

Male Individualization Based on Y-Chromosomal Short Tandem Repeats: A Comparative Information Theoretical Analysis of 16 Y-STR Loci in Central Anatolia and Iraqi Populations

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ABSTRACT The aim of this study is to investigate the discrimination capacity of 16 Y-Chromosomal Short Tandem Repeat markers (Y-STRs) based on their joint entropy for the purpose of male individualization on samples taken from Central Anatolia and Iraqi Populations. The Y-chromosome polymorphism of sixteen STR loci (DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, Y-GATA H4) were studied. Genomic DNA was extracted from buccal swabs using the QIAamp Mini kit and was co-amplified by using Applied Biosystems AmpF/STR® Yfiler™ PCR Amplification Kit. The Iraqi data set was readily available in the literature which is based on blood samples randomly collected from 100 healthy unrelated males living in middle or south of Iraq. The researchers observed 106 unique haplotypes in Central Anatolia data set. The genetic diversity values across the 16 Y-STR loci ranged from 0.564 (DYS391) to 0.876 (DYS385a/b). The complete male individualization with only 16 Y-STR markers in a genetically diverse local population is possible. In this study, haplotype diversity was 1.0 and discrimination capacity was 100 percent. The high discrimination capacity of the 16 Y-STR markers makes them valuable for male individualization for forensic purposes in Central Anatolia Region of Turkey. The researchers also show that, the *pointwise mutual information* and the *joint entropy* between allele pairs measure the discrimination power of markers more accurately than individual genetic diversity values and provide a better insight into the interaction between the genetic profile of the population and the given Y-STR marker set.