Announcement of Population Data

Microsatellite autosomal genotyping data in four indigenous populations from El Salvador

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Abstract

Fifteen microsatellite loci (D3S1358, TH01, D21S11, D18S51, PENTA E, D5S818, D13S317, D7S820, D16S539, CSF1PO, PENTA D, vWA, D8S1179, TPOX, and FGA) have been genotyped in four indigenous populations from El Salvador (Central America), namely, Conchagua, Izalco, Panchimalco, and San Alejo. Here we have obtained values for several indices of forensic interest for these population samples. Population differentiation test showed no significant statistical differences between these four populations, and an AMOVA test indicates that most of the genetic variation (~100%) occurs within individuals. Population pairwise genetic comparisons with other population samples seem to indicate the existence of a major Native American component in the populations from El Salvador.
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Keywords: STRs; Microsatellite; Population data; Conchagua; Izalco; Panchimalco; San Alejo; Native American; El Salvador

Population: Unrelated individuals from four indigenous populations from El Salvador: Izalco and Panchimalco in northwest towards the Ocean Pacific coast, and Conchagua and San Alejo in the south, also close to the coastal line. Fig. 1 shows the location of these populations.

PCR: PCR amplification was performed using the Power-Plex[16] kit and following the manufacturer conditions (Promega Corporation, Madison, WI, USA).

Typing: Amplicons were separated using an ABI PRISM 3100 Genetic Analyser (Applied Biosystems, Foster City, CA). Genescan analysis version 3.1.2 and Genotyper version 2.5.2 software were used for data analysis.

Results: See Tables 1–5 for results. Tables 1–4 show allele frequencies for the 15 STRs genotyped and various statistical parameters of forensic interest.

Quality control: Proficiency testing of the Spanish and Portuguese group of the International Society of Forensic Genetics (GEP-ISFG; http://www.gep-isfg.org).

Analysis of data: Heterozigosity values (observed and expected) were calculated according to Nei [1]. Several forensic and population parameters were estimated using the PowerStats v.12 (http://www.promega.com/; more information about statistical indices in Refs. [2,3]) software, Arlequin 3.0 [4], and Genepop [5].

Access to the data: apimlase@usc.es.

Other remarks: Deviation from Hardy–Weinberg equilibrium has been detected for the FGA ($P = 0.0165 \pm 0.0002$) in Conchagua, vWA ($P = 0.0132 \pm 0.0003$) in San Alejo, and D8S1179 ($P = 0.0220 \pm 0.0003$). These departures from equilibrium disappear under a (conservative) Bonferroni correction. Linkage disequilibrium has been tested using shuffling test for all possible combinations between loci. We have obtained a probability higher than 0.05 in most of the cases, indicating (most likely) independence of loci. We observed sporadic slight deviations from linkage disequilibrium but not more than those expected under a scenario of multiple testing.

Table 5 shows the expected and observed heterozygosities by populations; San Alejo shows the highest values. Population differentiation test (as performed in the Arlequin software) between all pairs of population samples shows non-significant
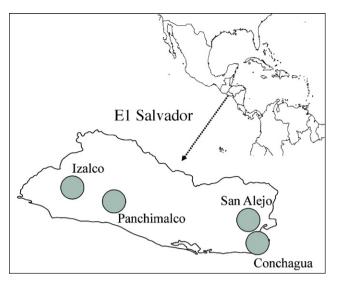

Fig. 1. Map showing the locations of the populations analyzed in the present study.

P-values. Population comparisons (based on frequency data) with other populations from America show that the populations from El Salvador analyzed in the present study cluster with other Native Americans, be while showing a clear differentiation with those of a main European and/or African ancestry (data not shown). Although there is not data about the admixture proportions in these populations, these results seem to suggest that the predominant component is of a Native American nature. Analysis of molecular variance (AMOVA) test was carried out as implemented in Arlequin. The significance of the covariance components associated with the different possible levels of genetic structure was tested using non-parametric permutation procedure. AMOVA shows that most of the genetic variation (~100%) occurs within individuals, a result which could be not very informative taking into account the number of loci and sample sizes used in the present study (see below).

It is worth to mention that while the amount of population data available for other Latino-American countries is quite abundant (e.g. [6–10]; only few of them analyzed Native

Table 1
Allele frequencies distribution for 15 STR loci in the Conchagua population (El Salvador; $N = 49$)

Alelo	D3S1358	TH01	D21S11	D18S51	PENTA E	D5S818	D13S317	D7S820	D16S539	CSF1PO	PENTA D	vWA	D8S1179	TPOX	FGA
5					0.0204						0.0102				
6		0.5918													
7		0.1837			0.0408	0.0408									
8					0.0102	0.0204	0.0306	0.0102			0.0102				0.4796
9		0.0714				0.0612	0.1837	0.0204	0.1633	0.0204	0.1837		0.0102		0.0714
9.3		0.1531													
10					0.0204	0.0612	0.2041	0.3061	0.1735	0.2143	0.1939		0.0204		
11				0.0102	0.0510	0.5510	0.1633	0.3265	0.2449	0.2551	0.1122		0.0204	0.3367	
12				0.1020	0.2959	0.2347	0.2245	0.2755	0.3571	0.3673	0.1633		0.1122	0.1122	
13				0.1224	0.0510	0.0306	0.1020	0.0612	0.0408	0.1327	0.2449		0.2143		
14	0.0306			0.1939	0.1633		0.0816		0.0102	0.0102	0.0612	0.0612	0.5102		
15	0.6327			0.1735	0.0510		0.0102		0.0102		0.0204	0.0612	0.0816		
16	0.1735			0.0816	0.0918							0.4082	0.0306		
17	0.0714			0.2143	0.0204							0.3265			
18	0.0918			0.0612	0.0102							0.1122			
19				0.0204	0.1429							0.0306			0.2143
20				0.0204	0.0102										0.0408
21															0.0204
22					0.0102										0.0816
22.2			0.0102												0.0204
23															0.0408
24															0.1939
24.2			0.0102												
25					0.0102										0.1531
26															0.2143
27			0.0102												0.0204
28			0.0612												
29			0.0918												
30			0.3980												
30.2			0.0408												
31			0.0408												
31.2			0.0408												
32			0.0408												
32.2			0.2041												
33.2			0.0306												
36			0.0102												
39			0.0102												