



Genetic data of an X-STR decaplex in Ecuadorian population (P)

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ABSTRACT

X-chromosomal STRs have proven to be an efficient complement in some complex paternity or forensic cases. In this work, we report the results obtained from an Ecuadorian men's sample of ten STR X chromosome markers (DXS8378, DXS9902, DXS7132, DXS9898, DXS6809, DXS6789, DXS7133, GATA172D05, GATA31E08, and DXS7423). We typed 200 unrelated males from 19 provinces of Ecuador. Samples were processed following the recommendations of the GEP-ISFG collaborative study (2008). Our data showed that locus DXS6809 had the highest values of Power of Discrimination (PD) and Polymorphism Information Content (PIC) with 0.8051 and 0.7888, respectively. There was no evidence for statistically significant linkage disequilibrium among the loci studied. Decaplex showed to be a powerful tool in kinship and forensic analysis.

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1. Introduction

Ecuadorian population was influenced by a mixture of Native Americans, European (Spanish) and African descendants (slaves) [1]. Nowadays Ecuador has approximately 7.177.683 men distributed in all the territory [2]. STRs (short tandem repeats) have been used in many population studies in order to give information how to solve kinship or forensic cases [3]. However, X-STRs markers give an additional and useful information in many complex cases (certain genetic information is not available, lineage comparison, one or two mutation cases) where there is a woman involve and it cannot be reach a satisfactory conclusion with STRs [4]. The current study presents complete information of forensic parameters of Ecuadorian Population.

2. Material and methods

Randomly we selected 200 unrelated males from Ecuador distributed in 19 provinces. All individuals have signed the informed consent for population genetic studies. The sample was blood on FTA paper, collected in the Molecular Genetic Laboratory at Ecuadorian Red Cross-Cruz Vital.

DNA was extracted using FTA buffer according to manufacturer's recommendations (Whatman—GE Healthcare). X-STR

amplification was performed according GEP-ISFG collaborative study in one reaction with ten X-STR (DXS8378, DXS9902, DXS7132, DXS9898, DXS6809, DXS6789, DXS7133, GATA172D05, GATA31E08, and DXS7423). STR fragment separation and detection were done in ABI PRISM 3100 and 3130 Genetic Analyzers (Applied Biosystems). Results were collected with Data Collection v3.0 and analyzed by GeneMapper v3.1 and 3.2 (Applied Biosystems).

Also, with the samples we analyzed a positive control (9947A). In addition, we had participated in quality control programs organized by GHEP-ISFG, GCIH and SLAGE.

Frequencies, discrimination power (PD), Polymorphism Information Content (PIC) and linkage disequilibrium were calculated using Arlequin v3.5.2 and Microsoft Excel, power of exclusion (PE) in trios and duos were calculated according Desmarais et al. [5].

3. Results and discussion

Table S1 shows statistical parameters that were calculated. Allelic frequencies for each marker were between 0.005 in some X-STRs and 0.63 for allele 9 of DXS7133, which differs from previous article from Pichincha's population where the highest frequency was in DXS8378 [6].

After Bonferroni correction ($p < 0.0011$), no linkage disequilibrium was found, consistent with the physical distance for the markers of 5Mb (except for DXS6809 and DXS6789) [3].

The least polymorphic marker was DXS7133 and the most polymorphic was DXS6809, which is similar to the study reported by GEP-ISFG (2008) with Spain population (Galicia).

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4. Conclusion

X STRs decaplex is a great and powerful tool that can be used in Ecuadorian population in routine analysis in forensic and kinship testing.

Conflict of interest

None

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.fsigss.2015.09.037>.

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