FOR THE RECORD

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Population Data on Nine STR Loci in an El Salvadoran (Central American) Sample Population

POPULATION: El Salvador, Central America

KEYWORDS: forensic science, DNA typing, population genetics, El Salvador, Central America

Blood samples were obtained by venipuncture from unrelated individuals ($n = 323$) living in El Salvador. Approximately 1–3 ng of DNA were used in each PCR. The samples were amplified using the Profiler Plus™ kit (PE) and the alleles were separated and detected using an Applied Biosystems ABI310 genetic analyzer. The frequency of each allele for each locus was calculated from the numbers of each genotype in the sample set (i.e., the gene count method). Unbiased estimates of expected heterozygosity were computed as described by Edwards et al. (1). Possible divergence from Hardy-Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies (1–4) and the exact test (5), based on 2000 shufflings experiments. An interclass correlation criterion (6) for two-locus associations was used for detecting disequilibrium between the STR loci. The program for this analysis was kindly provided by R. Chakraborty (University of Texas, School of Biomedical Sciences, Houston, TX).

The distributions of the observed allele frequencies for the nine STR loci are shown in Table 1. The most informative loci are FGA and D18S51, and the least discriminating are D3S1358 and D5S818 (Table 2). Seven of the nine loci meet Hardy-Weinberg expectations. The loci FGA ($p = 0.046$) and vWA ($p = 0.028$) departed from expectations based on the exact test. These two departures are not significant after correction for sampling (i.e., Bonferroni (7)). There is little evidence for association of alleles between pairs of the nine loci. Only one (D3S1358/D7S820: $p = 0.006$) of 38 pairwise comparisons demonstrated a departure from expectations of independence. This number of departures is within expectations of departure by chance. The combined power of discrimination is >0.999999999, and the combined power of exclusion is 0.99982.

The complete data set can be accessed at www.gitad.org.

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TABLE 1—*Observed allele frequencies for the nine Profiler Plus™ loci.*

	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
5	...	...	...	...	...	...	...	...	...
6	...	...	...	...	...	...	...	...	...
7	...	...	...	...	...	...	0.040	...	0.005
8	...	...	...	0.005	...	...	0.015	0.068	0.074
9	...	...	...	0.009	...	0.002	0.059	0.187	0.076
9.3	...	...	...	...	...	...	...	...	...
10	...	...	...	0.065	...	0.005	0.062	0.105	0.270
11	...	...	...	0.071	...	0.014	0.450	0.221	0.285
12	...	...	...	0.108	...	0.099	0.280	0.204	0.228
13	0.002	0.002	...	0.303	...	0.119	0.085	0.155	0.048
14	0.076	0.067	...	0.289	...	0.186	0.008	0.057	0.006
15	0.449	0.105	...	0.135	...	0.153	...	0.002	...
16	0.245	0.337	...	0.014	...	0.139	...	...	...
17	0.130	0.283	...	...	...	0.149	...	...	...
18	0.091	0.169	0.005	...	...	0.060	...	...	...
18.2	...	...	0.002		...	...	...	...	...
19	0.008	0.037	0.076	...	...	0.034	...	...	...
19.2	...	...	0.002	...	...	...	...	...	...
20	...	...	0.056	...	...	0.017	...	...	...
21	...	...	0.090	...	...	0.012	...	...	...
22	...	...	0.108	...	...	0.005	...	...	...
22.2	...	...	0.002	...	...	...	...	...	...
23	...	...	0.139	...	...	0.006			
23.2	...	...	0.003	...	...	...	...	...	...
24	...	...	0.194	...	...	...	...	...	...
24.2	...	...	...	...	0.003	...	...	...	...
25	...	...	0.183	...	...	...	...	...	...
26	...	...	0.099	...	0.002	...	...	...	...
27	...	...	0.029	...	0.009	...	...	...	...
28	...	...	0.014	...	0.081	...	...	...	...
29	...	...	...	...	0.223	...	...	...	...
29.2	...	...	...	...	0.002	...	...	...	...
30	...	...	...	...	0.285	...	...	...	...
30.2	...	...	...	...	0.017	...	...	...	...
31	...	...	...	...	0.048	...	...	...	...
31.2	...	...	...	...	0.116	...	...	...	...
32	...	...	...	...	0.012	...	...	...	...
32.2	...	...	...	...	0.014	...	...	...	...
33	...	...	...	...	0.003	...	...	...	...
33.2	...	...	...	...	0.037	...	...	...	...
34.2	...	...	...	...	0.014	...	...	...	...
35	...	...	...	...	0.003	...	...	...	...
36	...	...	...	...	0.002	...	...	...	...

TABLE 2—*Observed and expected (unbiased) homozygosities. HWE-homozygosity test and exact test for nine STR loci.*

	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
Obs. Hom.	0.350	0.310	0.108	0.238	0.195	0.149	0.331	0.170	0.241
Exp. Hom.	0.291	0.238	0.128	0.214	0.175	0.128	0.297	0.168	0.223
Hom. Test (p)	0.021	0.003	0.281	0.287	0.335	0.260	0.175	0.894	0.424
Exact test (p)	0.155	0.046	0.028	0.919	0.781	0.226	0.252	0.770	0.179
P.D.	0.876	0.908	0.965	0.924	0.946	0.967	0.871	0.948	0.916
P.E.	0.480	0.544	0.739	0.588	0.658	0.739	0.478	0.661	0.565