CHARACTERIZATION OF Y-STR, AUTOSOMAL STR LOCI AND MTDNA CONTROL REGION IN A POPULATION FROM NICARAGUA AND STUDY OF THE POPULATION SUBSTRUCTURE

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Objectives: Genetically characterize the population of Nicaragua and evaluate the level of population stratification that could affect the statistical calculations for forensic purposes. The sample population was typed for 17 Y-STRs, 15 autosomal STRs and the mitochondrial DNA control region (HVSI/II).

Materials and Methods: Blood was collected from 163 unrelated, healthy mestizo males from Nicaragua. DNA was extracted using Chelex® 100 (Sigma, Steinheim, Germany), and the quantity was determined using the Quantifiler Human DNA Quantification kit. Amplification of the 17 Y-STR loci and 15 autosomal STR loci, was performed using the reagents provided in the AmpFLSTR ® Yfiler™ and AmpFlSTR® Identifiler® PCR Amplification kit, respectively. PCR products covering HVSI (15996-16401) and HVSII (29-408) regions were sequenced using the BigDye® Terminator v1.1 Cycle Sequencing kit. Genotypes were determined using the ABI PRISM 310 Genetic Analyzer, and automated allele sizing was performed using the GeneMapper ID v3.2.1 software for autosomal and Y-STRs. MtDNA sequences were analyzed by means of Sequencing Analysis software and compared with the rCRS with the SeqScape software. Statistical parameters were studied using a program developed by Chakraborty and Lee. Genetic parameters that impact forensic statistical calculations using these genetic systems were determined comparing Nicaragua with Caucasian and Hispanic populations from Texas.

Results: Y-STR and mtDNA haplotypes are highly polymorphic and have a high power of discrimination in this Central American Mestizo population. 155 Y-STR and 107 mtDNA haplotypes out of a total of 163 were observed only once in the dataset. The F_{st} values were very small for Nicaragua and Caucasian Texan population as well as for Nicaragua and Hispanic Texan population. Results from the test of independence based on mismatch distribution showed no departure from independence between the autosomal and Y-STR markers for Nicaraguans (p=0.1201), as well as between Y-STRs and mtDNA (p=0.2556).

Conclusions: Statistical calculations for forensic purposes can be carried out following standard recommended protocols when determining the rarity of a Nicaraguan profile based on 15 autosomal STR, 17 Y-STR and/or HVSI/II mtDNA. Additionally, the data herein support that a single locus or multilocus autosomal STR profile frequency can be multiplied by the upper bound Y-STR haplotype frequency to obtain a joint match probability.