B86 Pairwise Comparisons as a Means of Validating Iraqi Muslim and Christian Allele Frequency Databases

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After attending this presentation, attendees will have a better understanding of Iraqi Muslim and Christian allele frequencies as well as an understanding of a novel approach used to examine population substructure using pairwise comparisons.

This presentation will impact the forensic science community by providing a method that can be an additional measure of validity for sample populations used to develop allele frequency databases. Due to the weight placed on DNA evidence in criminal trials as well as civil actions such as establishing paternity or identifying human remains, an additional test of the validity of allele frequency databases can be utilized.

A total of 542 individuals (395 and 147 self-identified Muslims and Christians, respectively) from Baghdad were genotyped at 15 Short Tandem Repeat (STR) DNA markers (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, TH01, TPOX, CSF1PO, D19S433, D2S1338, and D16S539) using the AmpFlSTR® Identifiler™ Polymerase Chain Reaction (PCR) Amplification Kit from Applied Biosystems®. Thirty-two alleles previously unobserved in the Iraqi population were detected in these individuals.

Conventional tests for Hardy Weinberg Equilibrium (HWE) and pairwise Linkage Equilibrium (LE) were performed on these populations and suggested that they were suitable for generating allele frequencies to be used in forensic DNA profiling work within Iraq; however, samples of populations displaying unacceptably high degrees of substructure can pass tests for HWE and LE. As a further test of the possibility of high levels of population substructure, exhaustive pairwise comparisons of the individuals within the Iraqi Muslim and Christian populations (77,815 and 10,731, respectively) were also performed. The distributions of pairwise allele sharing among the populations of Muslims and Christians were roughly Gaussian. The extent of allele sharing between pairs of individuals within Muslim ($\bar{x}$=9.30, s=2.30) and Christian ($\bar{x}$=9.60, s=2.37) populations was comparable to what was observed in 100 repetitions of these analyses using populations of simulated individuals with the same allele frequencies [Muslim ($\bar{x}$=9.35, s=2.31) and Christian ($\bar{x}$=9.67, s=2.34)]. The slightly greater degree of average pairwise allele sharing within populations of simulated individuals than what was observed in the actual populations may be an artifact of the slightly greater number of homozygous loci in the actual populations and will be the subject of further analyses with other actual populations. The maximum number of shared alleles observed in pairwise comparisons of actual profiles was 22 of a possible 30, while comparisons of simulated individuals yielded shared alleles of ($\bar{x}$=19.65, s=0.76) for Muslims and ($\bar{x}$=18.88, s=0.70) for Christians across the 100 simulations of each, indicating that there are no specific pairs of individuals in the Christian or Muslim Baghdad populations that are very likely to be close relatives.

All loci across both populations show high Power of Discrimination (PD≥0.81). Two-parent expected Power of Exclusion (PE) is greater than 0.50 at all loci except CSF1PO and TPOX in both Baghdad Iraqi Muslims and Christians. Polymorphism Information Content (PIC) was found to be highest for the D2S1338 locus (PIC=0.87 and 0.86 in Muslims and Christians, respectively) and lowest for the TPOX locus (PIC=0.65 and 0.57 in Muslims and Christians, respectively) in both populations. The Combined Matching Probability (CMP) was estimated to be 1.29E^{-18} and 9.83E^{-18} for the Muslim and Christian populations, respectively.

Iraq, Pairwise Comparisons, Allele Frequencies