TEXAS FORENSIC SCIENCE COMMISSION
CLARIFICATION REGARDING THE TERM
"CURRENT AND PROPER MIXTURE INTERPRETATION PROTOCOLS"

In May 2015, the FBI notified the public that it had identified some errors in the population data used to generate statistical calculations when analyzing DNA cases by crime laboratories around the country. The changes in the population statistics were attributable to human error in data entry and technology limitations at the time the database was created in the 1990's. The errors, being nominal, were not expected to have any material impact on the statistics derived in criminal cases. Empirical studies in and outside of Texas showed the differences in statistical calculations were minor. Regardless, Texas laboratories sent notifications to the criminal justice community in an abundance of caution, offering to provide statistical re-analysis upon request.

Some prosecutors accepted the offer for re-analysis in the notices, not expecting any significant difference in statistics but making the requests in an abundance of caution in cases set for trial. When these prosecutors received their new reports, they noticed significant changes in the statistics results in some (but not all) of the cases. The cases involved complex DNA mixtures, usually with difficult evidentiary samples such as gun swabs, steering wheel swabs, items of clothing, or other examples of "touch DNA" where multiple people may have contributed DNA to the sample.

The prosecutors went back to the laboratories and also sought the Texas Forensic Science Commission's help in understanding the cause of the unexpected statistical changes. The changes were attributable to the fact that the evidence was originally analyzed *before* certain important revisions were made in laboratory mixture interpretation protocols. These revisions were made due to an evolving understanding among forensic scientists of how to apply certain statistical methods to increasingly complex biological samples, particularly a statistical method referred to as the Combined Probability of Inclusion/Exclusion ("CPI/CPE"). Though DNA analysis is based on sound science, well-defined guidelines for interpretation are necessary when analyzing DNA samples containing multiple contributors, because of the complexity of the samples and the possibility of missing data (e.g., allele dropout and other stochastic effects).

The results of the Texas re-analysis requests highlighted in one state what has been an issue of concern in the forensic DNA community for years—that mixture interpretation is challenging; there can be wide variation from laboratory to laboratory and even within laboratories on how mixture evidence is interpreted; guidance on how to interpret mixtures properly was described in various journal publications and websites but it was not as centralized or proscriptive as it could have been; and efforts by the federal government (in particular the National Institute of Standards and Technology) to train laboratories and raise red flags regarding mixture interpretation problems they observed in two major studies (MIX05 and MIX13) took many years to transfer to the local level.

On August 21, 2015, Dr. Vincent Di Maio, Presiding Officer of the Texas Forensic Science Commission, published a letter to the Texas Criminal Justice Community. The letter explained the issues identified above and suggested that any prosecutor, defendant or defense attorney with a currently pending case involving a DNA mixture in which the results could impact the conviction consider requesting confirmation that CPI/CPE was calculated by the laboratory using "current and proper mixture interpretation protocols."

Since the publication of that letter, some in the community have asked for clarification regarding what the Commission means by "current and proper mixture interpretation protocols" in its August 21, 2015 letter. In using this term, the Commission specifically refers to ensuring the laboratory observes the main principle of CPI/CPE, as follows:

> **Loci that have a reasonable probability of allele dropout should be disqualified from use in calculation of the CPI/CPE statistic. The entire profile must be evaluated to determine the likelihood of dropout, not just the observable peaks at a single locus.**

Laboratory protocols may allow for the reinstatement of loci in certain situations, as well as distinguishing a profile comprised of multiple major contributors and minor or trace contributors where the majors are clearly distinguishable from the minors. These concepts are represented in a memorandum regarding mixture interpretation protocols dated October 15, 2015, and available on the Commission's website at the following link: http://www.fsc.texas.gov/sites/default/files/Texas%20Forensic%20Lab%20Mixture%20Criteria%20101515%20(FINAL).pdf

Further information regarding implementation of these concepts is anticipated in an article by Drs. Frederick Bieber, John Buckleton, Bruce Budowle, John Butler and Michael Coble currently under review in the journal *FSI Genetics*. The Commission will provide a link to the article on its website as soon as it is publicly available.