



Frequency data for 15 STR loci and forensic use in a Beijing-Han population

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Abstract

Short tandem repeats (STR) are useful to forensic science and are characterized by their small range of alleles, their high sensitivity and their suitability if the DNA is degraded. In our research, allele frequencies of 15 STR loci (CSF1PO, TPOX, TH01, D5S818, D7S820, D13S317, D16S539, D21S11, D18S51, FGA, vWA, D8S1179, D3S1358, PentaE, PentaD), together with the Amelogenin locus, were obtained in a sample of over 200 people from the Beijing-Han population, China. The results suggest that the 15 loci are excellent markers for identity and paternity testing. This is the first report on statistical data of all the 15 loci in the Beijing-Han population.

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1. Introduction

The purpose of our study was to investigate the distribution of 15 STR loci (CSF1PO, TPOX, TH01, D5S818, D7S820, D13S317, D16S539, D21S11, D18S51, FGA, vWA, D8S1179, D3S1358, PentaE, PentaD) in the Beijing-Han population and evaluate these markers in identity and paternity testing in forensic science.

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2. Materials and methods

2.1. Sample collection

A total of 201 blood samples were obtained from unrelated Beijing-Han volunteer donors. DNA was extracted either with 5% chelex-100 or organic reagents.

2.2. DNA typing

Target DNA (about 2 ng) was amplified using the Powerplex™ 16 System kit (Promega) following the PCR protocol described in the Technical Manual [1]. The amplified fragments were separated and detected using the PE-310 Genetic Analyzer with reference to allelic ladders. The genotype results of the 15 loci were obtained through the Genotyper software applied by Promega [1]. Preliminary data has been used to generate the population statistics displayed in Table 1.

3. Results and discussions

The genotype frequencies of the 15 STR loci showed no deviations from HWE expectations based on the χ^2 test. The study of the genetic mode of two generations from 100 families demonstrated that all these loci conform to Mendelian laws of inheritance.

The combined matching probability (CPm) and the combined power of exclusion (CPE) of the 15 loci were 0.9999999999999999995 and 0.9999992, respectively, which were both enhanced when compared with the data of nine STR systems that we have already reported [2,3].

Through our genetic research on PentaE and PentaD in the Beijing-Han population, the 5-bp core repeat systems were found to cause none or minimal “stutter” [4].

The results suggest that all these 15 loci are excellent markers in forensic science. Multiplex PCR of all these 15 loci could help us in identity and paternity testing especially when dealing with degraded or trace evidence samples where no signals were obtained for the larger fragment loci but good results were obtained for many smaller fragment size loci.

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