Development of a 16 X-STR multiplex PCR system for kinship analysis and its applicability for the Sinhalese population in Sri Lanka

Nandika Perera [1] [2], Gayani Galhena [3], Gaya Ranawaka [4]
Affiliations

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Abstract

The study describes the development of a new multiplex PCR system that simultaneously amplifies 16 X chromosome short tandem repeats (X-STRs) loci in a single PCR reaction and its applicability on a sample of 200 from the Sinhalese population in Sri Lanka. 13 X-STR loci located in four clusters are selected for the assay (DXS10148-DXS10135-DXS8378, DXS7132-DXS10079-DXS10074-DXS10075, DXS6801-DXS6809-DXS6789 and DXS7424-DXS101-DXS7133). In addition, three single loci were also selected (DXS9902, HPRTB and DXS7423). Genomic DNA extracted using the Chelex-100 method was amplified with modified published primers and subjected to capillary gel electrophoresis. Complete DNA profiles were obtained with 0.20 ng 9947A DNA and the band sizes ranged between 100 and 320 bp with 10 loci having sizes below 237 bp. A total of 160 alleles were observed among the sample with 5-23 alleles for each locus. The forensic efficiency evaluation showed high values for the combined power of discrimination in males (1 in 1×10^{10}) and females (1 in 1×10^{17}). Combined mean exclusion chance (MEC) indices calculated for deficiency, normal trio and duo cases were equally high (> 0.99999). Application of the new multiplex system to two actual kinship cases of full sibling and deficient paternity suggested that these 16 short tandem repeat loci are highly appropriate for forensic and kinship testing among the Sinhalese population.

Keywords: Forensic; Haplotype; Population data; STR clusters.