

MITOCHONDRIAL DNA CONTROL REGION DATABASE IN BANCO NACIONAL DE DATOS GENÉTICOS-ARGENTINA

M.G. Fraga, F.L. Gagliardi, C. Chaul, T. Samsonowicz, A.H. Szöcs, D.H. Alcázar, J.H. Solimine, J. Maggiore, G. C Echenique, S.G. Cabeller, A.M. Arellano, M. B. Rodríguez Cardozo.

Banco Nacional de Datos Genéticos.Unidad Inmunología del Hospital Dr Carlos G Durand. GCABA- Ministerio de Ciencia Técnica e Innovación Productiva Presidencia de la Nación

Aim: To analyze the distribution of different haplotypes of Mitochondrial Control Region DNA in a large sample of Argentine population who assisted to the Banco Nacional de Datos Genéticos (BNDG) looking for their identity in cases of civil state suppression during the dictatorial government (1976-1983).

Methods: A total of 3933 unrelated Argentine individuals who assisted to the BNDG were sampled for the analysis. Mitochondrial DNA Control Region sequences were determined for both hypervariable regions 1 (HV1) and 2 (HV2).

Blood samples and buccal swabs were used as the DNA source. The amplification for both hypervariable regions was performed in a Perkin Elmer 9700 thermal cycler.

The cycle Sequencing was performed using the BigDye® Terminator v 1.1 Cycle Sequencing Kit (Applied Biosystems) and automated sequencing was performed in an ABI PRISM® 3100/3130 Genetic Analyzer (Applied Biosystems).

Analysis of mitochondrial DNA sequencing data was performed by manual method. The hypervariable region 1 (HV1) was analyzed between positions 16023 and 16428 and the hypervariable region 2 (HV2) between 73 and 480 according to the Anderson Sequence.

To analyze these results a data base was created and statistical parameters were calculated.

Results: From 3933 haplotypes analyzed, 2620 were unique. Haplotype frequencies were estimated by haplotype counting. Values of Genetic Identity (P) and Genetic Diversity (h) were calculated, being $2,229410^{-3}$ and 0.9980 respectively.

Conclusion: This Mitochondrial Control Region DNA database provides useful information for genetic profiles comparison and maternal lineage determination in our lab.