ALLELE FREQUENCIES OF 21 STRS LOCI IN AN ARGENTINE POPULATION SAMPLE

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INTRODUCTION

It is well described the importance of knowing the allele distribution of the genetic markers used in forensic laboratories, in the population they will be applied. Our aim is to study the allele frequencies for 21 STR loci and calculate the statistical parameters of forensic interest, in a sample provenient from different regions of Argentina. From the whole samples used, 25% came from different provinces of Argentina (Buenos Aires, Córdoba, Mendoza, Neuquén, Santa Fe, San Luis, Tucumán and Tierra del Fuego) and the rest are from Ciudad de Buenos Aires. These proportions simply reflect the samples of non related people processed in the BNDG during 2009-2013.

MATERIALS AND METHODS

Materials and Methods: A total of 500 unrelated individuals [1] from different provinces in Argentina, were included for the analysis. DNA was obtained from blood samples with QIAcube™ QIAGEN [2], and Powerplex ® 21HS System – Promega Corporation was applied, with a final reaction volume of 15 µl. Capillary electrophoresis of the amplification products were performed on an ABI PRISM® 3500 Genetic Analyzer (Applied Biosystems). The 3500 Data Collection Software – Versión 1.0, and the Gene Mapper® ID-X1.2 (All from Applied Biosystems) were used. Statistical analysis for allele frequencies, power of discrimination, matching probability and power of exclusion were calculated using PowerStats [3] software. Deviation from Hardy-Weinberg equilibrium, observed and expected heterozygosity were calculated using Michael H. Count (2005-2008) [4]

RESULTS

Allele frequencies of 21 STR loci studied are presented in Table 1. Minimum allelic frequencies were calculated using Patcan software.[5]

Statistical parameters of forensic interest, are shown in Table 2. Deviations from Hardy-Weinberg equilibrium were not observed for any of the loci presented. Penta E and D18S51 exhibited the highest heterozygosity (0,904 and 0,888, respectively) whereas TPOX shows the lowest polimorphism (0,6370), as expected.

For the 21 loci STR, the combined power of discrimination is 0,99999999 and the combined matching probability is 4,336521436 x 10^{-26}.

CONCLUSIONS

The allele frequencies presented for the 21 STRs included in this study are a useful tool for forensic identification and parentage testing in the population we are working with nowadays.

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