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IN THE SUPERIOR COURT OF THE STATE OF CALIFORNIA

IN AND FOR THE COUNTY OF SANTA CLARA

PEOPLE OF THE STATE OF CALIFORNIA, Plaintiff, vs. ANTOLIN GARCIA-TORRES, Defendant.	NO. 213515 Trial Motion No. 3 Supplemental Motion (Motion to Exclude DNA Evidence)

On September 20, 2016, the President's Council of Advisors on Science and Technology (PCAST) released a highly critical report entitled *Forensic Science in Criminal Courts: Ensuring Scientific Validity of Feature-Comparison Methods.*[1] PCAST is a body of highly regarded scientists in the United States, including molecular biologists, physicists, engineers, biologists and biochemists. For the report, PCAST consulted with numerous advisors including two statisticians and prominent judges, researchers at the FBI and NIST as well as forensic scientists and practitioners, judges, prosecutors, defense attorneys, academic researchers, criminal justice reform advocates, and representatives of

[1] [Exhibit X] https://www.whitehouse.gov/sites/default/files/microsites/ostp/PCAST/pcast_forensic_science_report_final.pdf

Federal agencies.[2] The report was in response to a question from the President regarding what scientific steps could be taken to increase the validity and reliability of forensic sciences.

> PCAST concluded that there are two important gaps: (1) the need for clarity about the scientific standards for the validity and reliability of forensic methods and (2) the need to evaluate specific forensic methods to determine whether they have been scientifically established to be valid and reliable. Our study aimed to help close these gaps for a number of forensic "feature-comparison" ***methods—specifically, methods for comparing DNA samples,*** bitemarks, latent fingerprints, firearm marks, footwear, and hair.[3]

PCAST distinguishes between two different types of validity:

> (1) Foundational validity for a forensic-science method requires that it be shown, based on empirical studies, to be ***repeatable, reproducible, and accurate,*** at levels that have been measured and are appropriate to the intended application. ***Foundational validity, then, means that a method can, in principle, be reliable.*** It is the scientific concept we mean to correspond to the legal requirement, in Rule 702(c), of "reliable principles and methods."
>
> (2) ***Validity as applied*** means that the method has been reliably applied in practice. It is the scientific concept we mean to correspond to the legal requirement, in Rule 702(d), that an expert "has reliably applied the principles and methods to the facts of the case."[4]

While acknowledging that the interpretation of single source and simple mixtures (2 individuals with one known contributor for instance), PCAST concludes that the "subjective analysis of complex DNA mixtures has not been established to be foundationally valid and is not a reliable methodology."[5] The basis of this statement is that

> ***DNA analysis of complex mixtures is inherently difficult.*** Such samples result in a DNA profile that superimposes multiple individual DNA profiles. Interpreting a mixed profile is different from and more challenging than interpreting a simple profile, for many reasons. ***It is often impossible to tell with certainty which genetic variants are present in the mixture or how many separate individuals contributed to the mixture, let alone accurately to infer the DNA profile of each one.***[6]

In discussing the overarching concept of validity, PCAST noted that "testimony based on forensic feature-comparison methods [including DNA comparisons] poses unique dangers of misleading jurors for two reasons," first, "[t]he vast majority of jurors have no independent ability to

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[2] *Id.* at viii-x.
[3] *Id.* at x [emphasis added].
[4] [4] *Id.*at 4-5 [emphasis added].
[5] *Id.* at 8, 43.
[6] *Id.* at 8 [emphasis added].

interpret the probative value of results," and second, "[t]he potential prejudicial impact is unusually high, because jurors are likely to overestimate the probative value of a 'match' between samples."[7] The latter concern arises, in part, from the fact that jurors tend to underestimate error rates by orders of magnitude.[8] PCAST suggests that rather than use a term like "match," analysts should use the term "'proposed identification' to appropriately convey the examiner's conclusion, ***along with the possibility that it might be wrong.***"[9]

A. Foundational Validity

"For a metrological method to be scientifically valid and reliable, the procedures that comprise it must be shown, based on empirical studies, to be repeatable, reproducible, and accurate, at levels that have been measured and are appropriate to the intended application."[10]

The PCAST report continues, "valid scientific knowledge can only be gained through empirical testing of specific propositions" and summarizes what empirical testing entails:

> Scientific validity and reliability require that a method has been subjected to empirical testing, under conditions appropriate to its intended use, that provides ***valid estimates of how often the method reaches an incorrect conclusion.*** For subjective feature-comparison methods, appropriately designed black-box studies are required, in which many examiners render decisions about many independent tests (typically, involving "questioned" samples and one or more "known" samples) and ***the error rates are determined. Without appropriate estimates of accuracy, an examiner's statement that two samples are similar—or even indistinguishable—is scientifically meaningless: it has no probative value, and considerable potential for prejudicial impact. Nothing—not training, personal experience nor professional practices—can substitute for adequate empirical demonstration of accuracy.***[11]

Below is a box taken from the PCAST report defining the terms underlying validity.[12]

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[7] *Id.* at 45.
[8] *Id.*
[9] *Id.* at 46 [emphasis added]
[10] *Id.* at 47.
[11] *Id.* at 46.
12 Id. at 47-48

BOX 2. Definition of key terms

By "repeatable," we mean that, with known probability, an examiner obtains the same result, when analyzing samples from the same sources.

By "reproducible," we mean that, with known probability, different examiners obtain the same result, when analyzing the same samples.

By "accurate," we mean that, with known probabilities, an examiner obtains correct results both (1) for samples from the same source (true positives) and (2) for samples from different sources (true negatives).

By "reliability," we mean repeatability, reproducibility, and accuracy.[107]

By "scientific validity," we mean that a method has shown, based on empirical studies, to be reliable with levels of repeatability, reproducibility, and accuracy that are appropriate to the intended application.

By an "empirical study," we mean test in which a method has been used to analyze a large number of independent sets of samples, similar in relevant aspects to those encountered in casework, in order to estimate the method's repeatability, reproducibility, and accuracy.

By a "black-box study," we mean an empirical study that assesses a subjective method by having examiners analyze samples and render opinions about the origin or similarity of samples.

To meet the scientific criteria of foundational validity, two key elements are required:

> (1) a ***reproducible and consistent procedure*** for (a) identifying features within evidence samples; (b) comparing the features in two samples; and (c) determining, based on the similarity between the features in two samples, whether the samples should be declared to be a proposed identification ("matching rule").
> (2) ***empirical measurements,*** from multiple independent studies, of (a) the ***method's false positive rate***—that is, the probability it declares a proposed identification between samples that actually come from different sources and (b) the ***method's sensitivity***—that is, probability that it declares a proposed identification between samples that actually come from the same source.[13]

1. **Reproducible and Consistent Procedures**

Subjective methods, such as the interpretation and comparison of complex DNA mixtures, require careful scrutiny because of "their heavy reliance on human judgment [which] means that they are especially vulnerable to human error, inconsistency across examiners, and cognitive bias." When conducting feature comparisons, "cognitive bias includes the phenomena that, in certain settings, humans (1) may tend naturally to focus on similarities between samples and discount differences and

[13] *Id.* at 48 [emphasis added].

(2) may also be influenced by extraneous information and external pressures about a case."[14] "[F]oundational validity of subjective methods can be established only through empirical studies of examiner's performance to determine whether they can provide accurate answers; such studies are referred to as 'black-box' studies."[15]

2. Empirical Measurements of Accuracy

In order to assess accuracy, it is necessary to have empirical studies of a methods false positive rate and sensitivity. Measurement of error -- false positives -- is essential in assessing the probative value of the evidence. "The false positive rate is the probability that the method declares a proposed identification between samples that actually come from different sources."[16]

A methods sensitivity is

> the probability that the method declares a proposed identification between samples that actually come from the same source. For example, a sensitivity of 90 percent means two samples from the same source will be declared to come from the same source 90 percent of the time, and declared to come from different sources 10 percent of the time.[17]

False positives occur from two different causes. The first is "coincidental matches (where samples from different sources nonetheless have features that fall within the tolerance of the objective matching rule) and [the second is] human/technical failures (where samples have features that fall outside the matching rule, but where a proposed identification was nonetheless declared due to a human or technical failure)."[18] "An empirical measurement of error rates is not simply a desirable feature; it is essential for determining whether a method is foundationally valid."[19] The reason an error rate is essential is that without knowing an empirical measure of the methods accuracy, the evidence has no probative value.[20]

For subjective methods, the two types of errors cannot be distinguished because there is no objective matching rule, thus requiring that "black box" assessments of overall error be conducted.[21]

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[14] *Id.* at 49.
[15] *Id.* at 49.
[16] *Id.* at 50 [emphasis original].
[17] *Id.* at 50.
[18] *Id.* at 50.
[19] *Id.* at 53. The error rate cannot be determined through case work analysis.
[20] *Id.*
[21] *Id.* at 51.

Validation studies with pre-set parameters and sufficient number of samples can be used to determine error rates, but must be conducted with "representative of the quality of evidentiary samples seen in real cases," and "should be conducted so that neither the examiner nor those with whom the examiner interacts have any information about the correct answer."[22]

The PCAST report concludes that "experience" or "judgment" cannot be a substitute for empirical studies because experience with forensic case work in which the answer is not known, "cannot accurately [reflect] how often [analysts] erroneously declare matches and cannot readily [allow the analysts to] hone their accuracy by learning from their mistakes in the course of casework."[23]

> good professional practices—such as the existence of professional societies, certification programs, accreditation programs, peer-reviewed articles, standardized protocols, proficiency testing, and codes of ethics—cannot substitute for actual evidence of scientific validity and reliability.[24]

An experts "confidence" based on experience, or "consensus" among analysts in the field that of the methods accuracy, also cannot substitute for empirical evidence of validity.[25]

3. Requirement for Scientifically Valid Testimony

Even when a method has been shown to be foundationally valid, expert should show restraint when testifying.

> Forensic examiners should therefore report findings of a proposed identification with clarity and restraint, explaining in each case that the fact that two samples satisfy a method's criteria for a proposed match does not necessarily imply that the samples come from a common source.[26]
>
> From the standpoint of scientific validity, experts should never be permitted to state or imply in court that they can draw conclusions with certainty or near-certainty (such as "zero," "vanishingly small," "essentially zero," "negligible," "minimal," or "microscopic" error rates; "100 percent certainty" or "to a reasonable degree of scientific certainty;" or identification "to the exclusion of all other sources."[27]

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[22] *Id.* at 52.
[23] *Id.* at 55.
[24] *Id.* at 55.
[25] *Id.*
[26] *Id.* at 54.
[27] *Id.*

B. Validity as Applied

When a method has been shown to be foundationally valid, it must still be shown to be valid as applied. The PCAST report explains validity as applied as being the intersection of science and the law. Validity as applied is "the scientific concept we mean to correspond to the legal requirement, in Rule 702(d), that an expert 'has reliably applied the principles and methods to the facts of the case.'"[28] In order to show validity as applied, the PCAST Report describes a number of key criteria.

The first is "[d]emonstrating that an examiner is capable of reliably applying the method …especially for subjective methods, in which human judgment plays a central role. From a scientific standpoint, the ability to apply a method reliably can be demonstrated only through empirical testing that measures how often the expert reaches the correct answer."[29]

In order to establish this first criteria, the lab must conduct proficiency testing which is defined as "ongoing empirical tests to 'evaluate the capability and performance of analysts.'"[30] The proficiency test should done under conditions representative of casework, and on samples that are representative of the full range of sample types and quality likely to be encountered in casework in the intended application and the testing preferably be done in a blind manner where the analyst is not aware that he or she is being tested.[31]

The second criteria is that "[a]ssertions about the probability of the observed features occurring by chance must be scientifically valid."[32] In order to demonstrate this,

> (a) The forensic examiner should report the overall false positive rate and sensitivity for the method established in the studies of foundational validity and ***should demonstrate that the samples used in the foundational studies are relevant to the facts of the case.***
> (b) Where applicable, the examiner should report the random match probability based on the specific features observed in the case.
> (c) An expert should not make claims or implications that go beyond the empirical evidence and the applications of valid statistical principles to that evidence.[33]

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[28] *Id.*
[29] *Id.* at 56.
[30] *Id.* at 57.
[31] *Id.* at 57-58. The PCAST report concludes that at this point in time it is unrealistic to impose a blind proficiency testing requirement.
[32] *Id.* at 56.
[33] *Id.* at 56 [emphasis added].

C. Foundation and As Applied Validity of DNA in complex mixtures

PCAST applied the above standards to DNA testing and concluded that while single source and simple two person mixtures, met their standards for both foundational and applied validity, complex mixtures did not.[34] In reaching this conclusion, the report described the subjective nature of the analysis of a complex mixture.

> DNA analysis of complex mixtures—defined as mixtures with more than two contributors—is ***inherently difficult*** and even more for small amounts of DNA. Such samples result in a DNA profile that superimposes multiple individual DNA profiles. Interpreting a mixed profile is different for multiple reasons: each individual may contribute two, one or zero alleles at each locus; the alleles may overlap with one another; the peak heights may differ considerably, owing to differences in the amount and state of preservation of the DNA from each source; and the "stutter peaks" that surround alleles (common artifacts of the DNA amplification process) can obscure alleles that are present or suggest alleles that are not present. ***It is often impossible to tell with certainty which alleles are present in the mixture or how many separate individuals contributed to the mixture, let alone accurately to infer the DNA profile of each individual.***[35]

The subjectivity of the process continues when the analyst must make decisions about which alleles to include in their statistical analysis. The PCAST report points to a number of articles and incidents in which DNA analysts were provided with the same data but came to very different conclusions as well as statistical weight for the evidence.[36] The articles found that when presented with the same data, analysts reported wildly different conclusions from inconclusive to inclusion to exclusion of the suspect.

The report also points to issues in Texas, where reanalysis of the statistics associated with case work resulted in large shifts in reported statistics, primarily due to changes made by labs in "how they dealt with phenomena such as 'allelic dropout' at particular DNA loci."[37]

In response to the issues articulated above, some authors have begun to formulate "rules" for

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[34] *Id.* at 75. Interesting, the report appears to define "simple mixtures" at those which include at least one known individual who can be subtracted out to allow interpretation of the second individual. *Id.* at 70, 73.
[35] *Id.* at 75-76 [emphasis added].
[36] *Id.* at 77 [citing de Keijser, J.W., Malsch, M., Luining, E.T., Kranenbarg, M.W., and D.J.H.M. Lenssen. "*Differential reporting of mixed DNA profiles and its impact on jurists' evaluation of evidence: An international analysis.*" **Forensic Science International: Genetics**, Vol. 23 (2016): 71-82 [Exhibit Y]; Dror, I.E., and G. Hampikian. "*Subjectivity and bias in forensic DNA mixture interpretation.*" **Science & Justice**, Vol. 51, No. 4 (2011): 204-8. [Exhibit Z].
[37] PCAST Report, *supra*, at 78.

interpretation.[38] The report notes that these rules are "necessary" but that given the timing of the publication, PCAST had not been able to assess whether the proposed rules were "sufficient to define an objective and scientifically valid method."[39] In addition to the attempt to define a new set of interpretation rules to mixtures, some have produced what is known as Probabilistic Genotyping Software (PGS) in order to standardize mixture interpretation. However, as noted by the PCAST report, these different software packages have been subjected to limited validation, primarily by the developers of the software and on mixtures that are "less challenging."[40]

D. Application of the PCAST Report in this case.

This Court should give the PCAST Report great weight in determining the admissibility of the DNA evidence in this case. The members of PCAST are some of the most influential scientists in the United States. For instance, the chair of the working group that produced the report is Eric Lander. Dr. Lander is president and founding director of the Broad Institute of MIT and Harvard. He is a geneticist, molecular biologist, and mathematician, and has played a pioneering role in all aspects of the reading, understanding, and biomedical application of the human genome. He was a principal leader of the international Human Genome Project from 1990 to 2003, with his group being the largest contributor to the mapping and sequencing of the human genome. Dr. Lander is professor of biology at MIT and professor of systems biology at Harvard Medical School. He has served on governing and advisory boards for various government agencies, academic institutions, and scientific societies, and has co-founded several successful biotechnology firms. Dr. Lander's numerous honors and awards include the MacArthur Fellowship, the Woodrow Wilson Prize for Public Service from Princeton University, the City of Medicine Award, the Gairdner Foundation International Award of Canada, the AAAS Award for Public Understanding of Science and Technology, the Albany Prize in Medicine and Biological

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[38] *Id.* at 78 [citing Bieber, F.R., Buckleton, J.S., Budowle, B., Butler, J.M., and M.D. Coble. "*Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion.*" **BMC Genetics**. bmcgenet.biomedcentral.com/articles/10.1186/s12863-016-0429-7][Exhibit AA].

[39] PCAST Report, at 78. The PCAST report focuses on the use of the CPI statistical analysis and does not address the use of the LR statistic that is applied by SCCCL in this case. Regardless, the same issues of interpretation including determining the number of contributors, the application of the ST to the data and the assumptions of allelic drop-out and other stochastic effects are similar in the use of the LR.

[40] *Id.* at 81.

Research, the Dan David Prize of Israel, the Mendel Medal of the Genetics Society in the UK, the Breakthrough Prize in Life Sciences, and the James R. Killian Jr. Faculty Achievement Award.

Another member of PCAST is Sylvester James Gates Jr., who is a Distinguished University Professor, University System of Maryland Regents Professor and John S. Toll Professor of Physics at the University of Maryland. Dr. Gates is known for his pioneering work in supersymmetry and supergravity, areas closely related to string theory. Dr. Gates earned two Bachelor of Science degrees in physics and mathematics and his Ph.D. in physics from the Massachusetts Institute of Technology.

Dr. William Press is the Warren J. and Viola M. Raymer Professor in Computer Science and in Integrative Biology at the University of Texas at Austin. He is affiliated with the Institute for Cellular and Molecular Biology (ICMB) and in the Institute for Computational Engineering and Sciences (ICES). Dr. Press is also a Senior Fellow (emeritus) at the Los Alamos National Laboratory (LANL) in the Statistical Sciences group. His research is on computational biology, genomics, and computational statistical methods. Prior to June, 2004, he served for five years as LANL's Deputy Laboratory Director for Science and Technology. Before that, he was a Professor of Astronomy and Physics at Harvard University, and a member of the Harvard-Smithsonian Center for Astrophysics for twenty years.

Additionally, one of the most respected researchers on issues relating to forensic DNA testing, Dr. John Butler, concurred in the conclusions drawn by PCAST the analysis of complex mixtures is not foundationally valid.[41]

While the PCAST Report focuses on the federal standard of admissibility found in Daubert,[42] which is different than California's Kelly standard, the reasoning of the report applies to Kelly[43] as well. As set forth in our Motion to Exclude DNA Evidence, the first prong of the Kelly test is that:

> It must be established, usually by expert testimony, that the scientific methods utilized are generally accepted as ***reliable by the relevant scientific community.***[44]

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[41] *Id.* at 81.
[42] *Daubert v. Merrell Dow Pharmaceuticals* (1993) 509 U.S. 579.
[43] *People v. Kelly* (1976) 17 Cal.3d 24
[44] *Kelly, supra*, 17 Cal.3d at p. 30 [emphasis original].

Scientific validity is defined as defined by PCAST is when a method has been shown, "based on empirical studies, to be reliable with levels of repeatability, reproducibility, and accuracy that are appropriate to the intended application."[45] This definition falls squarely into the reasoning of Kelly which requires not only general acceptance, but that acceptance is premised on the method being reliable.[46]

The process of interpretation and comparison of DNA samples has been described as:

> Profile interpretation and CPI calculation involves three steps: assessment of the profile, comparison with reference profiles and inclusion/exclusion determination, and calculation of the statistic.[47]

Although this paragraph mentions CPI calculations, the same steps, assessment, comparison and inclusion/exclusion, and calculation of a statistics, are the same steps carried out at SCCCL when interpreting mixtures and applying a LR statistic. And when using the LR statistic, unlike the CPI, assumptions must be made on the number of contributors to the sample in order to apply the statistical analysis. As described in the Defendant's moving papers, the task of determining the number of contributors is not an easy one, and if the underlying assumption is incorrect, the statistical analysis will also be incorrect.

As the PCAST report noted: "DNA analysis of complex mixtures—defined as mixtures with more than two contributors—is inherently difficult and even more for small amounts of DNA."[48] As Dr. Butler stated in 2014, "[d]ata interpretation uncertainties are highest and errors are most likely to be made in situations with DNA mixtures from three or more individuals, especially with low-template DNA 'touch' samples."[49] He continues "[w]ith greater sensitivity comes the need for greater responsibility in data interpretation. Unfortunately, inconsistencies with handling DNA interpretation of complex mixtures adds to the challenge of obtaining reproducible results from multiple analysts and/or forensic laboratories."[50] Dr. Butler is not alone in this concern. In a recent paper cited in the PCAST Report, the authors begin their discussion with the following:

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[45] PCAST Report, *supra*, at 48 [emphasis added].
[46] *Id.* at 42, n.90.
[47] Exhibit AA, at 2 or 15.
[48] *Id.* at 75.
[49] Exhibit R, at 5.
[50] *Id.*

> The evaluation and interpretation of forensic DNA mixture evidence faces greater interpretational challenges due to increasingly complex mixture evidence. Such challenges include: ***casework involving low quantity or degraded evidence leading to allele and locus dropout; allele sharing of contributors leading to allele stacking; and differentiation of PCR stutter artifacts from true alleles.***[51]

In our case, all but one sample tested by the lab, which appear to be relevant to the prosecution case, resulted in complex mixtures of at least three individuals. As set forth in Defendant's moving papers, samples taken from a pair of jeans, Item 169108 (samples 169108-5ec, 169108-12, 169108-13), swabs taken from the exterior of a glove, Item 170206-R, a swab of rear driver door interior arm rest, Item S7, ***all yielded complex mixtures of at least three individuals,*** all of the samples exhibited low level peaks in the stochastic range with some samples requiring the invocation of allelic drop-out, an artifact of LT DNA testing, in order to reach an opinion of inclusion. There is no doubt that these samples as described by SCCCL in their reports, fall within the definition of complex mixtures as defined by the PCAST Report.

Item 169108-5ec is an example of the difficulty of interpretation of a complex mixture.

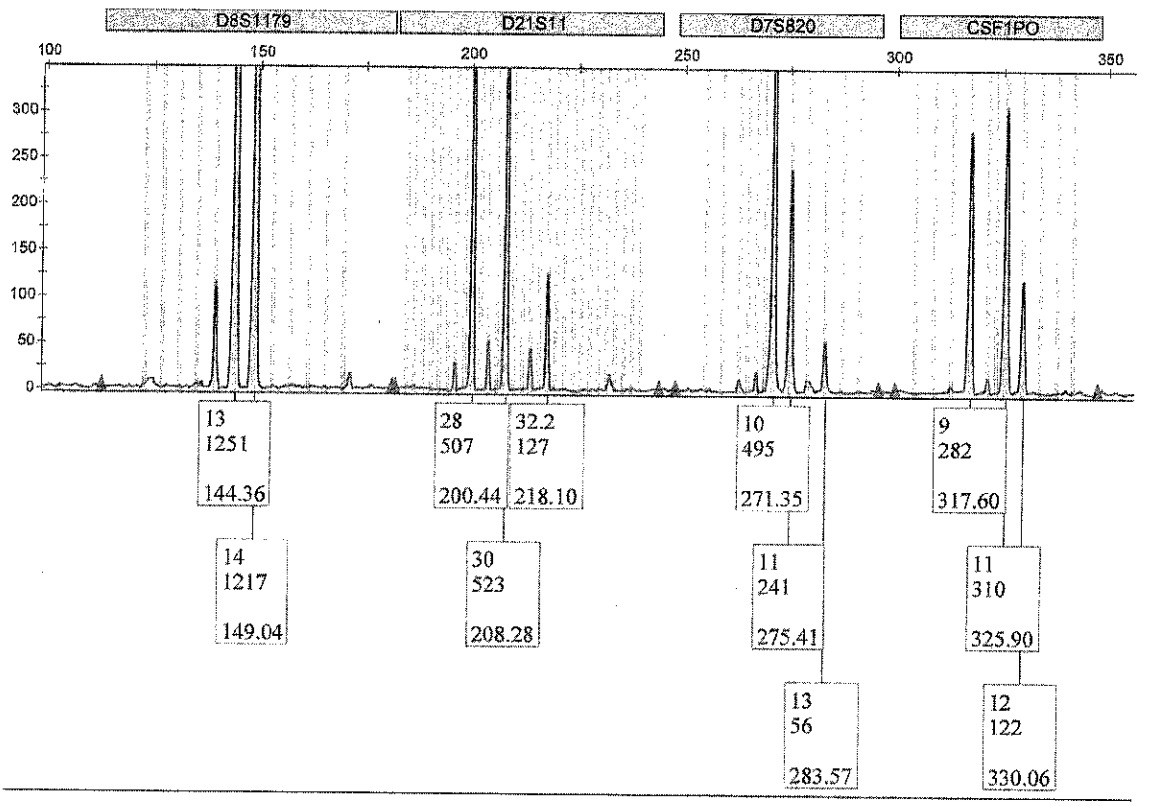
> ASSUMPTION: Three individuals are being detected in this profile. Although additional Y-STR data indicates four contributors (three males plus Sierra LaMar has already been determined to be the major contributor) the Y-STR kit is more sensitive than the autosomal kit and therefore the third minor Y contributor that was detected at one locus in the Y profile is most likely not being detected in the autosomal profile. The assumption in this calculation is that the third male contributor IS NOT being detected. This is 10 second injection."

In their initial testing, SCCCL described and interpreted this samples as being a mixture "of at least three individuals (including at least one male).[52]" The lab report stated that "Sierra LaMar is included as a possible major contributor to her own jeans."[53] Based on the assumption of three contributors,[54] the lab "deduced" a profile which was searched against the state CODIS database.[55] Later testing of the same sample with Y-STR (which tests only male DNA in the sample), the lab reported that the testing revealed a "mixture consisting of at least three males."[56] The Y-STR result was obtained prior to the

[51] Exhibit AA, *supra* [emphasis added].
[52] Bates Lab 0099
[53] *Id.*
[54] It appears that the lab assumed three contributors when the deduced profile was interpreted. However, no contemporaneous notes indicating the assumptions were made.
[55] Bates Lab 0099, 4466-4471
[56] Bates Lab 0447

statistical analysis of this sample and noted, however, when stating the assumptions for calculation of the LR, the analyst stated:[57] If, the assumption of only three contributors for the Identifiler Plus testing is incorrect, then the interpretation and statistical analysis may also be incorrect. Additionally, although not stated in the lab's notes, it appears that the lab also assumed only three contributors when deducing the profile uploaded to the state database.

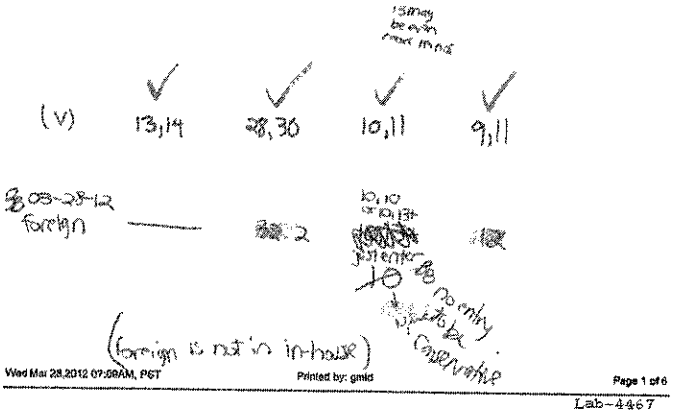
Much of the data falls within the stochastic range of the test for this sample. Below is one set of data from 169108-5ec.[58]



SCCCL's stochastic range for a 10 second injection ranges from 300-400 rfu.[59] Much of the data falls below this threshold. Again, however, there is no indication in the notes what threshold was applied during this process and how many contributors were assumed. In addition, although the lab report states "at least three" contributors, the assumption of only three first appears in the notes from the statistical analysis.

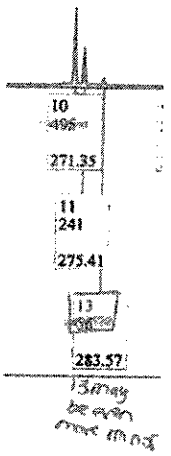
[57] Bates Lab 0309
[58] Bates Lab 0149
[59] Again, there are no indications in the notes for the interpretation of this sample as to the exact rfu value applied to this interpretation.

One set of notes from the deduction of the uploaded profile are show below.



The notes show that at certain loci, the lab was unsure of their interpretation. At locus D8, the lab found two peaks that are consistent with Sierra LaMar. The, as shown up on the far left hand side of the image, chose not to interpret this locus for upload.

At D7, the data showed three alleles, 10, 11 and 13. Sierra LaMar is a 10, 11. Again the lab showed uncertainty and chose to upload nothing, even though the 13 allele is foreign to Sierra LaMar, because looking at the data below, the 10 and 11 alleles are unbalanced, meaning that either the data is suffering from stochastic effect, or there is one or perhaps two other individuals in the mixture that have that 10 as well. This is the issue described in the PCAST report of allele stacking. Given this data, there is no way to tell what is causing this imbalance. The lab chose not to interpret this data for upload to the database.



These same issues appear at additional loci.

The SCCCL's protocols are minimal in addressing the issue of mixture interpretation and allow analyst great leeway to use their "training and experience" in the process. In the introduction to the lab manual it states:

> This manual has been compiled as a basic information source and is not intended as a substitute for proper training. The methods described require that they be used in association with adequate training in the subject and with knowledge of how to interpret the results obtained.
>
> It is recognized that every case and every exhibit is unique. In forensic science, the individual skill, judgment, and experience of the scientist should determine what specific tests are required in each instance.[60]

Much of the protocol is written expressly to allow analysts to use their training and experience and does not create what PCAST described, a reproducible and consistent procedure for identification and comparison. In defining the stochastic threshold the manual states:

> As a general guideline single peaks should not be called as homozygote alleles unless the peak is above 200 rfu for standard and reduced injection times, and above 300 rfus (larger loci) - 400 rfu (smaller loci) for enhanced injection times. Different stochastic thresholds can be applied to individual loci. ***The assignment of stochastic thresholds should be made with the following in mind***: presence of degradation and/or inhibition, zygosity and peak heights at flanking loci, stutter, and allele size. The threshold for a particular locus should generally not exceed the threshold set for a smaller locus within the same dye channel. Loci of similar size in different dye channels should have similar thresholds. Selection of the stochastic threshold should be documented and justified when necessary.[61]

Although the paragraph states what should be considered in setting the threshold, the manual does not offer any guidance in how to assess the various criteria set forth. For instance, what should the analyst consider and how should they act when assessing whether there is degradation or inhibition? This type of protocol allows the analyst far too much leeway. An interesting change to this paragraph can be found in the latest protocol, where this sentence has been added:

> These thresholds were determined using low level single source samples and may not be suitable for all mixture samples.[62]

The problem with this language is that while providing a cautionary statement, the manual offers no guidance to the analyst in assessing whether or not the stochastic threshold is correctly applied to the

[60] FB Manual, Introduction, pg 1 of 2 (Issue date: 11/16/2010, rev. 1)
[61] FB Manual, Interpretation, Sec. 21, pg 9 of 31 (Issue date: 11/16/20; rev 8)
[62] FB Manual, Interpretation, Sec. 21 pg 9 of 32 (Issue date: 11/16/20; rev 10)

sample at issue. If the stochastic threshold was set on low level single source sample, then how can it be applied to complex mixtures? The protocol offers no criteria for this assessment or an alternative threshold for the particular sample in question. Rather than having a procedures that are reproducible and consistent, the analyst is left to rely upon his or her training. As clearly articulated in the PCAST report, training and experience are no substitute for empirical studies and reproducible and consistent protocols.

In a section labeled Profile Characterization, the terms inhibition and degradation are described, but again, there are no criteria that an analyst can apply to assess the impact of either on the sample and what should be done if either is suspected or deemed to be present.[63]

Additional examples of this type of language are found throughout the manual. The lab has an analytical threshold which is set at 150 rfu. However, the same paragraph that defines that threshold also states that "[p]eaks below this level (50-149 rfus) can be interpreted with caution."[64] There is nothing in the manual such as objective criteria which provides an analyst with a procedure to determine is data that falls below the analytical threshold is appropriate for interpretation. There also is no discussion of what the word "caution" means in this context, and in this case all of the samples relevant to the prosecution theory have been analyzed below this threshold.

The only guidance offered in determining the number of contributors to the sample in the manual is:

> For autosomal STRs, the minimum number of contributors in a mixed sample is typically determined by taking the locus with the most alleles above the analytical threshold, and dividing by two (to represent the possibility that all contributors are heterozygous).[65]

The manual address the interpretation of mixtures in a relatively short section of the interpretation section and prefaces the mixture resolution with the following:

> It should be noted that mixture deconvolution can be aided by guidelines and mathematical calculations; ***however there will be instances that require an analyst to draw upon his or her training, experience, and knowledge to determine possible contributors to a mixture.***[66]

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[63] *Id.* at pg 15-16 of 32.
[64] *Id.*at pg 8 of 32.
[65] FB Manual, Interpretation, Sec. 21, pg 18 of 31 (Issue date: 11/16/2010; rev. 8)
[66] *Id.* at pg 19 of 31 [emphasis added].

In addressing the type of mixture found here, a complex mixture of at least three individuals, the manual states:

> Major/minor mixtures are commonly seen in samples with more than two individuals. In the case where the profile consists of one major and ***more than one minor contributor, it may be possible to deduce to the major contribution,*** taking into account peak height ratio expectations, an evaluation of all potential genotypic combinations, size of alleles at flanking loci, stutter, allelic drop-out, allele sharing/masking, presence/absence of degradation and/or inhibition. ***Resolving the multiple minor contributors in this situation is challenging and would rarely be appropriate.***[67]

Here in sample 169108-5ec, the "deduced" profile uploaded into CODIS is from one of two minor contributors, as something that "would rarely be appropriate.

Additionally, in conducting its validation, SCCCL did mixture and sensitivity studies. As articulated in the latest version of the lab manual, the sensitivity study was done on single source low level samples. The mixture study was also restricted to examining mixtures of two individuals.[68] The mixture study "will establish the mixture ratio at which the minor component drops out and will determine if the peaks heights can be used to accurately estimate the mixture ratio."[69] The lab selected for the study four reference samples to test in various mixtures, and it appears that they did not conduct any studies on mixed samples with three or more individuals or on samples from degraded or inhibited DNA.

The PCAST Report states in no uncertain terms that the empirical studies that must be done to establish foundational validity of a method must be conducted on samples that reflect the types of samples seen in the actual use of the method, namely in testing complex mixtures. Since the validation study did not address this fundamental question, they cannot assert that they have validated the use of the Identifiler Plus kit on complex mixtures such as the ones here.

Additionally, the lab has not established an error rate even though in its validation studies on mixtures and single source samples, it reports that allelic drop-out occurred at low levels and that alleles that were not part of the actual known profiles, did appear. This latter could be from contamination or

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[67] *Id.* [emphasis added].
[68] Identifiler Plus Validation-Sensitivity, Mixtures and Known Sample studies, at 302-303 of 736. The documents provided from SCCCL are not Bates stamped so will be referred to as the pdf name and page number.
[69] *Id.* at 302.

the stochastic effect known as allelic drop-in. In a case sample, this type of occurrence would not be apparent because by definition, the results are unknown. The lab must establish a false positive error rate in order to assess the foundational validity of the testing done in the lab. That has not been done in this case.

CONCLUSION

Samples from the jeans (169108-12,[70] 169108-13), the glove (170206-R) and the interior armrest (S7) are all complex mixtures of at least three individuals. All have data in the stochastic range defined by the lab. Based on the conclusions in PCAST Report, the lack of rigor in the lab's protocols, and the inadequate validation studies, these samples and the conclusions drawn by the lab have no foundational validity and should be inadmissible under both the *Kelly* and *Daubert* standards of admissibility.

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Respectfully submitted,

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[70] The report for Item 169108-12 states that there is a mixture of at least two individuals but if an assumption that Sierra LaMar and Mr. Garcia-Torres are present, then there must be at least three individuals. This is because alleles are certain loci are inconsistent with either individual. If this assumption is incorrect, then the lab is basing their interpretation, conclusion and statistics on a false premise.