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Announcement of population data

Population data on 15 autosomal STRs in a sample from Colombia

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ABSTRACT

We present population genetic data of 15 STRs (CSF1PO, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, FGA, PENTA D, PENTA E, TH01, TPOX and VWA) obtained from a sample of 617 unrelated individuals from Colombia. Deviations from Hardy–Weinberg equilibrium were assessed and allele frequencies and parameters of forensic interest for each STR were calculated. The combined power of exclusion (PE) and the combined power of discrimination (PD) for the 15 tested STR loci were 0,99999895 and more than 0,9999999, respectively. The combined MP value was 1 in 1,07888 × 10⁻¹⁷. Population comparisons between our sample and neighbouring populations from Latin America were carried out. Significant differences in above six markers were observed between our sample and two populations from Rio de Janeiro.

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1. Population

Blood samples were obtained from 617 unrelated healthy individuals living in different regions scattered along Colombia after informed consent. The individuals come from Arauca, Atlántico, Boyacá, Caquetá, Casanare, Cauca, Cundinamarca, Guainía, Guaviare, Meta, Nariño, Tolima and Valle del Cauca departments.

2. Extraction

DNA was extracted using a standard FTA method.

3. PCR

According to the manufacturer's instructions (PowerPlex[®] 16 System, Promega Corporation, Madison, USA).

4. Typing

PCR products were analysed by capillary electrophoresis in an ABI 310 Genetic analyzer (Applied Biosystems, Foster City, CA). GeneScan 3.2.1 analysis software (AB) was used to determine fragments size.

5. Analysis of data

Arlequin software ver 3.0 [1] was used to calculate allele frequencies, gene diversities, exact test of population differentiation, population pairwise genetic distances (Fst), and also to assess Hardy–Weinberg equilibrium. Parameters of forensic interest, namely power of discrimination (PD), power of exclusion (PE) and matching probability (MP) were calculated using PowerStats v1.2 (Promega Corporation) software package.

6. Quality control

Proficiency testing of the GEP-ISFG (www.gep-isfg.org).

7. Results

The whole genotype data set, allele frequencies and genetic distances between the studied sample and other American populations [2–31] are available as e-component.

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8. Other remarks

No deviations from Hardy–Weinberg equilibrium were observed except in the case of CSF1PO ($p \geq 0.003$; significant level after Bonferroni correction) (see *e-component*). This deviation cannot be explained by an excess of homozygotes. The combined PE and the combined PD for the 15 tested STR loci were 0, 99999895 and more than 0, 9999999, respectively. The combined MP value was 1 in 1, 07888 $\times 10^{-17}$.

Allele frequencies of the population analysed here were compared with those available of other Latin American populations, including samples from different regions of Colombia, Brazil, Perú and Ecuador [2–31]. Although low genetic distances were found for all the samples, significant differences were observed between our sample and populations from Antioquia [2,3], Bogotá [5], Colombian Chocó groups [5,7,21], Boyacá [6], Cauca Valley [26] (Colombia); descendants from Terena group [11], Rio Grande do Norte [13], Santa Catarina [14] Rio de Janeiro [15,25], Piauí [16], Alagoas [17], European derived Brazilians [18], Brazilian mulattos [18], African derived Brazilians [18], Asian derived Brazilians [18] and Matto Grosso do Sul [25] (Brazil); Ecuador [19,20]; and Perú [24] (see *e-component*, genetic distances table). Genetic distances between Colombia and Rio de Janeiro population samples were significant in more than six markers, being the Brazilian populations the most differentiated from our sample. Those differences could be due to the different proportion of admixture of the populations, bearing in mind that so our sample as well as those from Rio de Janeiro are mixed populations consisted of Europeans, Amerindians and African individuals.

As conclusion, here we present a 15-STR database suitable for general forensic purposes in Colombia, being the first Colombian STR database which includes that number of markers.

This paper follows the guidelines for publication of population data requested by the journal [32].

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.fsigen.2008.08.002.

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