BONNIE M. DUMANIS
SAN DIEGO COUNTY DISTRICT ATTORNEY

August 18, 2016

Dear Counsel:

Earlier this year I established the Conviction Review Unit (CRU), which is staffed by two attorneys dedicated to examining post-conviction claims of innocence where credible and verifiable evidence of innocence exists, or where new technologies exist to test, retest or reassess remaining evidence. This type of work is not new for the office. In the early years of DNA testing the office initiated an unprecedented DNA Project—individuals previously convicted of serious crimes were offered DNA testing of biological evidence collected in their case. The Project was spearheaded by George "Woody" Clarke, and for whom the CRU is named.

As you know, DNA technology and testing methodologies have continued to advance over the years and will continue to do so. DNA analysis has moved from single source testing through the beginning of DNA mixture testing, and on to more complex touch DNA testing. These advancements benefit everyone, allowing those who commit crimes to be brought to justice and also protect the innocent before and well after trial. All of us should be familiar with the latest DNA testing guidelines that are utilized by our local crime labs to interpret DNA.

As you may know, the Scientific Working Group for DNA Analysis Methods (SWGDAM) is the independent scientific committee that provides quality assurance recommendations for forensic DNA analysis. In 2010, SWGDAM published DNA mixture interpretation guidelines. While the guidelines were simply recommendations, they were adopted by both the San Diego Police Department Forensic Biology Unit and the San Diego County Sheriff's Forensic Biology Section—state of the art and well-respected labs within the scientific community.

As the attached documents from the SDPD and SDSO labs further explain, the 2010 SWGDAM guidelines are a continuation of past practices. Furthermore, the guidelines alter how minor DNA contributors are interpreted and which DNA markers will be used for statistical calculations on inclusions. More simplistically, the guidelines have the potential to change the statistics and conclusions in mixture cases in which DNA testing occurred prior to the adoption of these guidelines. If you handled a case involving a DNA mixture prior to 2010 that you believe could be impacted by these mixture interpretation guidelines, please feel free to contact the Conviction Review Unit at CRU@sdcda.org.

Also, as you may already know, there are more recent developments in forensic DNA testing. For a decade and an half, the Combined DNA Index System (CODIS) has required 13 core loci for searching within the National DNA Index System (NDIS). CODIS has grown tremendously during that time, with more than fourteen million samples currently in the database. Due to the sheer size of the database, CODIS is expanding its core loci to 20 in order to reduce the number of adventitious matches, which will allow more efficient searching of profiles internationally, and increase the power of discrimination.

More mixtures can then be searched. The new requirement goes into effect on January 1, 2017, for every CODIS lab in the US, including the SDPD and SDSO labs.

Advancements in forensic DNA testing improve our criminal justice system as a whole. Though we may be adversaries in the courtroom, we share the same interest in protecting the innocent before, during, and after trial. I am proud of the professional working relationship we have forged together and look forward to working cooperatively in the future.

Sincerely,

Bonnie M. Dumanis

Bonnie M. Dumanis
San Diego County District Attorney

THE CITY OF SAN DIEGO

DATE: May 4, 2011

TO: Sophia Roach, Assistant Chief Appellate Division, San Diego County District Attorney's Office

FROM: Shawn Montpetit, DNA Technical Manager

SUBJECT: New DNA Interpretation Guidelines at the San Diego Police Department

---

In April the San Diego Police Department's (SDPD's) Forensic Biology Unit implemented an improved DNA testing kit for forensic casework. The validation of this new testing kit spanned several months and was conducted in accordance with the quality assurance guidelines for DNA testing labs (Scientific Working Group for DNA Analysis Methods - SWGDAM 2009). As part of the internal assessment, experiments were performed to provide the foundational data for the interpretation guidelines that would be used in forensic casework for the new testing kit.

In June 2010, SWGDAM published a set of mixture interpretation guidelines to provide guidance to the forensic DNA community. The San Diego Police Department's Forensic Biology Unit used this document as a basis for the interpretation guidelines for the new testing kit. The published SWGDAM mixture interpretation guidelines are largely a clarification of existing guidelines and recommendations and some points SWGDAM deemed warranted further explanation.

The interpretation guidelines implemented with the new DNA testing kit reflect changes made in accordance with the published SWGDAM documents as well as changes based on the data obtained from the extensive validation effort by the SDPD laboratory. The interpretation guidelines employed for the previous DNA testing kit were based on validation experiments as well as the combined knowledge and experience obtained through years of analysis.

Outlined below is a summary of the differences between the old and new SDPD guidelines organized by the sections of the SWGDAM mixture interpretation document.

1. Preliminary Evaluation of Data

The SDPD laboratory has always employed the recommended controls and had thresholds in place for DNA testing. The new testing kit, through its improved formulation has a better signal-to-noise ratio and has allowed the laboratory to lower the detection threshold slightly from that of the previous testing kit.

2. Allele Designation
The new SDPD guidelines document practices that have always been employed by the laboratory. The current guidelines do not differ from the previous guidelines to any significant degree.

3. Interpretation of DNA Typing Results
The SDPD laboratory has had the same basic definitions and practice of identifying artifact data and has been performing analyses in the manner section 3 of the SWGDAM mixture guidelines indicates since the implementation of Short Tandem Repeat (STR) testing. The new guidelines further refine many points addressed in section 3 and document practices that had not been formally addressed in prior SDPD interpretation guidelines.

SDPD validation studies have always contained data on peak height ratios; although the validation studies performed on the new testing kit exceed those that have been done in the past. The laboratory has had data for the stochastic thresholds for the kits we employ since approximately 2006 and have continued the practice with the validation of the new testing kit.

The laboratory previously refined mixture interpretation in August 2009 in response to the audit document published by SWGDAM. The 2009 changes involved creating a more defined method of determining major/minor contributors in mixtures and implementing a more consistent method for performing statistical analyses on minor contributor inclusions (modified again with the 2011 SDPD guidelines).

The new interpretation guidelines (2011) provide more detail about making assumptions and handling mixtures of DNA as well as provide additional statistical options (see section 5). A change in the SDPD interpretation guidelines relates to section 3.6.1 of the SWGDAM mixture guidelines, and specifically how comparisons are made with evidence samples.

4. Statistical Analysis of DNA Typing Results
The SDPD laboratory has always used the listed statistical approaches to dealing with mixtures of DNA. The new guidelines provide additional information and guidance to analysts in applying these approaches. Another change to the SDPD interpretation guidelines relates to section 4.6.3 of the SWGDAM mixture guidelines, specifically dealing with how statistics will be performed on samples with low level data when no assumptions can be made about a mixture.

5. Statistical Formulae
The SDPD laboratory has always used the statistical formulae recommended in the National Research Council's 1996 report (*The Evaluation of Forensic DNA Evidence – National Academy Press – 1996*) cited in the SWGDAM mixture guidelines. In August of 2010, the SDPD adopted the ability to use the 2p formula (SWGDAM Mixture Guidelines 5.2.1.3) to deal with situations of undetermined zygosity. The new SDPD guidelines continue the use of 2p and in addition provide information for the use of Random Match Probabilities in DNA mixtures.

In conclusion, the new SDPD mixture interpretation guidelines are a more detailed continuation of past practices employed, some not previously codified, and they provide additional information with respect to utilizing the various statistical options available. The main changes concern how comparisons are made to the evidence and which markers can be used for statistics in samples with low level data when no assumptions can be made. The effect of these changes

will be to alter how minor DNA contributors are interpreted and which DNA markers will be used for statistical calculations on inclusions. It is likely the new SDPD guidelines will result in more samples that cannot be interpreted due to their complexity and/or low level. With regards to the statistical significance applied to inclusions, samples where no assumptions can be made may have more common inclusion statistics estimates, whereas samples for which assumptions can be made are may have more discriminating inclusion statistics provided in the report.

Shawn Montpetit
DNA Technical Manager
SSDPD Crime Laboratory

Patrick O'Donnell
Supervising Criminalist
SDPD Crime Laboratory

San Diego County Sheriff's Forensic Biology Section's current compliance with SWGDAM's DNA Interpretation Guidelines

This document was written to clarify Sheriff's Crime Lab's compliance with the new SWGDAM Interpretation Guidelines (compliance may be either through our practices and/or protocols in our manual). Our current interpretation methods are based on our validation studies, scientific literature, and the collective experience of our casework qualified DNA examiners. These interpretation methods continue to evolve in order to address relevant and changing issues in DNA analysis. With a few isolated exceptions, our current methods and practices conform to the principles stated in the SWGDAM document. We are reviewing our policies and adapting our methods to address issues raised by the new SWGDAM guidelines. However, these adaptations generally will not call into question previous or currently reported results.

1. Preliminary Evaluation of Data

1.1- Analytical Threshold– We are in compliance with this guideline.

1.2 Internal Standards and Allelic Ladders- We are in compliance with this guideline.

1.3 Controls- We are in compliance with this guideline.

1.4 Redundantly analyzed loci- Not applicable, we do not use redundant loci.

2. Allele Designation

2.1 Criteria for Allele Designations– We are in compliance with this guideline.

3. Interpretation of DNA Typing Results

3.1 Non-Allelic Peaks- We are in compliance with this guideline.

3.2 Application of Peak Height Thresholds to Allelic Peaks-

3.2.1 We have established a stochastic threshold for interpretation of single source samples. We are currently examining methods of incorporating the threshold into the interpretation of mixtures. We plan to incorporate this by the end of the year with the implementation of a new amplification kit.

3.2.2 Not applicable

3.3 Peak Height Ratios- We are in compliance with this guideline.

3.4 Number of Contributors to a DNA Profile-

3.4.1 Guidelines for minimum contributor number- We are in compliance with this guideline.

3.4.2 Criteria for mixture determination- We are in compliance with this guideline.

3.4.3 Guidelines for data from multiple injections-We are in compliance with this guideline.

3.5 Interpretation of DNA Typing Results for Mixed Samples-

3.5.1 Guidelines for distinguishing contributors- We are in compliance with this guideline.

3.5.2 Assumptions used in mixture deconvolutions- We are in compliance with this guideline.

3.5.3 Use of "other quantitative characteristics" in deconvolutions- We are in compliance with this guideline.

3.5.4 Mixtures with single major contributor-

3.5.4.1 Major alleles from heterozygotes should meet PHR expectations- We are in compliance with this guideline.

3.5.4.2 Minor alleles from heterozygotes should meet PHR expectations- Not applicable; we generally do not determine minor contributor genotypes.

3.5.4.3 Minor contributor genotypes may not be distinguished– Not applicable; we generally do not determine minor contributor genotypes.

3.5.5 Determining multiple major contributors with PHR– Our current policy uses peak height ratios to determine what DNA types are considered minor. We plan to employ more defined guidelines by the end of the year with the implementation of a new amplification kit.

3.5.6 Determining indistinguishable mixtures with PHR- We are in compliance with this guideline.

3.5.7 Mixtures with known contributors- We are in compliance with this guideline.

3.5.8 Interpretation of potential stutter peaks–

3.5.8.1 Interpreting n-4 peaks- We are in compliance with this guideline. However, we do not specifically have an

"indistinguishable" from stutter category. We are reviewing the possibility of using "indistinguishable" from stutter category.

3.5.8.2 Reporting n-4 peaks- We are in compliance with this guideline

3.5.8.3 "Considering" low n-4 peaks as potential alleles- When a peak is at or below our established stutter cutoff, we designate that as a stutter peak. We only consider stutter as potentially masking a true allele when assessing if an individual is included or excluded in a mixture of DNA. We do not use stutter peaks for statistical purposes. We are reviewing this guideline and will further address it at the end of the year with the implementation of a new amplification kit.

3.6 Comparison of DNA Typing Results–

3.6.1 Guidelines for interpreting evidence before references– We are in compliance with this guideline.

3.6.2 Partial profiles- We are in compliance with this guideline.

3.6.3 Guidelines for conclusions- We are in compliance with this guideline.

3.6.4 Guidelines for assessing whether typing results are accounted for by known contributors- This recommendation is that we may establish guidelines for assessing whether all the DNA typing results are accounted for by the included individuals. We do not have this in our manual. Generally many analysts address this issue in their report. We are reviewing this guideline to determine if it is appropriate to add it to our manual.

3.6.5 Guidelines for documenting assumptions- We are in compliance with this guideline.

3.6.6 Guidelines for results without conclusions- We are in compliance with this guideline.

4 Statistical Analysis of DNA Typing Results

4.1 Statistical analysis in support of inclusions– We are in compliance with this guideline.

4.2 Statistics derived from evidence; only one statistic per mixture component- We derive statistics from evidence profiles only. Generally, in practice, we comply with this guideline of only reporting one statistic per mixture

component. We are reviewing our guidelines and will determine if more clarification is needed in our manual.

4.3 Inconclusive/uninterpretable data not used in statistics- We are in compliance with this guideline.

4.4 Exclusions don't require statistics- We are in compliance with this guideline.

4.5 Sources of population databases documented- We are in compliance with this guideline.

4.6 Statistical formulae must be documented- We are in compliance with this guideline.

4.6.2 Composite statistics not appropriate–We are in compliance with this guideline.

4.6.3 Loci with alleles below stochastic threshold not used for statistics– We do not currently have a guideline in our manual addressing this issue. We are not specifically using the stochastic threshold to determine the possibility of dropout but analysts are asked to consider the peak heights to determine possible dropout. In practice, we do not use loci where dropout is considered likely in CPI calculations. We are reviewing this guideline and plan to incorporate the use of a stochastic threshold for mixture interpretation by the end of the year with the implementation of a new amplification kit.

4.6.3.1 Alleles below stochastic threshold may be used for comparisons and mixture determination– We are in compliance with this guideline.

4.6.3.2 Restricted CPE/CPI may be used for multiple major contributors- We are in compliance with this guideline.

4.7 Criteria for source attribution statements- Not applicable; we do not use source attribution statements.

5 Statistical Formulae

5.1 Statistics not calculated for loci with potential dropped genotypes, product rule not applied if all included contributors not represented- We comply with this guideline in practice (see response in 4.6.3). General guidelines are available to analysts but will be further refined in the future.

5.2- Random Match Probability (RMP)–

5.2.1 Formulae derived from NRCII- We are in compliance with this guideline.

5.2.2 RMP may be used for mixtures with deconvolution- Not applicable; we do not currently use RMP on mixtures.

5.2.3 NRCII formulae used for relative hypotheses in the absence of direct comparison- We are in compliance with this guideline.

5.3 Combined Probability of Exclusion/Inclusion (CPE/CPI)- We are in compliance with the guidelines regarding formulae used for CPI calculation. We generally comply in practice with guideline 5.3.5.2 regarding loci included in CPI calculations (see discussion of 4.6.3 above), but we do not currently have a policy requiring it. We do not use CPE.

5.4 Likelihood Ratio (LR)

5.4.1 LR on single-source samples– Not applicable; we do not use LR on single-source samples.

5.4.2 LR examples- We currently use the unrestricted LR as described in guideline 5.4.2.1. We do not currently use the restricted LR.