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Short communication

Population data on 15 autosomal STRs in a sample from East Timor

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Abstract

Allele frequencies for the fifteen STRs included in the AmpF/STR Identifiler (CSF1PO, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D19S433, D21S11, FGA, TH01, TPO and VWA) were estimated from a sample of 186 unrelated individuals from East Timor. No deviations from Hardy–Weinberg equilibrium were observed (only after applying the Bonferroni correction in the cases of D2S1338, TPO and D5S818). Genetic parameters of forensic interest were calculated and comparison with geographically nearby populations was performed.

Keywords: East Timor; STRs; Population data; AmpF/STR identifiler

Population: 186 unrelated individuals from East Timor. This sample includes 107 individuals previously reported [1].

DNA extraction: Chelex method [2].

PCR: according to the manufacturers (AmpF/STR Identifiler PCR amplification kit, AB Applied Biosystems).

Typing: ABI 310 and reference sequenced ladders (AB Applied Biosystems).

Results: See Tables 1 and 2.

Quality control: Proficiency testing of the GEP-ISFG WG.

Analysis of data: Hardy–Weinberg equilibrium, expected and observed heterozygosity and population differentiation tests were carried out with the Arlequin software Version 2.000 [3]. Power of discrimination (PD) and probability of exclusion (PE) were calculated with the Powerstats Version 1.2 (Promega Corp.) [4].

Access to the data: http://www.bio.ua.pt/STR.

Other remarks: Population data regarding our sample for the 15 STRs from East Timor (Fig. 1) are shown in Table 1. No deviations from Hardy–Weinberg equilibrium were observed with the exception of the D2S1338, TPO and D5S818 loci. After employing the Bonferroni correction for the number of loci analysed, the departure observed at these loci was not significant (0.05/15 = 0.003).

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Fig. 1. Map of southern Asia indicating the origin of our sample (East Timor), and Indonesia and Malaysia regions to which our sample was compared with.

Table 1
Population data for AmpF/STR Identifiler in East Timor ($N = 186$)

Allele	CSF1PO	D2S1338	D3S1358	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D19S433	D21S11	FGA	TH01	TPO	VWA
6	–	–	–	–	–	–	–	–	–	–	–	–	0.081	0.003	–
7	–	–	–	0.003	0.008	–	–	–	–	–	–	–	0.177	–	–
7.2	–	–	–	–	0.003	–	–	–	–	–	–	–	–	–	–
8	0.003	–	–	–	0.260	0.003	0.272	0.030	–	–	–	–	0.339	0.304	–
9	0.065	–	–	0.024	0.027	–	0.097	0.145	–	–	–	–	0.341	0.296	–
9.3	–	–	–	–	–	–	–	–	–	–	–	–	0.019	–	–
10	0.249	–	–	0.301	0.223	0.054	0.126	0.167	–	–	–	–	0.043	0.035	–
10.2	–	–	–	–	0.003	–	–	0.003	0.011	–	–	–	–	–	–
11	0.304	–	–	0.223	0.290	0.102	0.247	0.338	0.011	0.003	–	–	–	0.327	–
11.2	–	–	–	–	–	–	–	–	0.004	–	–	–	–	–	–
12	0.304	–	0.005	0.320	0.156	0.099	0.185	0.202	0.040	0.046	–	–	–	0.035	–
12.2	–	–	–	–	–	–	–	–	–	0.003	–	–	–	–	–
13	0.070	–	0.011	0.124	0.027	0.204	0.054	0.099	0.075	0.322	–	–	–	–	0.003
13.2	–	–	–	–	–	–	–	–	–	0.019	–	–	–	–	–
14	0.005	–	0.013	0.005	0.003	0.235	0.019	0.011	0.198	0.249	–	–	–	–	0.094
14.2	–	–	–	–	–	–	–	–	0.008	0.081	–	–	–	–	–
15	–	–	0.337	–	–	0.142	–	0.005	0.155	0.070	–	–	–	–	0.081
15.2	–	–	–	–	–	–	–	–	–	0.150	–	–	–	–	–
16	–	–	0.306	–	–	0.097	–	–	0.136	0.024	–	–	–	–	0.172
16.2	–	–	–	–	–	–	–	–	–	0.027	–	–	–	–	–
17	–	0.059	0.266	–	–	0.059	–	–	0.158	0.003	–	–	–	–	0.241
17.2	–	–	–	–	–	–	–	–	–	0.003	–	–	–	–	–
18	–	0.040	0.059	–	–	0.005	–	–	0.073	–	–	0.008	–	–	0.287
19	–	0.240	0.003	–	–	–	–	–	0.059	–	–	0.086	–	–	0.097
20	–	0.046	–	–	–	–	–	–	0.024	–	–	0.051	–	–	0.022
21	–	0.032	–	–	–	–	–	–	0.019	–	–	0.124	–	–	0.003
22	–	0.105	–	–	–	–	–	–	0.027	–	–	0.167	–	–	–
23	–	0.196	–	–	–	–	–	–	0.005	–	–	0.180	–	–	–
24	–	0.204	–	–	–	–	–	–	–	–	–	0.174	–	–	–
25	–	0.065	–	–	–	–	–	–	0.005	–	–	0.099	–	–	–
26	–	0.008	–	–	–	–	–	–	0.003	–	–	0.081	–	–	–
27	–	0.005	–	–	–	–	–	–	–	–	0.008	0.027	–	–	–

Table 1 (*Continued*)

Allele	CSF1PO	D2S1338	D3S1358	D5S818	D7S820	D8S1179	D13S317	D16S539	D18S51	D19S433	D21S11	FGA	TH01	TPO	VWA
28	–	–	–	–	–	–	–	–	–	–	0.105	0.003	–	–	–
29	–	–	–	–	–	–	–	–	–	–	0.223	–	–	–	–
30	–	–	–	–	–	–	–	–	–	–	0.204	–	–	–	–
30.2	–	–	–	–	–	–	–	–	–	–	0.008	–	–	–	–
31	–	–	–	–	–	–	–	–	–	–	0.126	–	–	–	–
31.2	–	–	–	–	–	–	–	–	–	–	0.118	–	–	–	–
32	–	–	–	–	–	–	–	–	–	–	0.019	–	–	–	–
32.2	–	–	–	–	–	–	–	–	–	–	0.148	–	–	–	–
33	–	–	–	–	–	–	–	–	–	–	0.005	–	–	–	–
33.2	–	–	–	–	–	–	–	–	–	–	0.030	–	–	–	–
35.2	–	–	–	–	–	–	–	–	–	–	0.003	–	–	–	–
37.2	–	–	–	–	–	–	–	–	–	–	0.003	–	–	–	–
H_o	0.785	0.785	0.726	0.710	0.785	0.887	0.796	0.780	0.882	0.817	0.882	0.887	0.753	0.747	0.849
H_e	0.746	0.841	0.722	0.743	0.774	0.849	0.804	0.788	0.877	0.799	0.847	0.869	0.731	0.712	0.806
PD	0.884	0.953	0.867	0.886	0.903	0.953	0.928	0.924	0.966	0.927	0.950	0.962	0.872	0.848	0.925
PE	0.571	0.571	0.469	0.443	0.571	0.769	0.591	0.562	0.758	0.631	0.758	0.769	0.514	0.505	0.694
P	0.851	0.032[a]	0.351	0.046[a]	0.072	0.465	0.416	0.901	0.223	0.796	0.090	0.336	0.404	0.014[a]	0.153

H_o (observed heterozigosity), H_e (expected heterozigosity), PD (power of discrimination), PE (power of exclusion), P (Hardy–Weinberg equilibrium, exact test based on more than 2000 shufflings, for S.E. < 0.01).

[a] Bonferroni correction (0.05/15 = 0.003).

Table 2
Population differentiation test probability values resulting from the comparison of our sample (TIMOR) with four Indonesian ‘‘Malay’’ samples: INDON1 [6]; INDON2 [7]; INDON3 (which includes SULAWESI and SUMATRA [7]) plus a Malaysian ‘‘Malay’’ sample (MALAS, [8]) and a sample from MACAU [9]

Loci	TIMOR vs. INDON1 (Surabaya)	TIMOR vs. INDON2 (Jakarta, Surabaya)	TIMOR vs. INDON3 (Sulawesi/Sumatra)	TIMOR vs. MALAS	TIMOR vs. MACAU
CSF1PO	0.428	–	–	0.256	–
D2S1338	–	0.026[a]	0.192	0.005[a]	–
D3S1358	0.026[a]	0.643	0.646	0.062	0.664
D5S818	0.131	–	–	0.215	0.007
D7S820	0.088	–	–	0.879	0.620
D8S1179	–	0.646	0.764/0.192[b]	0.473	0.349
D13S317	0.244	–	–	0.342	0.674
D16S539	–	0.578	0.862	0.839	–
D18S51	–	0.130	0.456	0.036[a]	0.487
D19S433	–	0.110	0.890	0.312	–
D21S11	–	0.426	0.927	0.341	0.292
FGA	0.003[a]	0.439	0.797	0.354	0.097
TH01	0.000	0.000	0.000	0.0000	–
TPO	0.000	0.000	–	0.0000	–
VWA	0.147	0.126	0.845	0.251	0.003[a]

[a] Not significant after Bonferroni correction (0.05/15 = 0.003).

[b] For D8S1179, comparison was done separately with the Sulawesi and Sumatra samples, since the authors [7] found significant differences between them and reported frequency data for each individually.

In our sample we found an individual with an ‘‘off-ladder’’ rare allele at the D21S11 locus (allele 37.2). This allele has only been reported in populations of Australia, namely Aborigine [5].

Single locus comparisons with available published data on other populations from the region (Table 2), revealed significant differences between all populations for two out of fifteen loci (TH01 and TPO). In some loci (footnote a in Table 2), differences were not significant only after Bonferroni's correction. Higher non-differentiation P values were obtained when comparing the East Timor sample with the Indonesian Sulawesi and Sumatra samples (except for TH01). A sample from Macau, a territory with secular relations with East Timor, was also considered for comparison and nonsignificant P values were obtained for the markers available.

Concerning discrimination capacity, the overall matching probability (15 STRs) for our sample is 1 in 2.57×10^{17} individuals and power of exclusion of 0.99999965.

This paper follows the guidelines for publication of population data requested by the journal [10].

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