ALLEL FREQUENCY DATABASE FOR QATARI POPULATION USING 13 RMY-STRS MULTIPLEX ASSAY

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Differentiating male lineages using non-recombining Y-chromosomal genetic markers is highly informative for tracing human migration and for forensic studies. Recently, it has been shown that the level of male lineage resolution can be enhanced by analysing Rapidly Mutating (RM) Y-STRs. The aim of this study was to develop an allelic frequency database for Qatari populatiom to evaluate the resolution power of 13 RM Y-STRs. The overall haplotype diversity (HD) was 100%. It was found that the markers which contributed the most toward high HD were DYF399S1 and DYF403S1a/b. Together with their value for paternal male relative differentiation, these RM Y-STRs will be a valuable asset for forensic casework. AMOVA test was performed between Qatari population in comparison to Gulf countries, Middle East, and several worldwide population data sets. F_{ST} values were also calculated. Geography was found to account considerably for the pattern of population sub structuring. The RM Y-STR markers showed remarkable haplotype resolution power in the Qatari population, high gene diversity and sufficient robustness for a diverse range of applications.