No. 25-5712

IN THE

Supreme Court of the United States

In re BLAINE KEITH MILAM,
Petitioner.

On Original Petition for a Writ of Habeas Corpus

APPENDIX

Exhibit A Laboratory Response to Texas Forensic Science Complaint

EXHIBIT A

DALLAS COUNTY
SOUTHWESTERN INSTITUTE OF FORENSIC SCIENCES

PHYSICAL EVIDENCE SECTION

2355 North Stemmons Freeway
Dallas, Texas 75235

Date: 9/19/2025
To: Texas Forensic Sciences Commission
From: Timothy J. Sliter, Ph.D., Section Chief, Physical Evidence
Re: Laboratory Response to Texas Forensic Science Complaint C25.52

Att: Guidelines for STR Interpretation – Profiler Plus and Cofiler Kits

The laboratory is in receipt of complaint C25.52 from Cynthia Cale on behalf of defendant Blaine Milam. The complaint is accompanied by supporting statements from Ms. Cale and from Dr. Dan Krane.

The complaint concerns the reinterpretation of DNA profiles originally obtained in 2009 and 2010 in laboratory case 08P02031. The reinterpretation was performed by Dr. Stacy McDonald at the request of the Rusk County District Attorney's Office and reported on 8/12/2025. The reinterpretation was performed using the laboratory's protocols that were revised following the 2015 state-wide review of mixture interpretation protocols sponsored by the Commission.

The complaint focuses on objections of Ms. Cale and Dr. Krane to the interpretation reported for Sample 20I, which is a swab collected by the medical examiner from the left elbow of the decedent in the case.

Consequently, this response will address only the interpretation performed for Sample 20I (swabbing of left elbow of decedent).

This response will consist of two parts:

Part 1. A detailed walk-through of the analysis and interpretation applied to sample 20I.

Part 2. A response to specific concerns expressed by Ms. Cale and Dr. Krane regarding the interpretation of the profile data from Sample 20I.

At the outset, however, I would make the following observation.

Both Ms. Cale and Dr. Krane in their statements do exactly what any competent expert for the defense should do – they evaluate scientific data from the perspective of what is most beneficial to the interests of their client. This approach is perfectly understandable, and it conforms to the ethical responsibilities of a defense expert.

However, this laboratory and its scientific staff operate under a different set of ethical standards. As licensed forensic scientists we do not have the option of shading our interpretations based upon what would benefit one side or the other in a legal proceeding. That approach would rightly be considered unethical. For that reason, the laboratory performs interpretations that are solely the product of objective evaluations of the relevant and available data.

Part 1. Description of analysis and interpretation

Workflow Overview. The laboratory's workflow for data analysis and interpretation is described in the Guidelines for STR Interpretation – Profiler Plus and Cofiler Kits (hereafter referred to as the Guidelines), which is provided as a supporting record to this response.

As stated in the Guidelines, the workflow is designed to reduce the potential for cognitive bias in profile interpretation. This is done by systematizing the analyst's evaluation of the data and basing each step of the interpretative process on objective criteria. The steps in the workflow are:

1. Step 1. Define the authentic alleles at each locus.
2. Step 2. Determine the number of contributors to the profile.
3. Step 3. For mixtures, define the principal components at each locus where possible.
4. Step 4. Assess the possibility of allelic dropout at each locus.
5. Step 5. For mixtures, deconvolute the profile using information about known or reasonably assumed contributors (subtraction).
6. Step 6. Define the set of not-excluded genotypes for each component at each locus.
7. Step 7. Evaluate the suitability of the profile as a whole and loci in the profile for statistical calculations of match probability.
8. Step 8. Compare the profile of the questioned sample to the profile of known individuals and draw conclusions regarding inclusion and exclusion (source attribution).

As part of the workflow, a protocol is included to determine the best estimate of the number of contributors to a profile. This protocol includes the evaluation of peaks below the analytical threshold that may be an indication of additional contributors to a sample.

Sample Description. Sample 20I was one (1) swab containing material collected at autopsy from the left elbow of the decedent. Because the swab was collected from the skin of the decedent, the decedent was an expected contributor to the DNA contained on sample 20I. Therefore, the interpretation of the DNA profile obtained from 20I was conditioned upon the decedent's expected contribution.

Serological Testing. Light brown staining was observed on sample 20I. A presumptive test for blood was negative.

DNA Extraction. Sample 20I was processed using the laboratory's QiaAmp extraction protocol. The protocol is a non-organic extraction protocol performed using the Qiagen QiaAmp extraction kit. Half of sample 20I swab was extracted. The remainder of the swab was retained for possible future testing. The final volume of extract obtained from the sample was approximately 30 μL.

DNA Quantification. The DNA extract was quantified using the Applied Biosystems Quantifiler Human DNA Quantification kit. This is a real-time PCR assay that was performed using the

Applied Biosystems 7900HT real time PCR instrument. The measured concentration of DNA in the extract was 0.0238 ng/µL

DNA Amplification. The DNA extract was amplified using the Applied Biosystems Profiler Plus DNA kit. The volume of extract that was amplified was 20 µL.

Electrophoresis and Data Analysis. The amplified DNA product was separated by capillary electrophoresis using the Applied Biosystems 310 Genetic Analyzer. Instrumental data files were then analyzed using the Applied Biosystems GeneMapper software (v3.2) using a 50 rfu analytical threshold.

Two rounds of electrophoresis were performed in the original processing in 2009-2010.

1. 5-second injection. In the first round of electrophoresis, the laboratory's standard 5-second injection was used. The resulting DNA profile showed label allele peaks above the 50 rfu analytical threshold at Amelogenin and two (2) STR loci (D3S1358 and D8S1179; see Figure 1). However, at several loci, additional peaks were observed below the analytical threshold but above the baseline instrumental noise level. At several loci (e.g., D5S818, Figure 2) more than two sub-analytical threshold peaks were observed, which suggested that the sample might be a mixture of DNA from more than one contributor.

   Note: In the 5-second injection, a single 11 allele was detected at 94 rfu at D8S1179. The laboratory's stochastic threshold is 85 rfu. If Sample 20I were interpreted as a single-source sample, then D18S1179 would be interpreted as being homozygous (11,11). However, given the suggestion by sub-analytical threshold peaks that Sample 20I might be a mixture, no conclusion was made regarding homozygosity at D8S1179 based on the 5-second injection data.

2. 15-second injections. In the second round, the amplified product was injected for 15-seconds. The profile obtained from the 5-second injection met the laboratory's requirements to qualify for 15-second injection.
   a. There was insufficient extract remaining to perform amplification.
   b. No peaks in the 5-second injection exceeded 900 rfu.

   Two replicate 15-second injections were performed (Figure 3 and Figure 4). These 15-second injections produced allelic peaks above the analytical threshold at Amelogenin and nine (9) STR loci.

   The 15-second injection data established that Sample 20I was indeed a mixture of DNA from more than contributor.

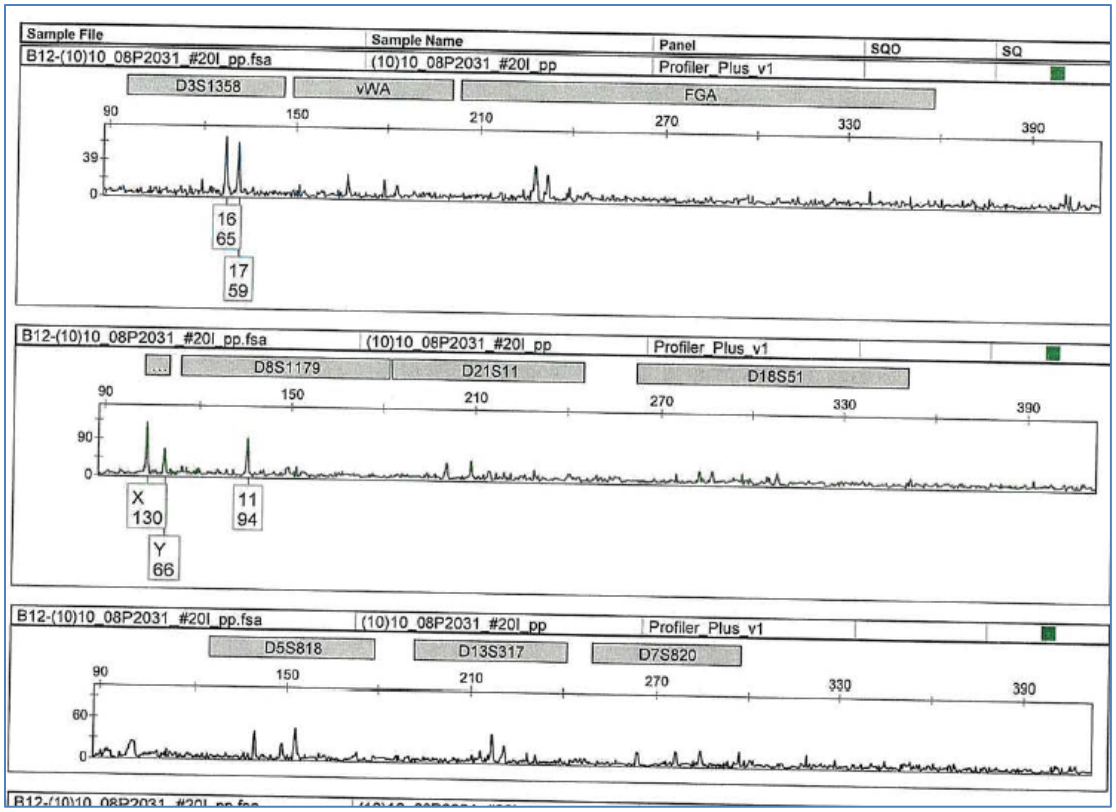

Figure 1. Electropherogram of sample 20I obtained using 5-second injection.

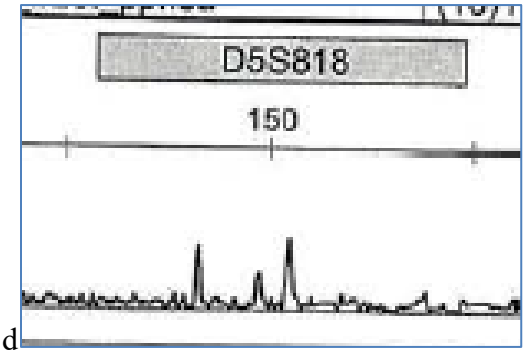

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Figure 2. Sub-analytical threshold peaks in 5-second injection of sample 20I (D5S818).

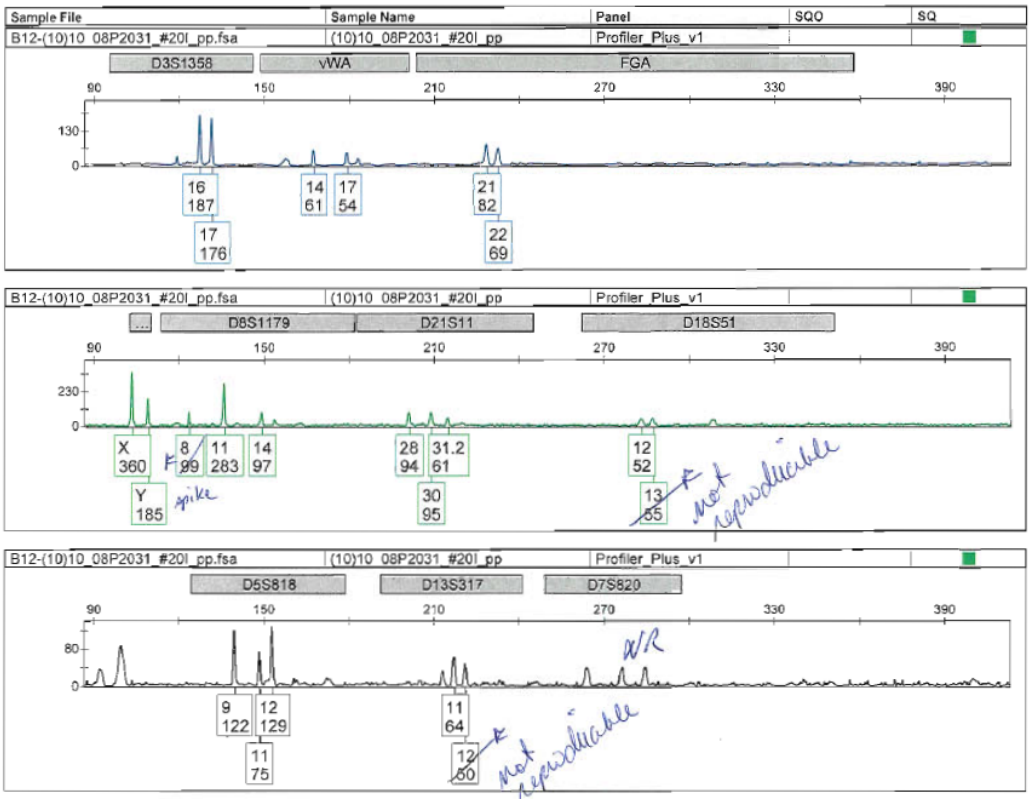

Figure 3. Sample 20I electropherogram – first 15-second injection.

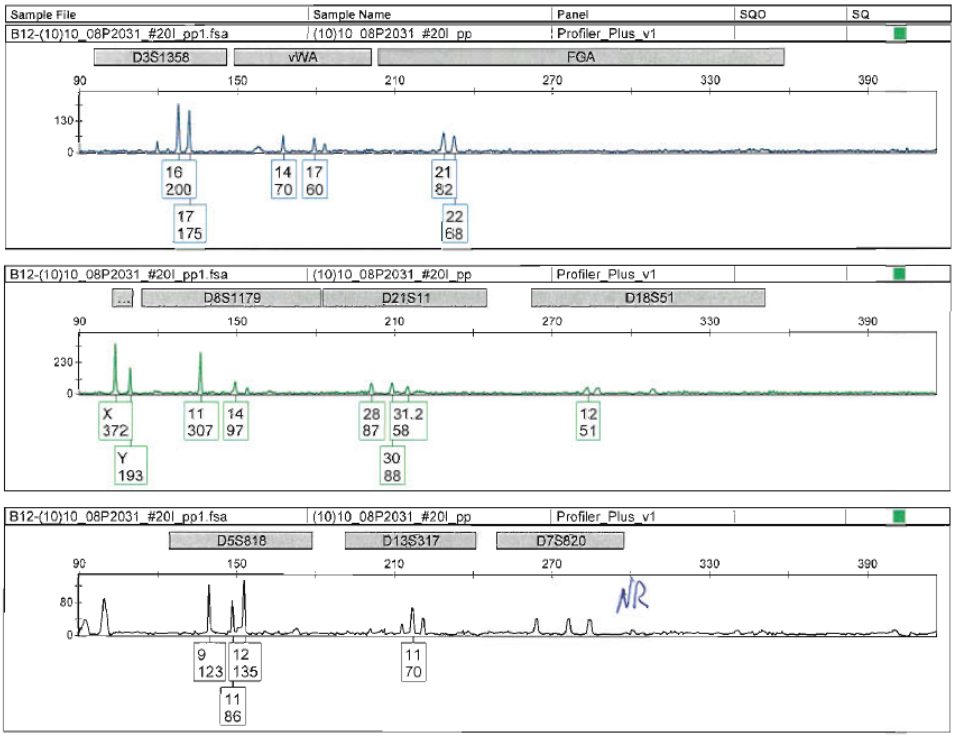

Figure 4. Sample 20I electropherogram - second 15-second injection.

Following data collection, the electropherogram data were analyzed to identify the authentic alleles present in the sample. Artifact peaks were identified. Additionally, the reproducibility of allele peaks in the two 15-second injections was evaluated.

At two loci, peaks in allelic positions were detected in only one of the two 15-second injections. Because these peaks were not reproducibly observed above the analytical threshold, they were not included in the final sample profile.

1. D18S51-13
2. D13S317-12

The analysis to determine the final reported sample profile is described in Table 1. The final reported profile for Sample 20I was the set of allele peaks reproducibly observed at each locus in the two 15-second injections.

Table 1. Sample 20I final reported profile, with individual injection results.

	5 Sec Injection		First 15 Sec Injection		Second 15 Sec Injection		Sample 20I Reported Profile
Locus	Allele	Peak Height	Allele	Peak Height	Allele	Peak Height	
D3S1358	16	65 rfu	16	187 rfu	16	200 rfu	**16,17**
	17	59 rfu	17	176 rfu	17	175 rfu	
vwa	--	--	14	61 rfu	14	70 rfu	**14,17**
			17	54 rfu	17	60 rfu	
FGA	--	--	21	82 rfu	21	82 rfu	**21,22**
			22	69 rfu	22	68 rfu	
Amelogenin	Amel-X	130 rfu	Amel-X	360 rfu	Amel-X	372 rfu	**Amel-X, Amel-Y**
	Amel-Y	66 rfu	Amel-Y	185 rfu	Amel-Y	193 rfu	
D8S1179	11	94 rfu	11	283 rfu	11	307 rfu	**11,14**
			14	97 rfu	14	97 rfu	
D21S11	--	--	28	94 rfu	28	87 rfu	**28,30,31.2**
			30	95 fru	30	30 rfu	
			31.2	61 rfu	31.2	58 rfu	
D18S51	--	--	12	52 rfu	12	12 rfu	**12**
			13 ***	55 rfu	--	--	
D5S818	--	--	9	122 rfu	9	123 rfu	**9,11,12**
			11	75 rfu	11	86 rfu	
			12	129 rfu	12	135 rfu	
D13S317	--	--	11	64 rfu	11	70 rfu	**11**
			12 ***	50 rfu	--	--	
D7S820	--	--	--	--	--	--	**--**

*** Not reproducible.
-- No result.

Profile Classification and Number of Contributors. The profile for sample 20I was classified as a 2-person mixture.

The classification as a 2-person mixture was based upon the observation of three alleles at both D21S11 and D5S818.

To be classified as a three-person would have required the observation of 5 or 6 alleles at one or more loci. However, there was no evidence of 5 or 6 alleles at any locus.

Identification of non-victim alleles. Sample 20I was a swabbing from the skin of the decedent. Therefore, the decedent was an expected contributor to the sample.

A subtraction was performed on the 20I profile using the decedent's DNA profile. At each locus, the decedent's contribution was subtracted from the sample profile to obtain the set of alleles that were attributable to the non-victim contributor to the sample. That subtraction process is outlined in Table 2.

The non-victim contributor was determined to be male based upon the observation of a Amelogenin-Y allele in 20I and the fact that the decedent was female.

All of the alleles attributable to the non-victim contributor were determined to be present at less than the stochastic threshold based upon the observed peak heights in the 5-second injection. Therefore, it was determined that dropout of non-contributor alleles was possible at all loci, except for D21S11 where two non-victim alleles were observed. At D21S11 the non-victim contributor was determined to be the (28,31.2) heterozygote.

Table 2. Sample 20I – Determination of the set of not-excluded genotypes for the non-victim contributor. X = any allele other than the observed allele. INC = inconclusive for homozygosity/heterozygosity, with detected alleles indicated in parentheses. <ST = allele observed at less than the stochastic threshold.

Locus	Sample 20I Reported Profile	Decedent	Non-Victim Contribution - Alleles Detected	Non-victim Contributor	Non-victim Contributor - Set of Not-Excluded Genotypes
D3S1358	**16,17**	14,16	17 (<ST)	**INC (17)**	(17,17) OR (17,X)
vwa	**14,17**	17,18	14 (<ST)	**INC (14)**	(14,14) OR (14,X)
FGA	**21,22**	20,22	21 (<ST)	**INC (21)**	(21,21) OR (21,X)
Amelogenin	**Amel-X, Amel-Y**	Amel-X, Amel-X	Amel-X, Amel-Y	**Amel-X, Amel-Y**	Amel-X, Amel-Y
D8S1179	**11,14**	11,15	14 (<ST)	**INC (14)**	(14,14) OR (14,X)
D21S11	**28,30,31.2**	30,30	28,31.2	**28,31.2**	28,31.2
D18S51	**12**	13,13	12 (<ST)	**INC (12)**	(12,12) OR (12,X)
D5S818	**9,11,12**	11, 12	9 (<ST)	**INC (9)**	(9,9) OR (9,X)
D13S317	**11**	8,10	11 (<ST)	**INC (11)**	(11,11) OR (11,X)
D7S820	**--**	8, 8	--	**--**	--

Inclusion/Exclusion Comparisons. The DNA profiles of each of the known reference samples submitted for testing were compared to the set of not-excluded genotypes for the non-victim contributor to sample 20I. These comparisons are described in Table 3.

At each locus, the DNA profile of Blaine Milam was included in the set of not-excluded genotypes for Sample 20I. Therefore, Blaine Milam was included as a possible source of the non-victim contribution to Sample 20I.

In contrast, the DNA profile of Jessica Carson was excluded from the set of not-excluded genotypes for Sample 20I at six STR loci.

Similarly, the DNA profile of Danny Milam was excluded from the set of not-excluded genotypes for Sample 20I at two STR loci. At D18S51, the non-victim contributor to Sample 20I had a 12 allele, which was not observed in Danny Milam's profile. Similarly, at D5S818 the non-victim contributor to Sample 20I had a 9 allele, which was not observed in Danny Milam's profile.

Table 3. Inclusion/exclusion comparisons for Sample 20I, non-victim contribution.

		Blaine Millam		Jessica Carson		Danny Milam	
Locus	Non-victim Contribution - Not Excluded Genotypes	Profile	Conclusion	Profile	Conclusion	Profile	Conclusion
D3S1358	(17,17) OR (17,X)	16,17	Included	16,17	Included	16,17	Included
vWA	(14,14) OR (14,X)	14,17	Included	17,18	Excluded	14,17	Included
FGA	(21,21) OR (21,X)	21,22	Included	22,23	Excluded	21,22	Included
Amel	Amel-X, Amel-Y	Amel-X, Amel-Y	Included	Amel-X, Amel-X	Excluded	Amel-X, Amel-Y	Included
D8S1179	(14,14) OR (14,X)	11,14	Included	11,11	Excluded	14,14	Included
D21S11	(28,31.2)	28,31.2	Included	28,30	Excluded	28,31.2	Included
D18S51	(12,12) OR (12,X)	12,18	Included	13,16	Excluded	15,18	Excluded
D5S818	(9,9) OR (9,X)	9,12	Included	11,11	Excluded	12,13	Excluded
D13S317	(11,11) OR (11 X)	11,12	Included	10,11	Included	11,12	Included
D7S820	(X, X)	11,13	Included	8,9	Included	11,13	Included

= Included as possible source of the non-victim contribution
= Excluded as possible source of the non-victim contribution

Part 2. Responses to concerns raised by Ms. Cale and Dr. Krane.

1. Ms. Cale states: "… elevating peaks above the stochastic threshold based on a longer injection time does not resolve the underlying problem of potential allele dropout. An allele cannot be confidently interpreted as homozygous merely because the peak height is now above the stochastic threshold; if a sister allele failed to amplify due to stochastic effects, it would remain undetected regardless of injection duration. This significantly limits the interpretability of the profile."

   Response. As made clear in Part 1, the laboratory recognized that profile peaks were in the stochastic dropout range and incorporated this information into the profile interpretation. As a result, the laboratory made no conclusions of homozygosity regarding the non-victim contribution to Sample 20I, based either on the 5-second or 15-second injections.

2. Ms. Cale states: "Given the degree of genetic overlap between Amora Carson, Blaine Milam, Jesseca Carson, and Danny Milam, the limited number of alleles present, and the compromised quality of the data, I believe this sample likely represents at least a three-person mixture, if not a four-person mixture. Under these conditions, the profile is unsuitable for interpretation and statistical calculation."

   Response: With both the 5-second and 15-injections, there is no objective evidence that supports the interpretation of the sample as anything greater than a 2-person mixture. Ms. Cale's belief that the sample is a three- or four-person mixture is therefore speculative and not grounded in the observed profile data.

   It is understandable that Ms. Cale, as an expert for the defense, would make interpretive choices that would tend to benefit the defense's position. However, for the laboratory that approach would be considered unethical. The laboratory's interpretation must be justified based upon objective criteria, and not whether the interpretation benefits one side or the other.

3. Ms. Cale states: "The manner in which this re-interpretation was conducted raises serious concerns about reference-driven analysis. Specifically, the analyst appears to have assigned

alleles to Blaine Milam first and then used those alleles in the subsequent statistical calculation."

Response: As was made clear in Part 1, the interpretation of the electropherogram data was in no way conditioned upon the DNA profile of Blaine Milam. The interpretation of the 5-second and 15-second injection data was based solely on the data collected from Sample 20I, and the parameters for profile interpretation described in the laboratory's protocols.

4. Ms. Cale states: "In this case, the re-interpretation was not performed in a neutral context." She then describes a series of statements made by DA Jimerson in written communications with the laboratory.

   Response: The laboratory's interpretation of Sample 20I was the result of an objective analysis of quantitative instrumental data. Both the data and the interpretation stand on their own and are fully justified based upon objective criteria.

5. Dr. Krane states: "…SWIFS has no protocols for reconciling peak height imbalances or for applying stochastic thresholds to assess the probability of dropout for any injection duration other than five seconds. Without such restrictions placed on its interpretation of sample 20I in this case, SWIFS is non-compliant with SWGDAM guidance and subject to errors of unknown rates and magnitudes."

   Response: As was made clear in Part 1, all non-victim allele peaks in the 15-second injections were determined to be below the stochastic threshold because they were less than the stochastic threshold in the 5-second injection.

   As a consequence, at no locus was the non-victim contributor determined to be homozygous. The laboratory's method is compliant with SWGDAM guidance.

6. Dr. Krane states: "If the assumption that two and only two contributors are present does not hold, the mRMP calculation is an inappropriate calculation of the probability that an unknown person could share the "non-victim" alleles."

   Response: The laboratory's data offers support for two contributors to Sample 20I and provides no support for three or more contributors. The suggestion that three or more contributors may be present in Sample 20I is therefore speculative and unsupported by the data.