B21 Population Data on 9 STR Loci in Crete (Greece)

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After attending this presentation the attendees will learn data on CSFPO D7S820 D13S317 D16S539 F13A01 FESFPS THO1 TPOX
and vWA STRs in the population of Crete and their validity for the use of forensic analysis.

This presentation will impact the forensic community by providing reliable STR data for probability calculations in cases where Cretan population is involved

Crete is the largest of the Greek islands and is located in the South East of the Mediterranean Sea. It is 260 km long and 60 km at its widest point. Being an island, it is considered to be fairly isolated and since geographically well separated, gene frequency differences were expected. There is a lack of population genetic data from most of these STRs despite the fact that the commercially available amplification kits are increasingly being used in forensic casework. Therefore we aimed to evaluate the data for the above-mentioned polymorphic loci, for an effective use in Crete and the suitability of the system for forensic applications.

Four hundred samples from unrelated individuals were tested for the systems as for their gene and phenotype frequencies. The sampling was done considering the population distribution in the four main residential areas of the island.

Following the DNA extraction and quantitation, the PCR amplification of the nine STR loci (CSFPO D7S820 D13 S317 D16S539 F13BA01 FESFPS THO1 TPOX and vWA) was performed using the commercially available triplex amplification kits provided by Promega, and the application was done according to the manufacturer's instructions.

Allele frequencies were estimated by gene counting. The expected genotype frequencies were calculated on the basis of estimated allele frequencies under the assumption of Hardy-Weinberg equilibrium. Accordance with Hardy-Weinberg equilibrium was checked using the software package Popgen32. Observed and expected heterozygosity, power of exclusion, power of discrimination, probability of match and paternity index was also calculated.

The observed genotype distributions of the nine STRs showed no deviations from Hardy-Weinberg expectations. The obtained results were compared to the present data for Greek population from different geographical areas and to the data for the rest of the Europe. No significant differences were observed between the populations for any of the STRs analysis.

In no cases the observed heterozygosity is less than that of expected. The discriminatory power and exclusion probability values for all the analyzed markers are significantly high and thus reveal high forensic significance. This allele frequency data will be useful for human identity testing in Cretan population.

STRs, Crete, Greece

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