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Population genetic study of three Sri Lankan ethnic groups with respect to three short tandem repeat (STR) loci

Identification of humans based on differences at the level of DNA or DNA profiling or typing, is now a widely accepted tool in forensic investigations. Typing by short tandem repeat (STR) analysis is the method of choice. Interpreting DNA typing evidence requires a method for estimating the probability of a random match between two DNA profiles, which is determined by multiplying the allele frequencies on the assumption that they segregate independently and that they are at a state of Hardy-Weinberg equilibrium. Tests for Hardy Weinberg equilibrium have important limitations in that they are relatively weak at detecting population substructure. In order to evaluate the average magnitude of this error, direct sampling and analysis of different population subgroups is recommended.

Blood samples form unrelated donors were collected from 85 Low Country Sinhalese, 56 Sri Lankan Tamils and 52 up Country Sinhalese. DNA was extracted and three STR loci, CSF1PO, TPOX and THO1 were amplified by unltiplex Polymerase Chain Reaction (PCR) and typed by polyacrylamide gel electrophoresis and silver staining.

Heterozygosity levels were high in all three population groups, at all loci except in the THO 1 locus (52.4% heterozygosity) of the UC Sinhala group. Only in the UC Sinhala group. Only in the UC Sinhala group the most common allele exceeded a frequency of 40% in all three loci. The alleles of all three loci in all three population groups conformed with Hardy-Weinberg expectations ($p>0.05$) and did not show any linkage disequilibrium ($p>0.05$), indicating independent segregation of alleles wihtin the

population groups conformed with Hardy-Weinberg expectations ($p>0.05$) and did not show any linkage disequilibrium ($p>0.05$), indicating independent segregation of alleles within the population groups. Wright's F_{st} test for inbreeding showed that for all three loci, the correlation fo alleles between individuals of the LC Sinhala/SL Tamil groups were below the leels of population substructure (F_{st} <0.01) but in the LC Sinhala/UC Sinhala and SL Tamil/UC Sinhal groups there was a marginal indication of population substructure. This is the first report of a population genetic study involving DNA typing of the Sri Lankan population at the ethnic level.