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Genetic Variation of Autosomal STR Loci from Unrelated Individual in Iraq

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Abstract : The aim of this study is twofold. One is to determine the genetic structure of Iraq population and the second objective of the study was to evaluate the importance of these loci for forensic genetic purposes. FTA® Technology (FTA™ paper DNA extraction) utilized to extract DNA. Twenty STR loci and Amelogenin including D3S1358, D13S317, PentaE, D16S539, D18S51, D2S1338, CSF1PO, Penta D, THO1, vWA, D21S11, D7S820, TPOX, D8S1179, FGA, D2S1338, D5S818, D6S1043, D12S391, D19S433, and Amelogenin amplified by using power plex21® kit. PCR products detected by genetic analyzer 3730xL then data analyzed by PowerStatsV1.2. Based on the allelic frequencies, several statistical parameters of genetic and forensic efficiency have been estimated. This includes the homozygosity and heterozygosity, effective number of alleles (n), the polymorphism information content (PIC), the power of discrimination (DP), and the power of exclusion (PE). The power of discrimination values for all tested loci was from 75% to 96% therefore, those loci can be safely used to establish a DNA-based database for Iraq population.

Keywords: autosomal STR, genetic variation, Middle and South of Iraq, statistical parameters **Conference Title:** ICSRD 2020: International Conference on Scientific Research and Development

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