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Letter to the Editor

Genetic data for D1S1677, D2S441, D4S2364, D10S1248, D14S1434 and D22S1045 miniSTR loci from Libya

We determined the allelic frequencies for six miniSTR loci D1S1677, D2S441, D4S2364 (miniplex NC02) and D10S1248, D14S1434, D22S1045 (miniplex NC01) in a sample of 124 unrelated Libyans. Libya, a Northern African country, was first inhabited by Berbers, followed by Phoenicians, Greeks, Romans, Arabs and Ottomans. Libya became independent in 1951 after a brief period as Italian colony.

Blood samples were collected from 124 unrelated Libyans, living in Tripoli area, with informed consent. The samples were identified and stored at room temperature for 1 year prior to genetic analysis. DNA extracted by different methods according the state of preservation of the sample. Three methods were used: (i) salting-out extraction procedure [1], (ii) PCIA [2] and (iii) DNA IQ on the Maxwell® 16 robot (Promega Corp.). DNA concentration was determined by the Quantifiler kit (Applied Biosystems) for some samples. Approximately 100 pg to 1 ng of DNA were amplified following the parameters outlined in [3] for the NC01 and NC02 miniplexes. Amplified products were electrophoresed on an Applied Biosystems 3130xl Genetic Analyzer. Allelic designation, with the corrected nomenclature [4], was determined using Applied Biosystems GeneMapper® 3.2 software, calibrated with standard DNA cell lines K562, 9947A, 9948 and 007 (www.cstl.nist.gov/div831/strbase/miniSTR/miniSTR_NC_loci_types.htm). The UNT Center for Human Identification is accredited under ISO 17025 for Forensic DNA analysis. All methods and procedures conducted during this study followed the established quality assurance measures developed by the laboratory and certified under ISO 17025.

Regarding analysis of the data, Hardy–Weinberg exact test (P), expected heterozigosity (He) and observed heterozigosity (Ho) were performed using the GDA Package [5]. Matching probability (MP), power of discrimination (PD), mean power of exclusion (Å), typical paternity index (PI) and polymorphic information content (PIC) were calculated using PowerStat version 1.2 (Promega Corp.) [6]. The observed allele frequencies and statistical parameters for forensic testing are summarized in supplementary Table 1. No significant deviations from Hardy–Weinberg expectations based on the Fisher's exact test were found after 10,000 shuffles. Linkage disequilibrium between all pair of loci was evaluated with all combinations returning a probability greater than 0.05, indicating independence of the loci (data not shown). The combined power of discrimination (PD) and mean power of exclusion (Å) for the NC01 and NC02 panels were 0.999992 and 0.976024, respectively. The genetic distance, F_{ST} (see supplementary Table 2) was calculated among Libyan population and US Caucasians, African Americans and Hispanics [7]. Also, a neighbor-joining tree of four population groups was generated (see supplementary Figure 1). Our data corroborates the notion that Libya population could be an admixture of North Africa, Sub-Sahara and European genetic contribution.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.fsigen.2009.08.004.

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