B216 Is the Factor of 10 Still Applicable Today?

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After attending this presentation, attendees will have an updated empirical measure of the variability inherent in the assignment of a match probability.

This presentation will impact the forensic science community by showing results for the variation of match probabilities obtained using different allele frequency database data from the same ethnic group. The results from this study indicate that this variation can be larger than a factor of 10 when comparing match probabilities obtained for different populations from around the world.

The assignment of the weight of DNA evidence depends on a number of factors (allele probability estimates, the population genetic model used, the value of the coancestry coefficient, etc.). One of these factors is the allele probability estimates from a database. Key considerations include, but are not restricted to, representativeness and size of the database. The appropriateness of any particular database to any given case is a matter of judgment. This judgment is often based on relevant background information such as the location of the crime. It involves an unavoidable subjective element.

In 1996, the National Research Council (NRC) Committee on DNA report stated that, "…empirical studies show that the differences between the frequencies of the individual profiles estimated by the product rule from adequate subpopulation databases (…) are within a factor of about 10 of each other...".[1] This statement has proven valuable as a gauge on variability caused by the database; however, it was developed at a time before Short Tandem Repeat (STR) multiplexes and is overdue for an update.

The present study examines the validity of the "factor of 10" method for the interpretation of DNA typing results today. It compares the match probabilities obtained using hundreds of different allele frequency databases from around the world. More specifically, this study first simulated sets of genotypes from a database of interest based on the allele frequencies of that database. Then, match probabilities were obtained using the allele frequency data from the original allele frequency database used for simulating the set of genotypes. Similarly, match probabilities were obtained using allele frequency data from each of the other databases in the study corresponding to the same ethnic group. The match probabilities obtained using the data from the other allele frequency databases were then compared with the match probabilities obtained using the original allele frequency database used for simulating the set of genotypes. The results of these comparisons indicate variation among the match probabilities that is greater than a factor of 10.

Reference(s):

1. National Research Council Committee on DNA Forensic Science. *The Evaluation of Forensic DNA*. National Academy Press, Washington D.C., 1996.

DNA Interpretation, Allele Probabilities, Subpopulations