B39 A Statistical and Allele Frequency Evaluation on the Methods of Kinship Calculations

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After attending this presentation, attendees will be better informed regarding the variations found in the statistical calculations used by commonly utilized DNA kinship analysis programs.

This presentation will impact the forensic science community by demonstrating that the variability present in statistical calculations of kinship analysis programs can have effects on kinship determination.

Kinship analysis of Short Tandem Repeat (STR) profiles is often used in cases of parentage testing. Kinship analysis programs calculate the likelihood ratios of paternity, maternity, and sibship using allele frequency databases. It is important to determine the extent of variation between numerical precision within these programs since small variances in value can yield different analyses and conclusions. The first portion of this presentation reports on the differences in numerical precision of these programs.

The choice of race-specific allele frequency databases brings additional variation in statistical calculations of kinship. Race-specific allele frequency databases provide for the genetic similarities and differences found within racial groups and become important for kinship analysis due to the expected genetic similarities of individuals within a biological family. Accuracy in kinship analysis is especially relevant in cases involving half siblings due to the increase of genetic dissimilarity. The second half of this presentation focuses on how the use of a race-specific allelic frequency database can affect accuracy in determining sibship between related individuals.

To identify the effects of using race-specific allele frequency databases for sibship determination, an analysis was conducted on the Short Tandem Repeat (STR) profiles collected from 96 families comprised of 415 individuals. The samples were sourced from the Applied Genetics Technology Corporation (AGTC) in Denver, CO, and were provided by the Department of Forensic Science at The George Washington University. The profiles were obtained from DNA samples collected from prior paternity and immigration testing and were self-defined as belonging to Asian, African American, Hispanic, or Caucasian backgrounds. Twenty-four families were chosen from each racial group to ensure equal representation within the data. The samples were quantified with Quantifiler® Duo DNA Quantification Kit, amplified with GlobalFiler™ and VeriFiler™, and analyzed using an Applied Biosystems® 3130 Genetic Analyzer and GeneMapper® ID-X software. Kinship analyses for the families were conducted on the software DNA•VIEW®. Sibship calculations yielded likelihood ratios that compared the likelihood of sibship with the likelihood of no biological relationship between the individuals. Four sibship likelihood ratios were calculated from four race-specific allelic frequency databases (Asian, African American, Caucasian, and Hispanic databases) for each sibship case, regardless of the individuals' reported backgrounds.

Preliminary analysis of the results conducted with DNA•VIEW® reported accurate determination of sibship for all cases involving full siblings and half siblings. In the cases determining full sibship, 94% demonstrated likelihood ratios as expected by race, with the true racial background of the family members showing the least discrimination. In cases determining half sibship, 50% demonstrated likelihood ratios expected by racial background. A chi-squared analysis of each case was conducted, and all cases showed no independence ($p \leq 2*10^{\wedge -18}$) between the likelihood ratios reported from the four race-specific allelic databases, thus demonstrating a significant difference in allele frequency values between the databases.

The results from the sibship analyses suggest that race-specific allelic frequencies have a diminishing effect on discriminating less related individuals versus more related individuals and supports prior research that half sibling analysis require highly discriminatory loci for accurate sibship determination.

Overall, this two-part evaluation of statistical calculation and allele frequencies seeks to inform the public of numerical variations involved within kinship programs and reaffirms the importance of race-based data for accuracy, allowing for the development of a more standard approach to kinship analysis.

Kinship Analysis, Statistics, Race

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