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POPULATION DATA

Population data of 15 autosomal STR markers from Afro-Bolivians of Nor Yungas Province (Bolivia)

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Abstract Allele frequencies and forensic parameters for 15 autosomal loci included in the AmpFlSTR® Identifiler kit were estimated in a sample of 57 unrelated Afro-descendants from Nor Yungas (Bolivia). Buccal swabs samples were obtained from voluntary donors, after consent was given. All loci were in Hardy-Weinberg equilibrium after Bonferroni correction. D21S11 was the most informative locus, while the least discriminating locus was D3S1358. The combined power of discrimination and the combined probability of exclusion were >0.99999999 and >0.99997, respectively. The multidimensional scaling (MDS) plot generated by Rst matrix supported that Afro-Bolivians of Nor Yungas preserved a stronger African descent compared to other admixed Latin American populations. These results amplified the Bolivian databases of autosomal STR loci and may provide a useful tool for human identification tests and population genetic studies.

Keywords Autosomal STRs · African ancestry · Bolivia · Population genetics

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During the sixteenth to nineteenth centuries, several million African slaves were brought to America as mine and farm laborers. Historical reports show that current Afro-Bolivians are descendants of that slave working force in Bolivia [1, 2]. According to the last official census carried out in Bolivia in 2001, a total of 6,000 Afro-Bolivians were registered. From those, only 23 % were citizens of the North and South Yungas and Inquisivi Department of La Paz region [3]. Their economy is mainly based on the cultivation of coca, citrus, and coffee. The genetic structure of the Afro-Bolivians is poorly known [4]. Besides, this is the first study of STRs autosomal markers in this African American population, which is partially isolated, both geographically and culturally. Autosomal STRs frequencies data will contribute to the understanding of the population genetic structure, and may provide a useful tool for human identification tests and population genetic analysis.

In this study, we analyzed a sample of 57 (30 males and 27 females) healthy unrelated Afro-descendant individuals. Buccal swabs were collected from volunteer donors, with the individual informed consents, who attended community cultural centers in Tocaña, Chijchipa, San Joaquín-San Martín Padilla, and Mururata in the Yungas Province of Bolivia (Supplemental Figure 1). The anonymity of the individuals investigated was preserved. DNA was extracted using the

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standard phenol-chloroform method. Multiplex PCR amplification of 15 autosomal STRs (D8S1179, D21S11, D7S820, C SF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S443, vWA, TPOX, D18S51, D5S818, and FGA) was performed using AmpFlSTR® Identifiler PCR Amplification kit (Applied Biosystems, Foster City, CA, USA) following the manufacturer's instructions. The amplified products were genotyped with the ABI Prism 3130 DNA Genetic Analyzer along with Gene-Mapper ID 3.2.1 software (Applied Biosystems, Foster City, CA). The quality of the genetic profiles was guaranteed through quality control testing by the International Society of Forensic Genetics (http://www.isfg.org) and the Argentine Society of Forensic Genetics (http://www.sagf.org.ar). The present study followed the guidelines and recommendations suggested by Carracedo et al. [5] and Poetsch et al. [6].

Allele frequencies, heterozygozities, exact test for Hardy-Weinberg (HW) equilibrium, and population differentiation tests were performed using the Arlequin version 3.5 [7]. The forensic statistical parameters were calculated using PowerStats v.1.2 software (Promega Corp.).

No significant deviations from HW equilibrium were observed after applying Bonferroni correction for the analyzed loci ($p>0.05/15=0.0033$). The most informative system was D21S11, which showed the highest average power of discrimination (PD=0.9530) and typical paternity index (TPI=4.000). Meanwhile, D3S1358 marker showed the lowest values for all analyzed parameters (Supplemental Table 1). The combined power of discrimination (PDc) and the combined probability of exclusion (PEc) for the 15 STR loci were >0.99999999 and >0.99997, respectively.

Pairwise genetic distances between populations (Rst) were estimated comparing the obtained results with published data of 18 worldwide populations: nine Latin American Mestizo, one South Amerindian, two European, and six African (Supplemental Table 2). Comparisons were carried out for 13 STR loci, since the loci D2S1338 and D19S433 were not available for all groups analyzed. Genotype datasets were reconstructed using R software (http://www.r-project.org). A multidimensional scaling (MDS) plot was performed for visualizing the Rst distances matrix.

After Bonferroni correction, no significant differences were observed between Afro-Bolivians and the populations of Mozambique ($p=0.089$), Angola ($p=0.009$), and Uganda ($p=0.009$). However, Afro-Bolivians differed significantly from all Latin American samples analyzed ($p<0.003$). These results were well represented in the MDS plot (Supplemental Figure 2), showing the Afro-Bolivian and African populations in a single cluster, and the Latin American and European populations in a separated group. Meanwhile, the admixed Bolivian sample was situated in an intermediate location between the Latin American and Amerindian populations. These differences highlight the importance of estimate STR frequencies and forensic parameters when the populations of interest involve diverse ethnical groups inhabiting the same geographical region [8, 9].

In conclusion, the analyses of the 15 autosomal STR show that Afro-Bolivians of Nor Yungas preserved a stronger African descent in contrast to other admixed Latin American populations, including other regions of Bolivia. This information amplified the Bolivian databases of autosomal STR loci and may provide a useful tool for human identification purposes, forensic calculations, and population genetic studies.

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