

ALLELIC DIVERSITY AND FORENSIC ESTIMATIONS OF THE BEIJING HANS: COMPARATIVE DATA ON SEQUENCE-BASED AND LENGTH-BASED STRS

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The analysis and profiling of short tandem repeat (STR) loci is routinely used in forensic genetics. At present, the analysis of STRs loci is mainly performed by PCR and capillary electrophoresis (CE). However, due to limitations of CE method, the study of STRs loci can only be limited to length polymorphisms and the nucleotide information is unknown. Fortunately, the Next generation sequencing (NGS) technology has been introduced into forensic science research. Here we present an STR profiling method based on the use of the Ion Torrent platform to simultaneously sequence 300 Beijing Han populations. The allele frequency analysis and forensic parameter analysis were carried out based on the sequence polymorphism and length polymorphism, respectively. We found that sequence polymorphism can provide higher discrimination than length polymorphism. Furthermore, we have a relatively comprehensive understanding of the forensic genetic characteristics of the Beijing population.