6 A laboratory shall not upload DNA profiles to NDIS in the event that the casework CODIS Administrator position is unoccupied.

STANDARD 5.4 The analyst shall be an employee or contract employee of the laboratory and meet the following qualifications:

5.4.1 Minimum educational requirements: The analyst shall have a bachelor's (or its equivalent) or an advanced degree in a biology-, chemistry-, or forensic science-, related area and shall have successfully completed course work (graduate or undergraduate level) covering the following subject areas: biochemistry, genetics, molecular biology; and course work and/or training in statistics and/or population genetics as it applies to forensic DNA analysis.

5.4.1.1. The specific subject areas listed in Standard 5.4.1. shall be an integral component of any coursework for compliance with this Standard.

5.4.1.2. Analysts appointed or hired after the effective date of these revisions shall have a minimum of nine cumulative semester hours or equivalent that cover the required subject areas.

5.4.1.3. Analysts who have completed course work with titles other than those listed in 5.4.1 above shall demonstrate compliance with this Standard through a combination of pertinent materials, such as a transcript, syllabus, letter from the instructor, or other document that supports the course content. The technical leader shall document approval of compliance with this Standard.

5.4.2 Minimum experience requirements: The analyst shall have six (6) months of forensic human DNA laboratory experience. If prior forensic human DNA laboratory experience is accepted by a laboratory, the prior experience shall be documented and augmented by additional training, as needed, in the analytical methodologies, platforms and interpretations of human DNA results used by the laboratory.

5.4.2.1 The analyst shall complete the analysis of a range of samples routinely encountered in forensic casework prior to independent work using DNA technology.

5.4.2.2 The analyst shall successfully complete a competency test before beginning independent DNA analysis.

STANDARD 5.5 The technical reviewer shall be an employee or contract employee of the laboratory and shall meet the following qualifications:

5.5.1 A current or previously qualified analyst in the methodologies being reviewed.

5.5.2 Successful completion of a competency test administered by the NDIS participating laboratory prior to participating in the technical review of DNA data.

5.5.3 Participation in an external proficiency testing program at an NDIS participating laboratory on the same technology, platform and typing amplification test kit used to generate the DNA data being reviewed.

STANDARD 5.6 The technician shall meet the following qualifications:

5.6.1 Documented training specific to their job function(s).

5.6.2 Successful completion of a competency test before participating in DNA analysis on evidence.

STANDARD 5.7 Laboratory technical support personnel shall have documented training specific to their job function(s).

6. FACILITIES

STANDARD 6.1 The laboratory shall have a facility that is designed to ensure the integrity of the analyses and the evidence.

6.1.1 Access to the laboratory shall be controlled and limited in a manner to prevent access by unauthorized personnel. All exterior entrance/exit points require security control. The distribution of all keys, combinations, etc., shall be documented and limited to the personnel designated by laboratory management.

6.1.2 Except as provided in 6.1.4., techniques performed prior to PCR amplification such as evidence examinations, DNA extractions, and PCR setup shall be conducted at separate times or in separate spaces from each other. Standard 6.1.4 is applicable if robotic workstations are used by the laboratory.

6.1.3 Except as provided in 6.1.4., amplified DNA product, including real time PCR, shall be generated, processed and maintained in a room(s) separate from the evidence examination, DNA extractions and PCR setup areas. The doors between rooms containing amplified DNA and other areas shall remain closed.

6.1.4 A robotic workstation may be used to carry out DNA extraction, quantitation, PCR setup, and/or amplification in a single room, provided that the analytical process has been validated in accordance with Standard 8. If the robot

performs analysis through amplification, the robot shall be housed in a separate room from that used for initial evidence examinations.

6.1.5 The laboratory shall have and follow written procedures for cleaning and decontaminating facilities and equipment.

7. EVIDENCE CONTROL

STANDARD 7.1 The laboratory shall have and follow a documented evidence control system to ensure the integrity of physical evidence.

7.1.1 Evidence shall be marked with a unique identifier on the evidence package. The laboratory shall clearly define what constitutes evidence and what constitutes work product. The laboratory shall have and follow a method to distinguish each sample throughout processing (such as plate or rack mapping) that may not require the assignment of unique identifiers or individual evidence seals for each specimen.

7.1.2 Chain of custody for all evidence shall be documented and maintained in hard or electronic format. The chain of custody shall include the signature, initials or electronic equivalent of each individual receiving or transferring the evidence, the corresponding date for each transfer, and the evidentiary item(s) transferred.

7.1.3 The laboratory shall have and follow documented procedures designed to minimize loss, contamination, and/or deleterious change of evidence and work product in progress.

7.1.4 The laboratory shall have secure, controlled access areas for evidence storage and work product in progress.

STANDARD 7.2 Where possible, the laboratory shall retain or return a portion of the evidence sample or extract.

STANDARD 7.3 The laboratory shall have and follow a documented policy for the disposition of evidence that includes a policy on sample consumption.

8. VALIDATION

STANDARD 8.1 The laboratory shall use validated methodologies for DNA analyses. There are two types of validations: developmental and internal.

STANDARD 8.2 Developmental validation shall precede the use of a novel methodology for forensic DNA analysis.

8.2.1 Developmental validation studies shall include, where applicable, characterization of the genetic marker, species specificity, sensitivity studies, stability studies, reproducibility, case-type samples, population studies, mixture studies, precision and accuracy studies, and PCR-based studies. PCR-based studies include reaction conditions, assessment of differential and preferential amplification, effects of multiplexing, assessment of appropriate controls, and product detection studies. All validation studies shall be documented.

8.2.2 Peer-reviewed publication of the underlying scientific principle(s) of a technology shall be required.

STANDARD 8.3 Except as provided in Standard 8.3.1.1, internal validation of all manual and robotic methods shall be conducted by each laboratory and reviewed and approved by the laboratory's technical leader prior to using a procedure for forensic applications.

8.3.1 Internal validation studies conducted after the date of this revision shall include as applicable: known and non-probative evidence samples or mock evidence samples, reproducibility and precision, sensitivity and stochastic studies, mixture studies, and contamination assessment. Internal validation studies shall be documented and summarized. The technical leader shall approve the internal validation studies.

8.3.1.1 Internal validation data may be shared by all locations in a multi-laboratory system. Each laboratory in a multi-laboratory system shall complete, document and maintain applicable precision, sensitivity, and contamination assessment studies. The summary of the validation data shall be available at each site.

8.3.2 Internal validation shall define quality assurance parameters and interpretation guidelines, including as applicable, guidelines for mixture interpretation.

8.3.3 A complete change of detection platform or test kit (or laboratory assembled equivalent) shall require internal validation studies.

STANDARD 8.4 Before the introduction of a methodology into the laboratory, the analyst or examination team shall successfully complete a competency test to the extent of his/her/their participation in casework analyses.

STANDARD 8.5 The performance of a modified procedure shall be evaluated by comparison with the original procedure using similar DNA samples.

STANDARD 8.6 Each additional critical instrument shall require a performance check. Modifications to an instrument, such as a detection platform, that do not affect the analytical portion of the instrument shall require a performance check.

STANDARD 8.7 Modifications to software, such as an upgrade, shall require a performance check prior to implementation. New software or significant software changes that may impact interpretation or the analytical process shall require a validation prior to implementation.

9. ANALYTICAL PROCEDURES

STANDARD 9.1 The laboratory shall have and follow written analytical procedures approved by the technical leader. The standard operating procedures are to be reviewed annually by the technical leader independent of the audit required by Standard 15 and this review shall be documented.

9.1.1 The laboratory shall have and follow a standard operating procedure for each analytical method used by the laboratory. The procedures shall specify reagents, sample preparation, extraction methods (to include differential extraction of nuclear DNA samples with adequate amount of sperm), equipment, and controls which are standard for DNA analysis and data interpretation.

STANDARD 9.2 The laboratory shall use reagents that are suitable for the methods employed.

9.2.1 The laboratory shall have written procedures for documenting commercial reagents and for the formulation of in-house reagents.

9.2.2 Commercial reagents shall be labeled with the identity of the reagent and the expiration date as provided by the manufacturer or as determined by the laboratory.

9.2.3 In-house reagents shall be labeled with the identity of the reagent, the date of preparation and/or expiration, and the identity of the individual preparing the reagent.

STANDARD 9.3 The laboratory shall identify critical reagents and evaluate them prior to use in casework. These critical reagents shall include but are not limited to the following:

9.3.1 Test kits or systems for performing quantitative PCR and genetic typing

9.3.2 Thermostable DNA polymerase, primer sets and allelic ladders used for genetic analysis that are not tested as test kit components under Standard 9.3.1.

STANDARD 9.4 The laboratory shall quantify the amount of human DNA in forensic samples prior to nuclear DNA amplification. Quantitation of human DNA is not required for casework reference samples if the laboratory has a validated system that has been demonstrated to reproducibly and reliably yield successful DNA amplification and typing without prior quantitation.

STANDARD 9.5 The laboratory shall monitor the analytical procedures using the following controls and standards.

9.5.1 Where quantitation is used, quantitation standards shall be used.

9.5.2 Positive and negative amplification controls associated with samples being typed shall be amplified concurrently in the same instrument with the samples at all loci and with the same primers as the forensic samples. All samples typed shall also have the corresponding amplification controls typed.

9.5.3 Reagent blank controls associated with each extraction set being analyzed shall be:

9.5.3.1 Extracted concurrently;

9.5.3.2 Amplified utilizing the same primers, instrument model and concentration conditions as required by the sample(s) containing the least amount of DNA; and

9.5.3.3 Typed utilizing the same instrument model, injection conditions and most sensitive volume conditions of the extraction set.

9.5.4 Allelic ladders and internal size makers for variable number tandem repeat sequence PCR based systems.

9.5.5 The laboratory shall check its DNA procedures annually or whenever substantial changes are made to a procedure against an appropriate and available NIST standard reference material or standard traceable to a NIST standard.

STANDARD 9.6 The laboratory shall have and follow written guidelines for the interpretation of data.

9.6.1 The laboratory shall verify that all control results meet the laboratory's interpretation guidelines for all reported results.

9.6.2 For a given population(s), the statistical interpretation of autosomal loci shall be made following the recommendations 4.1, 4.2 or 4.3 as deemed applicable of the National Research Council report entitled "The Evaluation of Forensic DNA Evidence" (1996) and/or court directed method. These calculations shall be derived from a documented population database appropriate for the calculation.

9.6.3 A laboratory performing genetic analyses not addressed by Standard 9.6.2, such as Y-chromosome or mtDNA typing shall have and follow documented statistical interpretation guidelines specific for such testing.

9.6.4 Laboratories analyzing forensic samples shall have and follow a documented procedure for mixture interpretation that addresses major and minor contributors, inclusions and exclusions, and policies for the reporting of results and statistics.

STANDARD 9.7 The laboratory shall have and follow a documented policy for the detection and control of contamination.

10. EQUIPMENT CALIBRATION AND MAINTENANCE

STANDARD 10.1 The laboratory shall use equipment suitable for the methods employed.

STANDARD 10.2 The laboratory shall have and follow a documented program for conducting performance checks and calibration of instruments and equipment.

10.2.1 At a minimum, the following critical instruments or equipment shall require annual performance checks:

10.2.1.1 Thermometer traceable to national or international standard(s) that is used for conducting performance checks.

10.2.1.2 Balance/scale

10.2.1.3 Thermal Cycler temperature verification system

10.2.1.4 Thermal Cycler, including quantitative-PCR

10.2.1.5 Electrophoresis detection systems

10.2.1.6 Robotic systems

10.2.1.7 Genetic Analyzers

10.2.1.8 Mechanical pipettes.

STANDARD 10.3 The laboratory shall have a schedule and follow a documented program to ensure that instruments and equipment are properly maintained. The laboratory shall retain documentation of maintenance, service or calibration.

STANDARD 10.4 New critical instruments and equipment, or critical instruments and equipment that have undergone repair, service or calibration, shall undergo a performance check before use in casework analysis.

10.4.1 At a minimum, the following critical equipment shall undergo a performance check following repair, service or calibration:

10.4.1.1 Electrophoresis detection systems

10.4.1.2 Robotic systems

10.4.1.3 Genetic Analyzers

10.4.1.4 Thermal cycler, including quantitative-PCR

11. REPORTS

STANDARD 11.1 The laboratory shall have and follow written procedures for taking and maintaining casework notes to support the conclusions drawn in laboratory reports. The laboratory shall maintain all analytical documentation generated by analysts related to case analyses. The laboratory shall retain, in hard or electronic format, sufficient documentation for each technical analysis to support the report conclusions such that another qualified individual could evaluate and interpret the data.

STANDARD 11.2 Casework reports shall include the following elements:

11.2.1 Case identifier;

11.2.2 Description of evidence examined;

11.2.3 A description of the technology;

11.2.4 Locus or amplification system;

11.2.5 Results and/or conclusions;

11.2.6 A quantitative or qualitative interpretative statement;

11.2.7 Date issued;

11.2.8 Disposition of evidence; and

11.2.9 A signature and title, or equivalent identification, of the person accepting responsibility for the content of the report.

STANDARD 11.3 Except as otherwise provided by state or federal law, reports, case files, DNA records and databases shall be confidential.

11.3.1 The laboratory shall have and follow written procedures to ensure the privacy of the reports, case files, DNA records and databases.

11.3.2 The laboratory shall have and follow written procedures for the release of reports, case files, DNA records and databases in accordance with applicable state or federal law.

11.3.3 Personally identifiable information shall only be released in accordance with applicable state and federal law.

12. REVIEW

STANDARD 12.1 The laboratory shall conduct and document administrative and technical reviews of all case files and reports to ensure conclusions and supporting data are reasonable and within the constraints of scientific knowledge. The review of data generated external to the laboratory is governed by Standard 17.

12.1.1 An individual conducting technical reviews shall be or have been an analyst qualified in the methodology being reviewed.

STANDARD 12.2 Completion of the technical review shall be documented and the technical review of forensic casework shall include the following elements:

12.2.1 A review of all case notes, all worksheets, and the electronic data (or printed electropherograms or images) supporting the conclusions.

12.2.2 A review of all DNA types to verify that they are supported by the raw or analyzed data (electropherograms or images).

12.2.3 A review of all profiles to verify correct inclusions and exclusions (if applicable) as well as a review of any inconclusive result for compliance with laboratory guidelines.

12.2.4 A review of all controls, internal lane standards and allelic ladders to verify that the expected results were obtained.

12.2.5 A review of statistical analysis, if applicable.

12.2.6 A review of the final report's content to verify that the results/conclusions are supported by the data. The report shall address each tested item or its probative fraction.

12.2.7 Verification that all profiles entered into CODIS are eligible, have the correct DNA types and correct specimen category

12.2.7.1 Prior to upload to or search of SDIS, verification of the following criteria for DNA profiles: eligibility for CODIS, correct DNA types, and appropriate specimen category.

12.2.7.2 For entry into a searchable category at SDIS, verification of the following criteria for DNA profiles by two concordant assessments by a qualified analyst or technical reviewer: eligibility for CODIS; correct DNA types; and appropriate specimen category.

STANDARD 12.3 The administrative review shall include the following elements, any or all of which may be included within the technical review:

12.3.1 A review of the case file and final report for clerical errors and that information specified in Standard 11.2 is present and accurate.

12.3.2 A review of chain of custody and disposition of evidence.

12.3.3 A procedure to document the completion of the administrative review.

STANDARD 12.4 The laboratory shall document the elements of a technical and administrative review. Case files shall be reviewed and documented according to the laboratory's procedure.

STANDARD 12.5 The laboratory shall have and follow a documented procedure to address unresolved discrepant conclusions between analysts and reviewer(s).

STANDARD 12.6 The laboratory shall have and follow a documented procedure for the verification and resolution of database matches.

STANDARD 12.7 The laboratory shall have and follow a program that documents the annual monitoring of the testimony of each analyst.

13. PROFICIENCY TESTING

STANDARD 13.1 Analysts, technical reviewers, technicians, and other personnel designated by the technical leader, shall undergo semi-annual external proficiency testing in each technology performed to the full extent in which they participate in casework. Semi-annual is used to describe an event that takes place two times during one calendar year, with the first event taking place in the first six months of that year and the second event taking place in the second six months of that year and where the interval between the two events is at least four months and not more than eight months. Such external proficiency testing shall be an open proficiency testing program and shall be submitted to the proficiency testing provider in order to be included in the provider's published external summary report.

13.1.1 Individuals routinely utilizing both manual and automated methods shall be proficiency tested in each at least once per year to the full extent in which they participate in casework.

13.1.2 Newly qualified individuals shall enter the external proficiency testing program within six months of the date of their qualification.

13.1.3 For purposes of tracking compliance with the semi-annual proficiency testing requirement, the laboratory shall define, document and consistently use the date that the proficiency test is performed as the received date, assigned date, submitted date, or the due date.

13.1.4 Except as provided in Standard 13.1.4.1, each analyst shall be assigned and complete his/her own external proficiency test.

13.1.4.1 Laboratories that use a team approach to casework examination may do so on external proficiency tests. However, all analysts, technicians, and technical reviewers shall be proficiency tested at least once per year in each of the DNA technologies, including test kits for DNA typing, and each platform in which they perform forensic DNA analysis.

13.1.5 Typing of all CODIS core loci or CODIS core sequence ranges shall be attempted for each technology performed.

13.1.6 The laboratory shall maintain the following records for proficiency tests:

13.1.6.1 The test set identifier,
13.1.6.2 Identity of the analyst, and other participants, if applicable,
13.1.6.3 Date of analysis and completion,
13.1.6.4 Copies of all data and notes supporting the conclusions,
13.1.6.5 The proficiency test results,
13.1.6.6 Any discrepancies noted, and
13.1.6.7 Corrective actions taken.

13.1.7 The laboratory shall include, at a minimum, the following criteria for evaluating proficiency test results:

13.1.7.1 Inclusions and exclusions as well as all reported genotypes and/or phenotypes are correct or incorrect according to consensus results or are within the laboratory's interpretation guidelines.

13.1.7.2 All results reported as inconclusive or not interpretable are consistent with written laboratory guidelines.

13.1.7.2.1 The technical leader shall review any inconclusive result for compliance with laboratory guidelines.

13.1.7.3 All discrepancies/errors and subsequent corrective actions shall be documented.

13.1.7.4 All final reports are graded as satisfactory or unsatisfactory.

13.1.7.4.1 A satisfactory grade is attained when there are no analytical errors for the DNA profile typing data.

13.1.7.4.1.1 Administrative errors and corrective actions, as applicable, shall be documented.

13.1.8 All proficiency test participants shall be informed of his/her final test results and this notification shall be documented.

13.1.9 The technical leader shall be informed of the results of all participants and this notification shall be documented. The technical leader shall inform the casework CODIS administrator of all non-administrative discrepancies that affect the typing results and/or conclusions at the time of discovery.

STANDARD 13.2 The laboratory shall use an external proficiency test provider that is in compliance with the current proficiency testing manufacturing guidelines established by the American Society of Crime Laboratory Directors/ Laboratory Accreditation Board or be in compliance with the current International Organization for Standardization.

14. CORRECTIVE ACTION

STANDARD 14.1 The laboratory shall establish and follow a corrective action plan to address when discrepancies are detected in proficiency tests and casework analysis. A laboratory corrective action plan shall define what level/type of discrepancies are applicable to this practice and identify (when possible) the cause, effect of the discrepancy, corrective actions taken and preventative measures taken (where applicable) to minimize its reoccurrence. Documentation of all corrective actions shall be maintained in accordance with Standard 3.2.

STANDARD 14.2 Corrective actions shall not be implemented without the documented approval of the technical leader.

15. AUDITS

STANDARD 15.1 The laboratory shall be audited annually in accordance with these standards. The annual audits shall occur every calendar year and shall be at least 6 months and no more than 18 months apart. Audits shall be conducted by an audit team comprised of qualified auditor(s) having at least one team member who is or has been an analyst previously qualified in the laboratory's current DNA technologies and platform.

STANDARD 15.2 At least once every two years, an external audit shall be conducted by an audit team comprised of qualified auditor(s) from a second agency(ies). and having at least one team member who is or has been an analyst previously qualified in the laboratory's current DNA technologies and platform.

15.2.1 Each analyst, casework CODIS administrator and technical leader shall have his/her education, experience and training qualifications evaluated and approved during two successive, separate external audits conducted after July 1, 2004. Approval of an individual's education, experience and training qualifications shall be documented in the audit document.

15.2.2 Each validation study shall be evaluated and approved during one external audit. Approved validation studies shall be documented in the audit document.

STANDARD 15.3. For internal audits, the auditor or audit team shall have the following expertise: currently qualified auditor and currently or previously qualified as an analyst in the laboratory's current DNA technologies and platform.

STANDARD 15.4 Internal and external audits shall be conducted utilizing the FBI DNA Quality Assurance Standards Audit Document.

STANDARD 15.5 Internal and external DNA Audit documents and, if applicable, corrective action(s) shall be submitted to the technical leader for review to ensure that findings, if any, were appropriately addressed.

15.5.1 For NDIS participating laboratories, all external audit documentation and laboratory responses shall be provided to the FBI within 30 days of laboratory receipt of the audit documents or report.

STANDARD 15.6 Internal and external audit documentation shall be retained and available for inspection during subsequent audits.

16. SAFETY

STANDARD 16.1 The laboratory shall have and follow a documented environmental health and safety program. This program shall include the following:

16.1.1 A blood borne pathogen and chemical hygiene plan

16.1.2 Documented training on the blood borne pathogen and chemical hygiene plan.

STANDARD 16.2 The laboratory's environmental health and safety program shall be reviewed once each calendar year and such review shall be documented.

STANDARD 17. OUTSOURCING

STANDARD 17.1 A vendor laboratory performing forensic DNA analysis shall comply with these Standards and the accreditation requirements of federal law.

17.1.1 An NDIS participating laboratory that outsources DNA sample(s) to a vendor laboratory to generate DNA data that will be entered into or searched in CODIS shall require the vendor laboratory to provide documentation of compliance with these Standards and the accreditation requirements of federal law. The NDIS participating laboratory shall maintain such documentation.

STANDARD 17.2 Except as provided in Standard 17.2.1, an NDIS participating laboratory's technical leader shall document approval of the technical specifications of the outsourcing agreement with a vendor laboratory before it is awarded. Such documentation shall be maintained by the NDIS participating laboratory.

17.2.1 A vendor laboratory that is performing forensic DNA analysis for a law enforcement agency or other entity and generating DNA data that may be entered into or searched in CODIS shall not initiate analysis for a specific case or set of cases until documented approval has been obtained from the appropriate NDIS participating laboratory's technical leader of acceptance of ownership of the DNA data.

STANDARD 17.3 An NDIS participating laboratory shall not upload or accept DNA data for upload to CODIS from any vendor laboratory or agency without the documented prior approval of the technical specifications of the outsourcing agreement and/or documented approval of acceptance of ownership of the DNA data by the NDIS participating laboratory's technical leader.

STANDARD 17.4 An NDIS participating laboratory shall have and follow a procedure to verify the integrity of the DNA data received through the performance of the technical review of DNA data from a vendor laboratory.

STANDARD 17.5 Prior to the upload or search of DNA data in SDIS, an analyst, casework CODIS Administrator or technical reviewer employed by an NDIS participating laboratory shall review the DNA data to verify specimen eligibility and the correct specimen category for entry into CODIS.

STANDARD 17.6 Prior to the upload of DNA data to SDIS or the reporting of search results, the technical review of a vendor laboratory's DNA data shall be performed by an analyst or technical reviewer employed by an NDIS participating laboratory who is qualified or previously qualified in the technology, platform and typing amplification test kit used to generate the data and participates in an NDIS laboratory's proficiency testing program.

17.6.1 The technical review shall include the following elements:

17.6.1.1 A review of all DNA types to verify that they are supported by the raw and/or analyzed data (electropherograms or images).

17.6.1.2 A review of all associated controls, internal lane standards and allelic ladders to verify that the expected results were obtained.

17.6.1.3 A review of the final report (if provided) to verify that the results/conclusions are supported by the data. The report shall address each tested items (or its probative fractions) submitted to the vendor laboratory.

17.6.1.4 Verification of the DNA types, eligibility, and the correct specimen category for entry into CODIS.

STANDARD 17.7 An NDIS participating laboratory or multi-laboratory system outsourcing DNA sample(s) to a vendor laboratory or accepting ownership of DNA data from a vendor laboratory shall have and follow a procedure to perform an on-site visit(s) of the vendor laboratory, provided, however, that an on-site visit shall not be required when only technical review services are being provided. The procedure to perform an on-site visit shall include, at a minimum, the following elements:

17.7.1 A documented initial on-site visit prior to the vendor laboratory's beginning of casework analysis for the laboratory.

17.7.1.1 The on-site visit shall be performed by the technical leader, or a designated employee of an NDIS participating laboratory, who is a qualified or previously qualified DNA analyst in the technology, platform and typing amplification test kit, used to generate the DNA data. Alternatively, the technical leader of the NDIS Participating Laboratory may accept an on-site visit conducted by a designated FBI employee.

17.7.2 If the outsourcing agreement extends beyond one year, an annual on-site visit shall be required. Each annual on-site visit shall occur every calendar year and shall be at least 6 months and no more than 18 months apart.

17.7.2.1 An NDIS participating laboratory may accept an on-site visit conducted by the FBI, or another NDIS participating laboratory using the same technology, platform and typing amplification test kit, for the generation of the DNA data and shall document the review and approval of such on-site visit.

Graham, E.A.M. and Rutty, G.N. (2008) Investigation into "normal" background DNA on adult necks: implications for DNA profiling of manual strangulation victims. *J. Forensic Sci.* 53: 1074-1082.

Ladd, C., Lee, H.C., Yang, N., Bieber, F.R. (2001) Interpretation of complex forensic DNA mixtures. *Croatian Med. J.* 42(3): 244-246.

Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Budowle, B. (2001) Validation of short tandem repeats (STRs) for forensic usage: performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. *J. Forensic Sci.* 46: 647-660.

Moretti, T.R., Baumstark, A.L., Defenbaugh, D.A., Keys, K.M., Budowle, B. (2001) Validation of STR typing by capillary electrophoresis. *J. Forensic Sci.* 46: 661-676.

Morling N., Bastisch, I., Gill, P., Schneider, P.M. (2007) Interpretation of DNA mixtures – European consensus on principles. *Forensic Sci. Int. Genet.* 1(3): 291–292.

Perlin, M. W. and Szabady, B. (2001) Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *J. Forensic Sci.* 46(6): 1372-1378.

Perlin, M.W., Kadane, J.B., Cotton, R.W. (2009) Match likelihood ratio for uncertain genotypes. *Law, Probability and Risk* 8(3):289-302.

Schneider, P.M., Gill, P., Carracedo, A. (2006) Editorial on the recommendations of the DNA commission of the ISFG on the interpretation of mixtures. *Forensic Sci. Int.* 160: 89.

Schneider, P.M., Fimmers, R., Keil, W., Molsberger, G., Patzelt, D., Pflug, W., Rothämel, T., Schmitter, H., Schneider, H., Brinkman, B. (2009) The German Stain Commission: recommendations for the interpretation of mixed stains. *Int. J. Legal Med.* 123: 1-5; originally published in German in 2006 *Rechtsmedizin* 16:401-404.

Stringer, P., Scheffer, J.W., Scott, P., Lee, J., Goetz, R., Ientile, V., Eckhoff, C., Turbett, G., Carroll, D., Harbison, S. (2009) Interpretation of DNA mixtures—Australian and New Zealand consensus on principles. *Forensic Sci. Int. Genet.* 3: 144-145.

Tomsey, C.S., Kurtz, M., Flowers, B., Fumea, J., Giles, B., Kucherer, S. (2001) Case work guidelines and interpretation of short tandem repeat complex mixture analysis. *Croatian Med. J.* 42(3): 276-280.

Torres, Y., Flores, I., Prieto, V., Lopez-Soto, M., Farfan, M.J., Carracedo, A., Sanz, P. (2003) DNA mixtures in forensic casework: a 4-year retrospective study. *Forensic Sci. Int.* 134: 180-186.

Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N. (2009) Estimating the probability of allelic drop-out of STR alleles in forensic genetics. *FSI Genetics* 3: 222-226.

Van Nieuwerburgh, F., Goetghebeur, E., Vandewoestyne, M., Deforce, D. (2009) Impact of allelic dropout on evidential value of forensic DNA profiles using RMNE. *Bioinformatics* 25: 225-229.

Wang, T., Xue, N., Birdwell, J.D. (2006) Least-squares deconvolution: a framework for interpreting short tandem repeat mixtures. *J. Forensic Sci.* 51(6): 1284-1297.

Weir, B.S., Triggs, C.M., Starling, L., Stowell, L.I., Walsh, K.A.J., Buckleton, J.S. (1997) Interpreting DNA mixtures. *J. Forensic Sci.* 42(2): 213-222.

Whitaker, J.P., Cotton, E.A., Gill, P. (2001) A comparison of the characteristics of profiles produced with the AmpFISTR SGM Plus multiplex system for both standard and low copy number (LCN) STR DNA analysis. *Forensic Sci. Int.* 123: 215-223.

Wickenheiser, R.A. (2006) General guidelines for categorization and interpretation of mixed STR DNA profiles. *Canadian Society of Forensic Science Journal* 39(4): 179-216.

Glossary for this document

Allelic dropout: failure to detect an allele within a sample or failure to amplify an allele during PCR.

Analytical threshold: the minimum height requirement at and above which detected peaks can be reliably distinguished from background noise; peaks above this threshold are generally not considered noise and are either artifacts or true alleles.

Artifact: a non-allelic product of the amplification process (e.g., stutter, non-templated nucleotide addition, or other non-specific product), an anomaly of the detection process (e.g., pull-up or spike), or a by-product of primer synthesis (e.g., "dye blob").

Coincidental match: a match which occurs by chance.

Composite profile: a DNA profile generated by combining typing results from different loci obtained from multiple injections of the same amplified sample and/or multiple amplifications of the same DNA extract. When separate extracts from different locations on a given evidentiary item are combined prior to amplification, the resultant DNA profile is not considered a composite profile.

Conditional: an interpretation category that incorporates assumption(s) as to the number of contributors.

CPE: combined probability of exclusion; produced by multiplying the probabilities of inclusion from each locus and subtract the product from 1; (i.e., 1-CPI).

CPI: combined probability of inclusion; produced by multiplying the probabilities of inclusion from each locus; (i.e., 1-CPE).

Deconvolution: separation of contributors to a mixed DNA profile based on quantitative peak height information and any underlying assumptions.

Deduced: inference of an unknown contributor's DNA profile after taking into consideration the contribution of a known/assumed contributor's DNA profile based on quantitative peak height information.

Differential Degradation: a DNA typing result in which contributors to a DNA mixture are subject to different levels of degradation (e.g., due to time of deposition), thereby impacting the mixture ratios across the entire profile.

Distinguishable Mixture: a DNA mixture in which relative peak height ratios allow deconvolution of the profiles of major/minor contributor(s).

Evidence sample: also known as Questioned sample.

Exclusion: a conclusion that eliminates an individual as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other).

Guidelines: a set of general principles used to provide directions and parameters for decision making.

Heterozygote: an individual having different alleles at a particular locus; usually manifested as two distinct peaks for a locus in an electropherogram.

Homozygote: an individual having the same (or indistinguishable) alleles at a particular locus; manifested as a single peak for a locus in an electropherogram.

Inclusion: a conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other).

Inconclusive/uninterpretable: an interpretation or conclusion in which the DNA typing results are insufficient, as defined by the laboratory, for comparison purposes.

Indistinguishable mixture: a DNA mixture in which relative peak height ratios are insufficient to attribute alleles to individual contributor(s).

Intimate sample: a biological sample from an evidence item that is obtained directly from an individual's body; it is not unexpected to detect that individual's allele(s) in the DNA typing results.

Known sample: biological material for which the identity of the donor is established and used for comparison purposes (referred to as a "K").

Likelihood ratio (LR): the ratio of two probabilities of the same event under different hypotheses; typically the numerator contains the prosecution's hypothesis and the denominator the defense's hypothesis.

Major contributor(s): an individual(s) who can account for the predominance of the DNA in a mixed profile.

Masked allele: an allele of the minor contributor that may not be readily distinguishable from the alleles of the major contributor or an artifact.

Minor contributor(s): an individual(s) who can account for the lesser portion of the DNA in a mixed profile.

Mixture: a DNA typing result originating from two or more individuals.

Mixture ratio: the relative ratio of the DNA contributions of multiple individuals to a mixed DNA typing result, as determined by the use of quantitative peak height information; may also be expressed as a percentage.

Noise: background signal detected by a data collection instrument.

No results: no allelic peaks detected above the analytical threshold.

Obligate allele: an allele in a mixed DNA typing result that is (a) foreign to an assumed contributor, or (b) based on quantitative peak height information, determined to be shared with the assumed contributor.

Partial profile: a DNA profile for which typing results are not obtained at all tested loci due, for example, to DNA degradation, inhibition of amplification and/or low- quantity template.

Peak height ratio (PHR): the relative ratio of two alleles at a given locus, as determined by dividing the peak height of an allele with a lower relative fluorescence unit (RFU) value by the peak height of an allele with a higher RFU value, and then multiplying this value by 100 to express the PHR as a percentage; used as an indication of which alleles may be heterozygous pairs and also in mixture deconvolution.

Probability of exclusion (PE): the percentage of the population that can be excluded as potential contributors to a DNA mixture.

Probability of inclusion (PI): the percentage of the population that can be included as potential contributors to a DNA mixture; also known as Random Man Not Excluded.

Questioned sample: biological sample recovered from a crime scene or collected from persons or objects associated with a crime (referred to as a "Q").

Random Match Probability (RMP): the probability of randomly selecting an unrelated individual from the population who could be a potential contributor to an evidentiary profile.

Reference sample: also known as Known sample.

Restricted: referring to a statistical approach conditioned on the number of contributors and with consideration of quantitative peak height information and inference of contributor mixture ratios; used to limit the genotypic combinations of possible contributors.

Signal-to-noise ratio: an assessment used to establish an analytical threshold to distinguish allelic peaks (signal) from background/instrumental noise.

Single-source profile: DNA typing results determined to originate from one individual based on peak height ratio assessments and the number of alleles at given loci.

Source attribution: a declaration which identifies an individual as the source of an evidentiary profile to a reasonable degree of scientific certainty based on a single-source or major contributor profile.

Stochastic effects: the observation of intra-locus peak imbalance and/or allele drop-out resulting from random, disproportionate amplification of alleles in low-quantity template samples.

Stochastic threshold: the peak height value above which it is reasonable to assume that, at a given locus, allelic dropout of a sister allele has not occurred.

Stutter: a minor peak typically observed one repeat unit smaller than a primary STR allele resulting from strand slippage during amplification.

Unrestricted: referring to a statistical approach performed without consideration of quantitative peak height information and inference of contributor mixture ratios; for CPE/CPI this may or may not be conditioned on the number of contributors.

KANSAS CITY POLICE CRIME LABORATORY REPORT

An ASCLD/LAB Accredited Laboratory
6633 Troost Avenue
Kansas City, MO 64131

Agency:	WESTON POLICE DEPARTMENT FORT LEAVENWORTH CID	**Lab Record #:**	A13-00353 #6
		Offense:	Rape/Sexual Assault
Agency Case #:	W09130166 – Weston 0104-13-CID055 – Fort Leavenworth	**Report Type:**	DNA
		Report Date:	April 29, 2014
		Examiner:	Jessica Hanna

Subject(s):

Suspect: Henning, Antiwan (B/M)
Victim: Nightengale, Sarah (W/F 11/26/1983)
Elimination: WEAVER, WILLIAM (U/M)

List of Evidence:

Item # 13-0166-001.3.2: cutting from stain E of black thong underwear
Item # 13-0166-001.3.3: cutting from stain F of black thong underwear

Results of Analysis:

A mixture of genetic profiles consisting of a minimal minor contribution was PREVIOUSLY developed from Item 13-0166-001.3.2 cutting from stain E of black thong underwear. Henning , Antiwan B/M is included as a possible contributor of the minor genetic information developed from Item 13-0166-001.3.2. The expected frequency of potential contributors to the alleles present in Item 13-0166-001.3.2 minimal minor is one in 220 unrelated individuals. Weaver, William is excluded as a possible contributor of the minor genetic information.

A mixture of genetic profiles consisting of a minimal minor contribution was PREVIOUSLY developed from Item 13-0166-001.3.3 cutting from stain F of black thong underwear. Henning , Antiwan B/M is excluded as a possible contributor of the minor genetic information developed from Item 13-0166-001.3.3. Weaver, William is included as a possible contributor of the minor genetic information developed from Item 13-0166-001.3.3. Statistical analysis was not performed at this time, but can be done upon request.

This report contains the conclusions, opinions, and/or interpretations of the below analyst.

Jessica Hanna

Jessica Hanna
Forensic Specialist IV
Jessica.Hanna@kcpd.org

This report must be disseminated in full.

----------END OF REPORT ----------

CONFIDENTIAL REPORT

United States Army Trial Judiciary
Third Judicial Circuit, Fort Riley, Kansas

UNITED STATES v. HENNING, Antiwan M. MAJ, U.S. Army HHC, Combined Arms Center Fort Leavenworth, Kansas 66027	)	FINDINGS AND CONCLUSIONS RE: DEFENSE MOTION IN LIMINE (PRECLUDE EXPERT TESTIMONY) 29 APRIL 2015

Defense has filed a motion to exclude Government expert DNA evidence and testimony as being unreliable. The Government opposes the motion.

Factual Findings:

1. The Accused is charged with entering Mrs. Nightengale's bedroom while she was asleep next to her husband in bed, awakening her by touching her breast with his hand, penetrating her vagina with his tongue, and then moving her to the floor and penetrating her vagina with his penis by unlawful force. Her husband remained unaware of this activity. The Accused denies any sexual contact with Mrs. Nightengale.

2. The Kansas City Police Crime Laboratory (KCPCL) tested Mrs. Nightengale's underwear for the presence of DNA using autosomal short tandem repeat (STR) typing and compared it to the Accused's submitted DNA sample. KCPCL concluded that the Accused was included as a potential contributor to a "minimal minor" DNA profile from the underwear. The Accused's DNA matched five alleles at four loci in the minimal minor profile from the underwear. The Accused's DNA and the evidentiary sample shared a 6 and a 9 allele at the THO1 locus and a homozygotic (two alleles with the same genetic information from both parents) 12 allele at the D13 locus. At the D2 locus, the Accused has 16 and 22 alleles while the evidentiary sample only showed a 16 allele. At the D18 locus, the Accused has 13 and 20 alleles while the evidentiary sample only showed a 13 allele. KCPCL concluded that 1 in 220 people would have the same alleles in the same loci in the minimal minor profile as the Accused did.

3. The Scientific Working Group on DNA Analysis Methods (SWGDAM) is a group of approximately 50 scientists representing federal, state, and local forensic DNA laboratories in the United States and Canada. SWGDAM subcommittees discuss topics of interest to the forensic DNA community and develop documents to provide direction and guidance for the community. In January 2010, SWGDAM published Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories (hereinafter, Guidelines). SWGDAM is the definitive authority on reliable procedures and methods for forensic DNA testing and analysis.

APPELLATE EXHIBIT XLI

4. The SWGDAM Guidelines are mostly that: guidelines. Almost every reference in the document is permissive, and much of the document defers to laboratories for individual implementation. However, the section entitled, "Statistical Analysis of DNA Typing Results," contains definitive, almost mandatory language. That section delineates three different statistical calculations: Random Match Probability (RMP); Likelihood Ratio (LR); and Combined Probability of Exclusion or Inclusion (CPE/I). The Guidelines refer to these in the disjunctive: "In forensic DNA testing, ... calculations are based on [RMP], [LR], or [CPE/I]." SWGDAM Guidelines, p. 12 (emphasis added). According to the Guidelines, RMP is only appropriate for a single contributor or a known number of multiple contributors. Id. at p.12 and para. 5.2.2. ("conditioned upon the assumption of a particular number of contributors greater than one...." (emphasis added)). A RMP calculation can account for allelic dropout, that is the failure to detect an allele within a sample or failure to amplify an allele. See, e.g., id. at para. 5.2.2.3. A CPE/I calculation is used when no assumption is made as to the number of contributors to a sample. Id., at p.12 and para. 4.6.3. Allelic dropout cannot be a possibility when using CPE/I. Id. at para. 4.6.3. In some of the strongest, non-permissive language in the document, the Guidelines clearly state that RMP and CPE/I are incompatible with each other. The Guidelines state that RMP calculations are "distinguished from" CPE/I. Id. at p. 12. The Guidelines state that because these calculations are only used on evidentiary samples (vice known samples), "[t]his precludes combining multiple CPE or RMP results for the same mixture component of an evidentiary sample." Id. at para. 4.2. While the Guidelines permit both CPE/I and RMP calculations to be applied to the same evidentiary sample, each calculation must be based on different underlying assumptions about the number of contributors and the possibility of allelic dropout. Id. However, "the CPI and RMP cannot be multiplied across loci in the statistical analysis of an individual DNA profile because they rely upon different fundamental assumptions about the number of contributors to the mixture." Id. at para. 4.6.2 (emphasis added). Finally, Table 1 in the Guidelines states, "The statistical methods [of RMP, CPE/I, and LR] listed in the table cannot be combined into one calculation." Id. at p. 22 (emphasis added).

5. KCPCL used a statistical calculation in this case that does precisely what the Guidelines state is "precluded." That is, KCPCL made no assumptions about the number of contributors (invoking the CPE/I calculation) but accounted for the possibility of allelic dropout (invoking the RMP calculation). Ms. Hanna, the KCPCL lab technician who performed the DNA testing in this case, called this a "modified unrestricted RMP" calculation. Mr. Hummel, Ms. Hanna's supervisor, confirmed that the modification of the RMP calculation was its application to an unknown number of contributors. Ms. Hanna alternatively called this an "alleles present statistic." She stated that, in order to be included as a potential contributor, a person must have all of the alleles that were detected in the evidentiary sample (in this case, all five alleles). Then this is compared to the number of people in the FBI's DNA database who share the same alleles at the same loci to develop a probability statistic. Mr. Hummel stated KCPCL did not originate such a formula, that such a formula is accepted in the scientific community, and that accreditors and auditors have looked at this formula and have continued to accredit KCPCL. Ms. Hanna said that KCPCL has been using such a formula for 15 years.

6. The amount of human, male DNA used in the testing process in this case that resulted in the conclusion that the Accused was included as a potential contributor to the genetic material in Mrs. Nightengale's underwear was the equivalent to three or four human cells. This was an "exceedingly small quantity" according to Dr. Krane. Dr. Krane testified that this was "the most difficult sample that could be interpreted" because it was a "minimal minor" sample, the quantity of testable DNA was extremely low, and because of the possibility of allelic dropout or drop-in (e.g., through contamination). Additionally, according to Dr. Krane's review of Ms. Hanna's laboratory notes, Ms. Hanna did not conclude, one way or another, whether allelic dropout had occurred in the sample.

Law:

As a threshold matter, when deciding whether an expert will be allowed to testify, the military judge is obligated to determine whether the expert testimony will be helpful to the panel. United States v. Flesher, 73 M.J. 303, 313 (C.A.A.F. 2014). M.R.E. 702 states that an expert witness may provide testimony if it "will assist the trier of fact to understand the evidence or determine a fact in issue." Thus, an expert may testify if his or her testimony is "helpful." United States v. Billings, 61 M.J. 163, 166 (C.A.A.F. 2005). A suggested test for deciding when experts may be used is "whether the untrained layman would be qualified to determine intelligently and to the best possible degree the particular issue without enlightenment from those having a specialized understanding of the subject . . . ." United States v. Meeks, 35 M.J. 64, 68 (C.M.A. 1992) (quoting F.R.E. 702 advisory committee's note). Where it is relevant to the case, courts have generally found DNA evidence to be helpful to panel members and beyond their ken. See, e.g., United States v. Youngberg, 43 M.J. 379, 386 (C.A.A.F. 1995); United States v. Allison, 63 M.J. 365, 369 (C.A.A.F. 2006).

Further, M.R.E. 702 permits expert testimony in the "form of an opinion or otherwise" only if the testimony: (1) is "based upon sufficient facts or data," (2) is "the product of reliable principles and methods," and (3) the principles and methods have been "applied . . . reliably to the facts of the case." In United States v. Houser, 36 M.J. 392 (C.M.A. 1993), the Court of Military Appeals examined M.R.E. 702 and set forth six factors that must be satisfiedby the proponent of expert testimony:

(1) the qualifications of the expert;

(2) the subject matter of the expert testimony;

(3) the basis for the expert testimony (M.R.E. 703);

(4) the legal relevance of the evidence (M.R.E. 401);

(5) the reliability of the evidence; and

(6) the standard balancing test outlined in M.R.E. 403.

Two months after Houser was decided, the Supreme Court decided Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579, 589 (1993), concerning scientific evidence offered under F.R.E. 702. The Supreme Court focused on the issues of reliability, 509 U.S. at 590, and relevance, id. at 591, holding that F.R.E. 702 assigns to the trial judge the duty to act as a gatekeeper, that is "the task of ensuring that an expert's testimony both rests on a reliable foundation and is relevant to the task at hand." Id. at 597. The Supreme Court, while disclaiming any attempt "to set out a definitive checklist or test," listed the following six factors to be considered by the trial judge in determining whether scientific evidence meets the requirements for reliability and relevance:

(1) Whether the theory or technique can be (and has been) tested;

(2) Whether the theory or technique has been subjected to peer review and publication;

(3) The known or potential error rate;

(4) The existence and maintenance of standards controlling the technique's operation;

(5) The degree of acceptance within the relevant scientific community; and

(6) Whether the probative value of the evidence is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury. Id. at 593-95. Although Houser was decided before Daubert, the two decisions are consistent, with Daubert providing more detailed guidance on the fourth and fifth Houser prongs pertaining to relevance and reliability. United States v. Griffin, 50 M.J. 278, 283-284 (C.A.A.F. 1999).

The focus is on the objective of the gatekeeping requirement, which is to ensure that the expert, "whether basing testimony upon professional studies or personal experience, employs in the courtroom the same level of intellectual rigor that characterizes the practice of an expert in the relevant field." United States v. Sanchez, 65 M.J. 145, 149 (C.A.A.F. 2007) (quoting Kumho Tire Co. v. Carmichael, 526 U.S. 137, 152 (1999)). The inquiry is "a flexible one," Daubert, 509 U.S. at 594, and "the gatekeeping inquiry must be tied to the facts of a particular case." Kumho Tire Co., 526 U.S. at 150. The focus of the inquiry into reliability is on the principles and methodology employed by the expert, without regard to the conclusions reached thereby. Daubert, 509 U.S. at 595. At a minimum, the military judge is required to determine whether the conclusion could reliably follow from the facts known to the expert and the methodology used, mindful that "conclusions and methodology are not entirely distinct from one another. Trained experts commonly extrapolate from existing data." Sanchez, 65 M.J. at 149-150 (quoting

General Electric Co. v. Joiner, 522 U.S. 136, 146 (1997)). Whether attempting to determine if there is "too great an analytical gap between the data and the opinion proffered," Joiner, 522 U.S. at 146, or whether the proffered testimony falls "outside the range where experts might reasonably differ," Kumho Tire Co., 526 U.S. at 153, the goal is to ensure that expert testimony or evidence admitted is relevant and reliable, as well as to shield the panel from junk science. Sanchez, 65 M.J. at 149-50.

Conclusions:

There is no real argument about the first four Houser factors in this case: they are satisfied. Ms. Hanna and Mr. Hummel are qualified to testify about forensic DNA testing and analysis. The DNA testing and analysis in this case is legally relevant, because it makes a fact of consequence—the Accused's sexual contact with Mrs. Nightengale—more likely in a case where Mrs. Nightengale and the Accused have opposing versions of the events and there are no other eyewitnesses. Ms. Hanna's and Mr. Hummel's expert testimony about the forensic DNA testing and analysis in this case would be helpful to the panel members, who cannot be expected to understand this complex subject on their own. Ms. Hanna will base her expert testimony on her own testing rather than on the conclusions of others or on hypotheticals.

The real issue is the reliability of this evidence. Specifically, it is about the reliability of the formula KCPCL applied to the DNA test results in order to conclude that the Accused was a possible contributor to the genetic material found in Mrs. Nightengale's underwear. KCPCL's testing procedures (i.e., the extraction of DNA from an evidentiary sample and the identification therefrom of a constellation of specific alleles at specific loci) are not in question; they are reliable under a Daubert analysis. They are testable, are subject to peer review (including internal technical reviews, audits, and accreditation), are governed by known standards, and are widely accepted in the scientific community. However, the Government, as the proponent of the evidence, bore the burden of persuasion and failed to demonstrate by a preponderance of the evidence that the "modified" formula KCPCL applied to draw conclusions about potential contributors in this case is reliable.

Although the KCPCL formula is testable and subject to peer review, a preponderance of the evidence does not indicate it is widely accepted in the field of forensic DNA testing despite Mr. Hummel's testimony to the contrary. SWGDAM appears to represent the scientific community with regard to forensic DNA testing. The parties agree that SWGDAM is the definitive authority in this regard. SWGDAM is comprised of a representative sample of all persons involved in this field who meet regularly and make recommendations to the field of practitioners. While Ms. Hanna testified that KCPCL has been using the "alleles present statistic" for 15 years, such a formula has never made it into (much less mentioned by) the SWGDAM Guidelines. In fact, such a formula appears wholly contradictory to the only portion of the Guidelines that sound non-permissive. The Guidelines from the "definitive authority" reject KCPCL's approach. The Guidelines preclude the combination of CPE/I and RMP calculations in a given sample, because

they rely on fundamentally different underlying assumptions. Some of the apparent flaws with KCPCL's formula follow. First, if you assume two contributors to the sample in this case, then the Accused could not have contributed all five of the alleles detected; the second person would have had to contribute at least one of the alleles (and possibly more). This is true regardless whether allelic dropout had occurred. In that case, a reliable formula could account for the possibility that the Accused contributed the least number of alleles possible. If allelic dropout definitely occurred, it could have occurred at the D13 locus where only one allele (12) was detected. If so, it would also be possible that the D13 locus contained heterozygous alleles, and that would exclude the Accused (who has homozygous alleles at that locus) as a contributor. In either of the above cases, this would presumably result in a different formula producing a different statistic than the one KCPCL developed (1 in 220). On the other hand, if you assume no allelic dropout occurred, the Accused must be excluded as a contributor regardless of the number of contributors. If no allelic dropout occurred, then all alleles are present and the D2 and D18 loci contain homozygotic alleles: a 16, 16 at the D2 and a 13, 13 at the D18. The Accused is a 16, 22 at the D2 and a 13, 20 at the D18. This means he would not match the evidentiary sample and must be excluded. The formula KCPCL used did not rely on a conclusive determination whether allelic dropout had occurred or on a specific number of contributors, making its probability statistic misleading at best. Further, the Government provided no evidence of error rates with regard to KCPCL's formula or what the statistical cutoff is for inclusion as a possible contributor (e.g., is 1 in 100,000 a permissible statistic to be included?).

Even if this Court were to determine that KCPCL's formula, its application in this case, and the resulting statistical conclusion were reliable, the evidence fails the M.R.E. 403 balancing test. The probative value is minimal. While it does add to the Government's side of the scales, it concludes merely that the Accused is a "possible" contributor. This is based on three to four human cells (an "exceedingly small quantity of starting material") in a "minimal minor" profile where the Accused matched up to (but possibly less than) 5 of 32 alleles, and allelic dropout or drop-in could have occurred—"the most difficult sample that could be interpreted". This battle of the experts would certainly be a mini-trial within the trial, with multiple experts being called and recalled to rebut one another on a highly technical issue the panel members will likely have a difficult time understanding. There is a danger that the panel members will put aside the "technical" issue they do not understand and default to the more straightforward conclusion of "included as a possible contributor." Because DNA evidence is powerful (and ubiquitous on television and the movies), this danger is high. KCPCL's statistic compounds this problem. Despite the small amount of DNA in a minimal minor profile, the statistic KCPCL produced can be viewed as significant. Using the 1 in 220 statistic, in a population as small as Weston, Missouri (1,641 in the 2010 census—see, http://www.census.gov/popfinder/), only 7 people could be contributors to the genetic material in Mrs. Nightengale's underwear. The Government is sure to point out that of those seven possible people, only one was in Mrs. Nightengale's house. Consequently, the probative value is substantially outweighed by the danger of unfair prejudice, misleading the panel members, and waste of time.

CERTIFICATE OF FILING AND SERVICE

I certify that the foregoing was filed electronically with the court (efiling@armfor.uscourts.gov) and contemporaneously served electronically on appellate defense counsel on the 23rd day of October 2015 and.

JIHAN WALKER
Captain, JA
Branch Chief
Government Appellate Division
9275 Gunston Road
Fort Belvoir, Virginia 22060
(703) 693-0783