D-35: Polymerase chain reaction based typing of Sri Lankan human DNA isolates at three short tandem repeat loci

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Short tandem repeat (STR) loci, which are composed of tandemly repeated sequences of 1-7 bp in length, are highly polymorphic and are well distributed in the human genome. STR alleles are small in size, generally < 350 bp in length, and thus are amenable to amplification by Polymerase Chain reaction (PCR). DNA typing by STR analysis has the advantage of requiring only a small amount of DNA, and works well in situations where the DNA may be degraded.

Three tetraameric STR loci HUMCSF1PO, HUMTPOX, and HUMTHO1 (GenePrint multiplex system, Promega, USA) were simultaneously amplified by PCR (Perkin-Elmer GeneAmp 2400) employing the following amplification protocol: 96°C for 2 min, 10 cycles (after addition of *Taq* polymerase) of 94°C,1 min; 60°C, 1 min; 70°C 1.5 min, and 20 cycles of 90°C, 1 min; 60°C, 1 min; 70°C 1.5 min. PCR products were size fractionated by polyacrylamide gel electrophoresis, visualized by silver staining, and allele size determined by comparison with an allelic ladder marker.

The allele sizes of the 3 loci, 179-203 (HUMTHO1), 224-252 (HUMTPOX), and 291-327 (HUMCSF1PO) do not overlap in length. Of the 9 human DNA samples examined 3 samples were found to be heterozygous at all 3 STR loci while 5 samples were heterozygous at 2 of the 3 loci. The high degree of polymorphism of the Sri Lankan population with respect to the 3 STR loci HUMCSF1PO, HUMTPOX, and HUMTHO1 demonstrate the suitability of these loci for forensic identification of humans in Sri Lanka.

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