GENOTYPES AND CONSERVATIVE STATISTICS: ALLOWING FOR MORE CONTRIBUTORS IN THE INTERPRETATION SHOULD GIVE A MORE CONSERVATIVE NUMBER

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As forensic DNA examiners, we strive to be certain to not make more of our evidence than is proper. The combined probability of inclusion (CPI) is a statistical method that is generally agreed to be the most "conservative." In this context, the term conservative means the lowest weight, or the smallest number calculated. This is important, because in the U.S. justice system, all persons are presumed to be innocent, and a low(er) weighting is generally considered to be preferred.

The random match probability (RMP) is often times very similar to the CPI, especially in a mixture of balanced contributors. The CPI is the more conservative statistic because it includes the most genotypes in the calculation. The RMP allows for a refinement of the statistic at times by restricting the number of genotypes considered by assuming a specific number of contributors. Additional genotypes may be restricted by either assuming a donor and/or using quantitative information such as peak heights to distinguish between major and minor genotypes. This refinement of the RMP (i.e., restricted RMP) typically results in fewer genotypes included, which gives a larger RMP value (i.e., more informative number) than the CPI. In general, the fewer the included genotypes, the more informative the number, and the more genotypes, the more conservative the number calculated. The advent of probabilistic systems has resulted in the use of software packages that require, among other things, little to no input by the examiner other than the number of contributors. These systems all use the Likelihood Ratio (LR) and examiner input is typically limited to setting propositions. The resulting output may contain more or fewer genotypes than an experienced examiner may have considered otherwise.

This presentation compares CPI, RMP, LR, and probabilistic LR statistical approaches to investigate this trend of more genotypes being more conservative in terms of the weight assigned to the mixture. The examples will all be worked by hand, and the genotype count for each approach will be compared to the resulting "number" that is calculated. Let's find out if we can predict the probabilistic output, and whether or not it really is true that an interpretation based on more genotypes is more conservative.