CRITERIA FOR EVALUATION OF DNA MIXTURE INTERPRETATION PROTOCOLS

On October 7, 2015, the Texas Forensic Science Commission ("Commission") requested that Texas laboratories provide copies of their DNA mixture interpretation protocols to a panel of international experts (see below) for review. The primary purpose of the exercise is to provide proactive and constructive feedback to Texas laboratories about their current protocols, with a particular focus on the way in which laboratories evaluate and interpret forensic casework involving DNA mixtures, including calculation and expression of Combined Probability of Inclusion/Exclusion (CPI/CPE) in final laboratory reports. A secondary purpose is to ensure legal end-users that Texas forensic laboratories are using scientifically appropriate protocols for all DNA mixture cases involving CPI/CPE calculations that are currently pending disposition in the criminal justice system.

Some laboratories have requested the Commission announce criteria the panel will consider in evaluating current laboratory protocols. In response, the Commission worked with members of the expert panel to develop the criteria set forth herein. We are extremely grateful to Drs., Frederick Bieber, John Buckleton, Bruce Budowle, John Butler, and Michael Coble for their expertise and generous commitment of time to this effort.

N.B. The presence or absence of any particular criteria in a laboratory's protocol should not be interpreted as a definitive indication of the scientific acceptability of that protocol. For protocols that may not explicitly reference all criteria, the expert panel will work with the laboratory to assess how the issues are being considered in casework.

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1. Does the protocol contain both an analytical threshold (AT) and a stochastic threshold (ST)? Is each threshold clearly defined? How were these thresholds chosen in the laboratory?

2. Does the protocol address **the main limitation of CPI**, *i.e.,* that loci *having a reasonable probability of allele dropout* should be disqualified from being used in computing the CPI/CPE statistic?

3. Does the protocol consider the following concepts in deciding which loci survive the main limitation of CPI/CPE?

    a. Any locus with an allelic peak below the ST and above the AT should not be used in computation of CPI/CPE.

    b. Any locus with subthreshold peaks below the AT that the analyst deems likely to be a "true" allele should not be used for CPI/CPE calculations. A peak deemed likely to be allelic should be distinct from the local noise, should not

be in a forward, single or double backward stutter position (also referred to as +/– stutter in the U.S.) and should have Gaussian morphology.

c. Any locus with no allelic peaks below the ST or the AT but which looks likely to have an unseen contributor in the stochastic zone (below the ST) is disqualified and should not be used in computation of CPI/CPE. This is often determined by reference to adjacent loci or a pattern across multiple loci.

4. Stutter Rule: Does the laboratory have a "stutter threshold"? Does the protocol consider that if the height of minor peaks is similar to that of the stutter peaks then the stutter peaks should be included as potentially allelic in the mixture interpretation and in subsequent CPI/CPE calculation?

5. Considering Exceptions: Does the protocol consider scenarios in which it is possible to reinstate some loci? For example, if an assumption of one minor contributor can be made, then if both minor alleles can be seen below the ST the locus may be used. Does the protocol set forth a policy on how to handle scenarios *where there is no evidence of dropout below the ST*?

6. Interpreting Major Clusters Using CPI/CPE. Does the protocol consider application of CPI/CPE for situations in which a set of peaks representing more than one donor is distinct from one or more minor or trace peaks? Does the protocol provide guidance for qualifying a locus as a major cluster?

7. Avoiding "Suspect-Driven CPI/CPE". Does the protocol explain (or implicitly account for in some way) the concept of suspect-driven CPI/CPE (i.e., where the comparison of each suspect results in a different statistic)? Does it provide guidance regarding how to avoid "suspect-driven CPI/CPE"? Does it emphasize the importance of calculating the CPI/CPE statistic from the evidence profile, and not calculating the CPI/CPE estimate based on the reference profile?