A53 Characterization of Y-STR Loci in a Population From Nicaragua (Central America) and Study of Population Substructure

Miriam Baeta, Carolina Núñez, Cecilia Sosa, PhD, Yolanda Casalod, PhD, and Santiago Gascon, PhD, Department of Legal Medicine, University of Zaragoza, Faculty of Medicine, Domingo Miral s/n, Zaragoza, 50.009, SPAIN; Jianye Ge, PhD, Department of Biomedical Engineering, University of Cincinnati, Ohio, Cincinnati, OH 45220; Ranajit Chakraborty, Department of Environmental Health, Univesity of Cincinnati College of Medicine, Cincinnati, OH 45267; Begona Martinez-Jarreta, PhD, Department Forensic Medicine, Faculty of Medicine, Univ Zaragoza, c/Domingo Miral, Zaragoza, 50.009, SPAIN; and Bruce Budowle, PhD, FBI Laboratory, 2501 Investigation Parkway, Quantico, VA 22135*

After attending this presentation, attendees will have been provided with information on the Nicaraguan genetic population data for the most used forensic genetic markers of Y-chromosome and on population substructure.

This presentation will impact the forensic community by providing Y-chromosome genetic data with a great potential for forensic applications in the Nicaraguan population and by assessing if the population substructure affects forensic statistical calculations.

Population genetic databases are of utmost importance in forensic genetics. However there are still some important population groups not enough characterized genetically. This is the case of certain Central American populations as those from Nicaragua. There is a lack of information on Nicaraguan population from a genetic point of view and this can be an issue when solving criminal, paternity and identification problems. On the other hand, it is important to determine the degree of substructure within the population and the effects that it may exert on the forensic statistical calculations.

In this survey, a population of healthy Mestizo male individuals from Nicaragua (Central America) were typed for 16 Y-STR markers and tested for the degree of substructure within them. For sampling, blood drops from 147 healthy unrelated donors born and living in Nicaragua were collected on FTA cards. DNA extraction and Quantification: Genomic DNA from the blood stains was extracted using Chelex® 100 (Sigma, Germany), and the quantity of human DNA was determined by real time PCR using the Quantifiler Human DNA Quantification kit (Applied Biosystems, Inc.). PCR and typing were carried out by using the AmpfℓSTR® Yfiler kit (Applied Biosystems, Inc.). Amplification was performed in a GeneAmp® Thermal Cycler 2720, and typing was carried out in an ABI Prism 310. Fragment size and allele designation of different loci was determined by comparison with allellic ladders provided with the kit and analysed using the GeneMapper ID v3.2.1 software (Applied Biosystems, Inc.).

The recommendations of the DNA Commission of the International Society of Forensic Genetics for analysis of STRs systems were followed. Gene diversity at each locus, the number of haplotypes and haplotype diversity were calculated using a program developed by Chakraborty and Lee (http://cgi.uc.edu/download/haplo). Linkage disequilibria tests, with 5000 permutations, were performed using the same program. The F_{ST} values were calculated according to Weir and Cockerham (1984). The analyses performed on the 16 Y-chromosome loci studied in the present study have a great potential for forensic applications in this population.

Y-Chromosome, DNA Typing, Population Substructure

** Presenting Author*