



Announcement of Population Data

Population genetic data for 15 STR loci (Identifiler™ kit) in Bolivia

Omar Rocabado^a, Patricia Taboada^a, Francisco Javier Inda^b, Inaki Yurrebaso^c, Oscar García^{c,*}^a Laboratorio de Genética Forense, Instituto de Investigaciones Forenses, Indaburo 946, La Paz, Bolivia^b Basque Country Government, Larrauri Mendotxe 18, 48950 Erandio, Bizkaia, Spain^c Basque Country Forensic Genetics Laboratory, Larrauri Mendotxe 18, 48950 Erandio, Bizkaia, Spain

ARTICLE INFO

Article history:

Received 19 October 2008

Received in revised form 12 July 2009

Accepted 13 July 2009

Available online 8 September 2009

Keywords:

Short tandem repeats (STRs)

Population study

Bolivia

ABSTRACT

Allele frequencies for 15 STR autosomal loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D18S51, D5S818 and FGA) were obtained from a sample of 200 unrelated individuals from Bolivia, South America.

© 2009 Elsevier Ireland Ltd. All rights reserved.

Population: Samples in this study were collected from 200 unrelated healthy individuals of Amerindian (Aymara) and mestizo populations of the metropolitan area of the city of La Paz, north-west area of Bolivia, previous informed consent.

Extraction: DNA was extracted by organic phenol–chloroform–isoamyl alcohol method.

PCR: PCR amplifications were performed using the AmpFISTR Identifiler PCR Amplification kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturers' recommendations.

Typing: Amplified products were analyzed using an ABI 3100 Avant DNA sequencer (Applied Biosystems, Foster City, CA, USA). Allele designations were made according to recommendations of the DNA Commission of the ISFG [1] with the aid of allelic ladders provided by the manufacturers.

Quality control: Proficiency testing of the Spanish–Portuguese Speaking Working Group of International Society for Forensic Genetics (GEP-ISFG) (<http://www.gep-isfg.org>).

Results: See Tables 1 and 2.

Analysis of data: Statistical evaluations were carried out with the aid of GDA and PowerStats software packages [2,3]. Statistical parameters such as power of discrimination (PD) and a priori chance of exclusion (CE) for each loci were estimated as described by Huston [4]. Also we calculated the polymorphic information content (PIC) according to Botstein et al. [5]. The Hardy–Weinberg

equilibrium for each loci were verified using the GDA program. AMOVA and population differentiation exact test were calculated with the Arlequin program [6], using the Bonferroni's correction [7].

Access of data: Available upon request to orocabadoc@hotmail.com.

Other remarks: No significant deviations from Hardy–Weinberg expectations based on the exact test (in all cases, the data were shuffled 2000 times) were found. The combined power of discrimination (PD) and the combined chance of exclusion (CE) for the 15 studied loci were >0.999999999 and 0.999984, respectively.

The allelic frequencies for each locus in Bolivia were compared with those in other Central and South American populations [8–16]. AMOVA results revealed that most of the molecular variation was due to variation within populations rather than among them, with all fixation indexes (Fst) below 0.044 (see Table 2).

In the exact test of population differentiation, statistically significant differences (after Bonferroni's correction; $P < 0.0033$) were found with the populations of Costa Rica [8], El Salvador [9], Venezuela [10], Honduras [11], Argentina [13], Brazil [14] and Mexico [15]. No differences were observed with the population of Peru [12]. Moreover, the results of this study have been also compared with other populations of Bolivia [16]. Statistically significant differences were found with the Beni population whereas no differences were observed with the Quechua and Aymara populations.

In conclusion, a Bolivian population database has been established for the 15 STR systems studied. These systems have been shown to be useful tool for personal identification.

* Corresponding author. Tel.: +34 94 6079533; fax: +34 94 6079500.
E-mail address: gobies01@euskalnet.net (O. García).

Table 1
Observed allele frequencies for 15 STR loci in the Bolivian population.

Allele	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	VWA	TPOX	D18S51	D5S818	FGA
6						0.226						0.003			
7			0.003			0.563								0.158	
8			0.040	0.005		0.015	0.013	0.005				0.663	0.003		
9	0.003		0.050	0.008		0.028	0.345	0.318				0.020		0.088	
9.3						0.168									
10	0.058		0.253	0.223		0.003	0.138	0.238				0.010	0.005	0.028	
10.2									0.003						
11	0.065		0.398	0.328			0.160	0.170	0.008			0.200	0.008	0.540	
12	0.130		0.230	0.370			0.123	0.190	0.028			0.105	0.095	0.153	
12.2									0.013						
13	0.290		0.028	0.060			0.143	0.073	0.163	0.008			0.170	0.035	
13.2									0.163						
14	0.225			0.008	0.025		0.073	0.008	0.330	0.013			0.250		
14.2									0.060						
15	0.213				0.510		0.008		0.148	0.045			0.173		
15.2									0.040						
16	0.015				0.310				0.035	0.348			0.115		
16.2									0.008						
17	0.003				0.123				0.178	0.003	0.400		0.118		
17.2									0.003						
18					0.030				0.068		0.138		0.030		0.013
19					0.003				0.343		0.048		0.020		0.145
20									0.135	0.003			0.008		0.050
21									0.028				0.005		0.085
22									0.045						0.065
23									0.138				0.003		0.068
24									0.045						0.163
25									0.010						0.233
26															0.145
27									0.003						0.033
28		0.045													0.003
29		0.215													
30		0.188													
30.2		0.020													
31		0.030													
31.2		0.220													
32		0.010													
32.2		0.195													
33.2		0.060													
34.2		0.013													
35		0.003													
35.2		0.003													
N	200	200	200	200	200	200	200	200	200	200	200	200	200	200	200
H	0.765	0.860	0.735	0.745	0.610	0.615	0.800	0.775	0.755	0.825	0.710	0.495	0.840	0.635	0.840
PD	0.930	0.940	0.874	0.850	0.793	0.792	0.929	0.912	0.939	0.937	0.856	0.716	0.953	0.834	0.962
CE	0.536	0.716	0.485	0.501	0.303	0.309	0.599	0.554	0.518	0.646	0.444	0.183	0.675	0.335	0.675
PIC	0.766	0.802	0.674	0.647	0.565	0.551	0.770	0.736	0.782	0.786	0.644	0.463	0.822	0.615	0.842
p	0.794	0.379	0.283	0.514	0.544	0.627	0.345	0.536	0.518	0.487	0.823	0.704	0.942	0.636	0.153

N, sample size; H, observed heterozygosity; PD, power of discrimination; CE, probability of paternity exclusion; PIC, polymorphic information content; p, Hardy–Weinberg equilibrium. Exact test based on 2000 shufflings.

Table 2
P values of population differentiation tested for each locus by an exact test and result for variation, for each locus, among populations (Fst) between this sample of Bolivia (BO) and other neighboring populations: Costa Rica (CR) [8], El Salvador (ES) [9], Venezuela (VE) [10], Honduras (HO) [11], Peru (PE) [12], Argentina (AR) [13], Brazil (BR) [14], Mexico (ME) [15] and other population of Bolivia (Beni -BO2-, Quechua -BO3- and Aymara -BO4-) [16].

Locus	BO vs. CR	BO vs. ES	BO vs. VE	BO vs. HO	BO vs. PE	BO vs. AR	HO vs. BR	BO vs. ME	BO vs. BO2	BO vs. BO3	BO vs. BO4	Fst**
D8S1179	0.0000*	0.2600	0.1594	0.7863	0.3636	0.7335	0.8306	0.1306				0.0006
D21S11	0.0000*	0.0340	0.0000*	0.0139	0.6752	0.0018*	0.0000*	0.0196				0.0048
D7S820	0.0005*	0.0682	0.0005*	0.0266	0.5718	0.0000*	0.0000*	0.0107				0.0035
CSF1PO	0.5950	0.6603	0.8141	0.6230	0.5028	0.6728	0.1235	0.7352	0.3632	0.7330	0.9578	0.0011
D3S1358	0.0000*	0.0122	0.0000*	0.0023*	0.9594	0.0000*		0.0000*				0.0113
TH01	0.0000*	0.0000*	0.0000*	0.0000*	0.0642	0.0000*	0.0000*	0.0000*	0.0000*	0.9050	0.6746	0.0441
D13S317	0.0000*	0.0002*	0.0000*	0.0001*	0.4231	0.0000*	0.0000*	0.0000*				0.0127
D16S539	0.0000*	0.0000*	0.0000*	0.0003*	0.5406	0.0000*	0.0000*	0.0000*				0.0074
D2S1338	0.0000*		0.0000*	0.0005*				0.0278				0.0109
D19S433	0.0000*		0.0029*	0.7614				0.0466				0.0053
VWA	0.0000*	0.0532	0.0000*	0.0077	0.4785	0.0000*	0.0003*	0.0000*	0.0000*	0.0811	0.3482	0.0201
TPOX	0.0000*	0.0003*	0.0000*	0.0022*	0.0091	0.0000*	0.0000*	0.0029*	0.0000*	0.0345	0.5755	0.0158
D18S51	0.0000*	0.0094	0.1997	0.0139	0.9437	0.1163	0.0055	0.4185				0.0009
D5S818	0.0000*	0.0000*	0.0000*	0.0000*	0.1288	0.0000*		0.0000*				0.0118
FGA	0.0009*	0.0659	0.0001*	0.0018*	0.7015	0.0000*	0.0000*					0.0031

* Significant differentiation test P-values, after Bonferroni correction.

** Variation among populations.

References

- [1] DNA recommendations. Report concerning further recommendations of the DNA commission of the ISFH regarding PCR-based polymorphisms in STR (short tandem repeat) system. *Forensic Sci Int* 1994;69:103–4.
- [2] Lewis PO, Zaykin D. Genetic Data Analysis, a computer program for the analysis of allelic data. Version 1.1, 2002. Free program distributed by the authors over the internet from the GDA home page. Available from: <http://alleyn.eeb.uconn.edu/gda/>.
- [3] PowerStats. A computer program for the analysis of population statistics, 1999. Free program distributed by the authors over the internet. Available from: <http://www.promega.com/geneticidtools/>.
- [4] Huston KA. Statistical analysis of STR data. *Profiles DNA* 1998;1(3):14–5.
- [5] Botstein D, White RL, Skolnick M, Davis RW. Construction of a genetic linkage map in man using restriction fragment length polymorphism. *Am J Hum Genet* 1980;32:314–31.
- [6] Excoffier L, Laval G, Schneider S. Arlequin ver 3.0: an integrated software package for population genetics data analysis. *Evol Bioinform Online* 2005;1:47–50.
- [7] Weir BS. Genetic data analysis II. USA: Sinauer Associates; 1996. p. 134.
- [8] Rodríguez A, Arrieta G, Sanóu I, Vargas MC, García O, Yurrebaso I, et al. Population genetic data for 18 STR loci in Costa Rica. *Forensic Sci Int* 2007; 168(1):85–8.
- [9] Monterrosa JC, Morales JA, García O. Genetic variation for 15 short tandem repeat loci in an El Salvadoran (Central America) population. *J Forensic Sci* 2006;51(2):451–2.
- [10] Chiurillo MA, Morales A, Mendes AM, Lander N, Tovar F, Fuentes A, et al. Genetic profiling of a central Venezuelan population using 15 STR markers that may be of forensic importance. *Forensic Sci Int* 2003;136(1–3):99–101.
- [11] Matamoros M, Pinto Y, Inda FJ, García O. Population genetic data for 15 STR loci (Identifiler™ kit) in Honduras. *Legal Med* 2008;10:281–3.
- [12] Pérez L, Hau J, Izarra F, Ochoa O, Zubieta U, García O. Allele frequencies for the 13 CODIS STR loci in Peru. *Forensic Sci Int* 2003;132(2):164–5.
- [13] Marino M, Sala A, Corach D. Population genetic analysis of 15 STRs loci in the central region of Argentina. *Forensic Sci Int* 2006;161(1):72–7.
- [14] Gomes AV, Mauricio-da-Silva L, Raposo G, Vieira JR, dos Santos Silva R. 13 STR loci frequencies in the population from Paraíba, Northeast Brazil. *Forensic Sci Int* 2007;173(2–3):231–4.
- [15] Hernández-Gutiérrez S, Hernández-Franco P, Martínez-Tripp S, Ramos-Kuri M, Rangel-Villalobos H. STR data for 15 loci in a population sample from the central region of Mexico. *Forensic Sci Int* 2005;151(1):97–100.
- [16] Corella A, Bert F, Pérez-Pérez A, Gené M, Turbón D. HUMTH01, HUMVWA31A, HUMCSF1PO and HUMTPOX polymorphisms in Amerindian populations living in the Beni Department of Bolivia. *Ann Hum Biol* 2008; 35(5):556–64.