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STUDY OF INSERTION-DELETION POLYMORPHISMS (INDELS) IN THE UAE POPULATION

by

Maryam M. Matar Almheiri

Faculty Advisor

Dr. Ranjit Vijayan, Department of Biology

College of Science

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Abstract

Insertion-deletion polymorphisms (indels) have been used less in forensic identification of individuals in comparison to short tandem repeat (STR) and single nucleotide polymorphism (SNP) systems. The use of indels has many advantages including low costs, simple typing methods as well as a small amplicon size of under 160 bp making them suitable for genotyping highly degraded DNA. They can also be valuable as a complementary tool to help resolve kinship cases, with the advantage of lower mutation rates when compared to STRs. The main objective of this study was to investigate the polymorphism of 30 indel loci in the UAE population and to evaluate its suitability for forensic applications. The Qiagen Investigator[®] DIPplex kit was used to amplify 30 biallelic indel loci and the amelogenin locus in 500 blood samples. This technique was robust, relatively simple, and the results were analysed using the same capillary electrophoresis equipment and software used for STR typing. Allele frequencies were evaluated and forensic parameters (match probability, power of discrimination, polymorphism information content, power of exclusion and typical paternity index) were estimated for the 30 autosomal indel loci. No significant departure from Hardy-Weinberg equilibrium (HWE) expectations were observed for most of the indel loci analyzed in the samples obtained from the UAE population. The combined power of discrimination (CPD) and combined match probability (CMP) values were 0.999999999999754 and 2.46×10^{-13} , respectively, which indicated that the 30 indel loci are highly polymorphic and are appropriate for forensic human identification purposes. Even when the match probability of STRs was low, indels gave an acceptable value for forensic application.

Keywords: polymorphism, indels, short tandem repeats, single nucleotide polymorphisms, allele frequencies, Hardy-Weinberg equilibrium, forensic parameters, power of discrimination, match probability.