

FOR THE RECORD

Sinthia Pagano,¹ M.S.; *Mónica Sans*,² Ph.D.; *Ville Pimenoff*;³ *Ana M. Cantera*,⁴ Ph.D.; *J. Carlos Alvarez*,⁵ Ph.D.; *Jose A. Lorente*,⁵ M.D., Ph.D.; *Jose M. Peco*,⁵ M.D.; *Pablo Mones*,² and *Antti Sajantila*,³ M.D.

Assessment of HV1 and HV2 mtDNA Variation for Forensic Purposes in an Uruguayan Population Sample

POPULATION: 120 unrelated Caucasians living in Uruguay (Southern America)

KEYWORDS: forensic science, DNA typing, population genetics, mtDNA, Uruguay, Hv1, Hv2

In order to assess the utility of mtDNA typing for forensic purposes in Uruguay, a population sample of 120 maternally unrelated individuals were amplified and directly sequenced for the HV1 and for the HV2 segments in the control region of the human mtDNA, following previous international recommendations (1).

Blood and saliva samples were taken from 120 unrelated individuals and deposited into FTA cards (FTA card, Whatman WB 12-0205). The DNA was extracted in a 1.2 mm punch according to the manufacturer recommendations. DNA amplification and sequencing was performed according to previously published paper (2). All statistical analysis were calculated using the Arlequin Software ver. 2.000 (3).

Results are shown in Table 1. In this population sample, 107 different mtDNA sequences were observed out of 120 individuals. Of these, 97 sequences were observed once (80.8%), 8 sequences were observed twice (13.3%), one sequence was observed three times

(2.5%), and another four times (3.3%). The variation of mtDNA HV1 and HV2 regions was confined to 146 positions, of which 99 was observed in the HV1 and 47 in the HV2. Sequence variation consisted of 120 transitions, 21 transversions, and 11 indels. The genetic diversity value for combined HV1 and HV2 regions was 0.998 (± 0.002) in this Uruguayan population sample, and the nucleotide diversity was 0.068 (± 0.035).

The complete dataset is available to any interested researcher at: <http://www.lorgen.com/forense>

References

1. Wilson MR, DiZinno JA, Polansky D, Replogle J, Budowle B. [Validation of mitochondrial DNA sequencing for forensic casework analysis](#). *Int J Legal Med* 1995; 108:68–74. [PubMed]
2. Sans M, Weimer T, Franco M, Salzano f, Bentancor N, Alvarez I, Bianchi N, Chakraborty R. [Unequal contributions of male and female gene pools from parental populations in the African descendants of the City of Melo, Uruguay](#). *Am J Phys Anthropology* 2002;118:33–44.
3. Schneider S, Roessli D, Excoffier L. 2000. arlequin ver. 2.000: A software for population genetic data analysis. University of Geneva, Switzerland: Genetics and Biometry Laboratory.

Additional information and reprint requests:
Jose A. Lorente, M.D., Ph.D.
Dept. Medicina Legal — University of Granada
Av. Madrid 11
E-18012 Granada, Spain
E-mail: jlorente@ugr.es

¹ Laboratorio Biologico, Direccion Nacional de Policia Tecnica, San Martin 2676, CP 11800, Montevideo, Uruguay.

² Sección de Antropología Biológica, Facultad de Humanidades. Universidad de la República, 11200 Montevideo, Uruguay.

³ Laboratory of Forensic Biology, Department of Forensic Medicine, P.O. Box 40 University of Helsinki, Helsinki, Finland.

⁴ Catedra de Bioquímica, Facultad de Química, UDELAR, Gral. Flores 2124, CP 11400, CC 1157 Montevideo, Uruguay.

⁵ Department of Legal Medicine, University of Granada, 18012 Granada, Spain.

