

Presenting Mitochondrial DNA Statistics in the Courtroom

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Mitochondrial DNA (mtDNA) evidence is increasingly used in criminal trials. As with nuclear DNA, courts typically require that the prosecution present a number reflecting the statistical significance of a mtDNA “inclusion” so that the jury can assess its probative value. Not withstanding that mtDNA is not a unique identifier, such “inclusion” evidence and accompanying frequency statistics can have a powerful effect on a jury.

Laboratory analysts typically determine mtDNA sequence frequencies by comparing the suspect’s profile to the SWGDAM database. As of June 2005, the database has 5071 mtDNA sequences in fourteen “racial” sub-categories ranging in size from 8 sequences (“Pakistan”) to 1814 sequences (“Caucasian”). To estimate sequence frequencies in the population, forensic scientists use the “counting method.” Analysts literally count the number of observations of the suspect’s profile in a database, calculate a frequency estimate by dividing the number of observations by the size of the database, and report the upper and lower bounds of a confidence interval around this estimate. Members of the scientific and legal communities have increasingly voiced concern that this kind of reporting inaccurately portrays the significance of a mtDNA inclusion. One concern is that the SWGDAM database is neither sufficiently large nor sufficiently representative to provide a valid basis for estimating sequence frequencies in a particular population or the population as a whole. For example, molecular anthropologists’ studies of the “African-American,” “Apache,” and “Navajo” subdatabases have found that the SWGDAM database fails to account for historic and more recent migration patterns, geographic clustering of haplotypes, and consequent regional mtDNA differences, leading to potentially inaccurate and misleading frequency estimates. A second concern is whether to count the suspect’s mtDNA profile and the crime scene mtDNA profiles as additional observations to those found in the SWGDAM database.

Other discussions in the scientific community include database construction methods, quality assurance of the sequence information in the database, and the utility of confidence intervals to correct for sampling error. Further research and changes to current reporting practices are necessary to resolve these issues. Larger, regional databases, which at least one national laboratory already is attempting to develop, may become an effective, reasonable, and feasible alternative to use of the SWGDAM database for calculating meaningful sequence frequency estimates. Meanwhile, forensic scientists and other courtroom participants should account for the abovementioned concerns when reporting the significance of mtDNA “inclusions” to jurors.