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COMPARATIVE STUDY OF 15 STR FORENSIC LOCI BETWEEN A BOLIVIAN POPULATION AND CENTRAL AND SOUTH AMERICA POPULATIONS

Abstract: A population of 117 individuals of La Paz was typed for 15 STR loci using the AmpFISTR® Identifiler™ PCR kit (Applied Biosystems). Allelic frequencies and parameters of forensic interest (power of discrimination and probability of exclusion) were calculated. A comparative study with populations from Central and South America was done, using the calculation of genetic distances between them and the phylogenetic tree.

Introduction

The study of autosomal short tandem repeats (STRs) in a Bolivian population from La Paz is important since this is a country with a high genetic variability, according to previous studies made in mitochondrial DNA [1]. Allelic frequencies of 15 STR forensic loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 e FGA) were calculated in a sample from La Paz and a comparative study with other populations from Central and South America [2-11] was done.

Material and Methods

DNA from 117 unrelated healthy individuals of La Paz, Bolivia was extracted, using Chelex100 method [12]. Samples were amplified using the AmpFISTR® Identifiler™ PCR kit (Applied Biosystems) [13] according to manufacturer's instructions. Amplified products were separated and detected using an ABI Prism™ 310 Genetic Analyzer (Applied Biosystems), analyzed with GeneScan software version 3.1. and typed using the reference sequenced ladder.

Allelic frequencies (see table 1), observed and expected heterozygosity and Hardy-Weinberg (HW) equilibrium were calculated using the Arlequin population genetics software v3.1 [14]. Matching probability, power of discrimination and power of exclusion were achieved using the PowerStats v1.2 software. Software *Phylip* v3.5c [15] was used to establish phylogenetic relationships between population of La Paz and other Central and South American populations, by calculating the genetic distances.

Neighbor-Joining method produced the phylogenetic tree, visualized by application of software *TreeView* v1.6.6 [16].

Results

Results are founded in figure 1, table 1 and table 2.

Discussion

This Bolivian population is in Hardy-Weinberg equilibrium for all markers, except for CSF1PO ($P < 0,05$). The observed heterozygosity (H_o) is between 0.573 (D5S818) and 0,872 (FGA). The power of discrimination (PD) varies between 0.760 (TPOX) and 0.963 (FGA) and the combined power of discrimination for the 15 loci is 0.9999999. The probability of exclusion (PE) varies between 0.259 (D5S818) and 0.738 (FGA), and the combined probability of exclusion for all loci is 0.999987 (see table 2).

Phylogenetic analysis (figure 1) revealed that La Paz is distant from the remaining populations, mainly the Brazilians, with genetic distances greater than 0.1319. The population that reveals the smaller distance from La Paz population is Valley of Mexico (0.0381). Populations of El Salvador and Mexico have genetic distances of 0.0519 and 0.0439 respectively, Central region of Mexico (0.0719), Buenos Aires (0.0814), Caracas (0.1012) and Maracaibo-Venezuela (0.1031).

Conclusions

Our results are important to determine the genetic background of La Paz population and the combination of the studied 15 STR loci presents a powerful strategy for individual identification and parentage analysis.

The geographical situation of La Paz, namely the location at highlands around Lake Titicaca, could explain the higher genetic distances between other populations from Central and South American.

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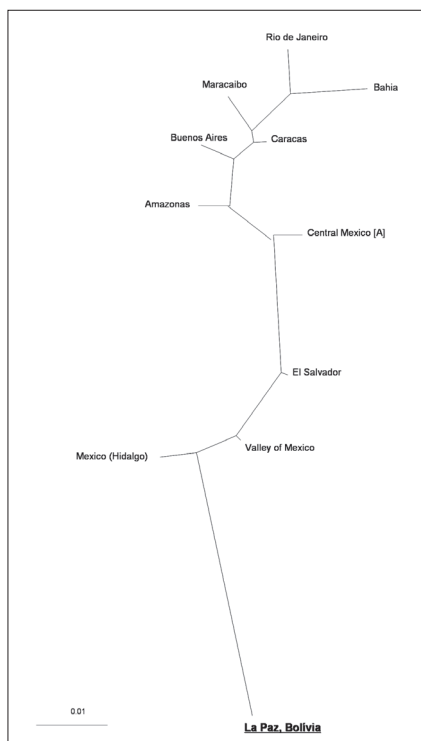


Figure 1 – Phylogenetic tree – genetic distances between Bolivia and other populations [1-10]; [A] Mestizos from the central region of Mexico.

Alleles	CSF1PO	D2S1338	D3S1358	D7S820	D8S1179	D13S317	D16S539	D19S433	D21S11	TH01	vWA	TPOX	D18S51	D5S818	FGA
6										0,1880					
7				0,0170						0,5170				0,1370	
8	0,0130		0,0210		0,0260	0,0090				0,0560	0,6030			0,0040	
9	0,0040		0,0380	0,0040	0,3590	0,2820				0,0340		0,0210		0,0850	
9.3										0,2010					
10	0,2260		0,3080	0,0510	0,0980	0,2480				0,0040	0,0300	0,0040		0,0040	
11	0,2610		0,3720	0,0680	0,1580	0,1790	0,0040					0,2090	0,0040	0,5850	
12	0,4060		0,2220	0,0980	0,1750	0,1880	0,0260					0,1320	0,1280	0,1410	
12.2								0,0170							
13	0,0810		0,0210	0,3420	0,1200	0,0810	0,1370				0,0040	0,0040	0,1410	0,0430	
13.2								0,1840							
14	0,0040	0,0260		0,2260	0,0640	0,0130	0,3500				0,0130			0,2560	
14.2								0,0260							
15		0,4700		0,1790				0,1710			0,0510			0,1410	
15.2								0,0510							
16	0,0170	0,3420		0,0260				0,0210			0,3550			0,1200	
16.2								0,0090							
17	0,1240	0,1150					0,0040				0,4020			0,1200	
18	0,0680	0,0470		0,0040							0,1150			0,0470	0,0130
19		0,3460									0,0560			0,0210	0,1320
20	0,0040	0,1450									0,0040			0,0040	0,0560
21		0,0170												0,0090	0,0680
22		0,0130												0,0040	0,0840
23		0,1880													0,1110
24		0,0510													0,1970
25		0,0260													0,1970
26		0,0040													0,1150
27									0,0040						0,0090
28									0,0470						0,0090
29									0,1880						
30									0,1670						
30.2									0,0090						
31									0,0510						
31.2									0,2090						
32									0,0040						
32.2									0,2440						
33.2									0,0600						
34.2									0,0090						
35.2									0,0090						

Table 1 – Allelic frequencies of 15 STR in a Bolivian population from La Paz

	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
H _o	0,78923	0,80342	0,70385	0,68378	0,69667	0,70385	0,78632	0,88325	0,78923	0,73604	0,71796	0,58120	0,85470	0,57285	0,87179
H _e	0,78530	0,82857	0,71810	0,70967	0,84673	0,85544	0,78007	0,78796	0,80326	0,78707	0,68658	0,57891	0,85023	0,81208	0,89629
MP	0,079	0,090	0,127	0,136	0,169	0,168	0,075	0,087	0,075	0,070	0,148	0,240	0,048	0,191	0,037
PD	0,921	0,940	0,873	0,884	0,801	0,832	0,923	0,903	0,925	0,930	0,851	0,780	0,954	0,809	0,963
PIC	0,750	0,800	0,660	0,660	0,580	0,810	0,780	0,750	0,780	0,840	0,530	0,830	0,830	0,580	0,850
PE	0,543	0,621	0,430	0,404	0,379	0,430	0,574	0,721	0,543	0,485	0,457	0,269	0,704	0,259	0,738
<i>P exact test for Hardy-Weinberg equilibrium</i>	0,36616	0,41568	0,95814	0,03977	0,19850	0,96090	0,60668	0,05423	0,07985	0,37911	0,88536	0,10465	0,88244	0,13142	0,85485

H_o, observed heterozygosity; H_e, expected heterozygosity; MP, matching probability; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion; P, probability value of exact test for Hardy-Weinberg equilibrium.

Table 2 – Forensic statistical parameters of La Paz population