Polymorphic Positions, Haplotypes, and Mutations Detected In The Mitochonderial DNA Coding Region By Sanger Sequence Technique

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Abstract : The aim of this research is to study the mitochonderial coding region by using the Sanger sequencing technique and establish the degree of variation characteristic of a fragment. FTA® Technology (FTATM paper DNA extraction) utilized to extract DNA. Portion of coding region encompassing positions 11719 - 12384 amplified in accordance with the Anderson reference sequence. PCR products purified by EZ-10 spin column then sequenced and Detected by using the ABI 3730xL DNA Analyzer. Five new polymorphic positions 11741, 11756, 11878, 11887 and 12133 are described may be suitable sources for identification purpose in future. The calculated value D= 0.95 and RMP=0.048 of the genetic diversity should be understood as high in the context of coding function of the analysed DNA fragment. The relatively high gene diversity and a relatively low random match probability were observed in Iraq population. The obtained data can be used to identify the variable nucleotide positions characterized by frequent occurrence which is most promising for various identifications.

Keywords : coding region, Iraq, mitochondrial DNA, polymorphic positions, sanger technique

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