B169 Defining Appropriate Peak Ratios for the STR DNA Analysis of Pristine Single Source Samples

John H. Ryan, PhD*, Myriad Genetic Laboratories, 320 Wakara Way, Salt Lake City, UT 84108; Dennis Loockerman, PhD, Crime Laboratory Services, Building B, 5805 North Lamar Boulevard, Austin, TX 78752; Jeffrey Barrus, BS and Brian Ward, PhD, Myriad Genetic Laboratories, 320 Wakara Way, Salt Lake City, UT 84108

This presentation will impact the forensic community and/or humanity by defining appropriate guidelines for DNA data analysis of pristine single source DNA samples.

In casework DNA samples, the relative peak height or area of heterozygous STR alleles are useful indicators to detect the presence of a potential sample mixture. However, in pristine single source DNA samples, sample mixtures are not common or expected. To date, defining acceptable peak ratios in pristine single source DNA samples has largely been based on the rules used to define mixtures in casework samples. These peak ratios are often defined as the height of the secondary peak in a heterozygous marker to be greater than or equal to 60% of the height of the main peak. While such a conservative peak ratio may be appropriate for defining mixtures in casework type DNA samples it is potentially restrictive for pristine single source DNA samples. A defined peak ratio of 60% can potentially create unnecessary work for the DNA data analyst by excluding scientifically robust data. The acceptable peak ratio for pristine single source DNA samples should be defined by the accuracy of the resulting STR DNA profile.

We will present the results of a study comparing STR profiles generated from over 130,000 single source DNA samples, in which the acceptable peak ratio will be changed from 60% to a series of more liberal peak ratios. The resulting STR profiles generated from each defined peak ratio will be checked for accuracy. The results of this study will enable the forensic community to define an appropriate peak ratio for heterozygous STR markers, of pristine single source DNA samples, that will produce an accurate profile. In addition, the results of this study will quantify the amount of work saved by employing a more liberal peak ratio for heterozygous STR markers of pristine single source DNA samples.

Peak Imbalance, STR Profiles, Single Source DNA Samples