



Paul R. LePage
Governor

STATE OF MAINE
Maine State Police Crime Laboratory
26 Hospital Street
133 State House Station
Augusta, Maine
04333-0133

A Nationally Accredited Laboratory



Lt. William Harwood
Director

October 10, 2015

Criminal Justice Community,

The purpose of this letter is to inform you of an important issue brought to our attention related to forensic biology (DNA) population statistics estimates relied upon by this laboratory. We have used the FBI STR Population database to predict random match probabilities on DNA evidence since June 1, 2005. We were informed that there were allelic frequency errors due to clerical mistakes and limitations of the old technology and software. The FBI has made the corrected data available to all crime laboratories. We have since transitioned from the old database to a newly established, corrected, and expanded database.

On June 1, 2015 we suspended the release of forensic biology (DNA) reports and began a process of evaluating the differences between the old data and the new. We have learned that the differences between statistics calculated using the original tables and the corrected tables are not great. In some instances the random match probability estimates increase slightly and in other instances there are slight decreases in the estimates. In other instances there are no changes in the estimates whereas not all alleles are affected by these errors. Cases in which a person was included or excluded as a donor of DNA would not change with the old versus the new calculations. We have begun using the newly corrected estimates in casework. All reports released from this laboratory after June 12, 2015 reference corrected tables.

It would be impossible for us to know what, if any, impact statistical estimate variations would have had on the adjudication of a past case. For example, in one experiment with old and new data a random match probability changed from a genetic sequence being estimated to be found in 1 of every 236 quadrillion people to 1 in every 219 quadrillion people. With low level partial DNA sequences, such is often found in touch DNA, we believe the statistical impact could be more significant. In one experiment with low level DNA we attempted to produce a scenario that would create a more significant difference in the results from using old and new data. In this case we assumed a two locus DNA profile. The random match probability changed from a sequence found in 1 in every 32,960 people to 1 in every 28,570 people.

We endeavor to be proactive in our efforts to ensure that all stakeholders in the criminal justice system have accurate and reliable forensic results. **In response we offer to recalculate the statistics in any DNA report issued on, or between 6/1/2005 to 6/1/2015. We will issue an addendum to a report if statistics change as a result of the recalculation using the new data. All attorneys should send requests through the appropriate prosecutor's office of jurisdiction. A form is attached for this purpose.**

We are committed to accurate and reliable results and transparency when there are possible concerns with the quality of our analysis. Please contact me with any questions or requests for more information.

Lt. William S. Harwood
Maine State Police Crime Laboratory

INTEGRITY * FAIRNESS * COMPASSION * EXCELLENCE



MAINE STATE POLICE CRIME LABORATORY

26 HOSPITAL STREET

AUGUSTA, MAINE 04330

REQUEST FOR ALLELE FREQUENCY STATISTIC COMPARISONS

REQUESTING ATTORNEY _____

ADDRESS _____

EMAIL/PHONE _____

INVESTIGATING AGENCY CASE # _____

DOCKET # _____

LAB # _____

DEFENDANT'S NAME _____

VICTIM'S NAME _____

TYPE OF OFFENSE _____

DATE OF OFFENSE _____

*Please complete this form and return to the prosecutor's office of jurisdiction