

ANALYSIS OF 55 KIDD ANCESTRY SNP OF QATARI POPULATION USING STRUCTURE SOFTWARE

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SNPs are good predictors of ethnicity and several panels have been published (1). The ForenSeq Signature kit (Illumina) offers coverage of 230 different markers including 55 ancestry SNPs (AISNPs). The ForenSeq Universal Analysis Software (UAS) brings the capability to analyse the sequencing data, represent results and accomplish statistical estimates of biogeographic ancestry. The ancestry prediction results in UAS are based on Principal Component Analysis (PCA) collected on several reference populations comprised in the 1000 Genomes project. This set does not include Qatari population. Therefore, the ancestry prediction facilities of the ForenSeq kit were assessed by profiling 124 Qatari population samples. The samples were collected from native Qatari population from various districts in Qatar. The data was analysed using STRUCTURE software. These data serve as an addition to the existing Middle Eastern population data for the 55 AISNPs. This study also confirmed some of the previously determined alleles in several loci. The MPS kit included 55 Ancestry Informative Marker SNPs (AISNPs). The Qatari population has been a melting pot of various populations and this forensic study was the first of its kind to generate new data on the genetics of Qatari population. The 55-ancestry marker allele frequency data for 150 samples were analysed and compared to 139 world populations using STRUCTURE software. The Qatari population data for the Kidd AISNPs were found to be similar in patterns when compared to other Middle Eastern populations. FROG-kb analysis led to all Qatari samples being correctly assigned to Middle Eastern populations showing that the Illumina software needs to be enhanced by adding more databases from the Middle East. In conclusion, the results have clearly demonstrated the potential use of MPS methods to study the genetics of Qatari population.

Keywords: MPS, Ancestry SNPs; Illumina, ForenSeq™ kit; Forensic; MPS; Qatar.