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Announcement of Population Data

STR data for the AmpFℓSTR® SGM Plus® loci from two South Asian populations

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ABSTRACT

Using the Applied Biosystems' AmpFℓSTR® SGM Plus® PCR amplification kit, we studied the allele frequency distribution of 10 STR loci in two south Asian populations: one from the Gujarat region of India represented by 172 unrelated Gujaratis, now resident in England; and a Pakistani population, represented by 155 unrelated individuals. Gujarat borders southeast Pakistan. There were no significant deviations from Hardy–Weinberg equilibrium in either population after Bonferroni correction. The combined power of discrimination and exclusion for the Indian population were 0.999999999999544 and 0.9999785, respectively; for the Pakistani population, they were 0.999999999999865 and 0.9998975, respectively. F_{ST} (or θ) between these two populations was estimated as 0.00146.

Population: Samples were taken from 172 unrelated individuals of Gujarati origin (from the Gujarat region of Western India) living in Preston, England. A further 155 samples collected from Pakistan, comprised of Punjabi (40), Pushtoon (61) and Sindi (54) individuals. Prior to sample collection, written informed consent was obtained. Individuals were grouped according to self-classification of their ancestry.

Extraction: DNA was extracted using the QIAamp® DNA Blood Mini Kit (Qiagen, Hilden, Germany) in accordance with manufacturer's guidelines.

PCR amplification: PCR was performed using the AmpFℓSTR® SGM Plus® PCR amplification kit (Applied Biosystems, Foster City, USA) using the GeneAmp® PCR System 2700 (Applied Biosystems) in accordance with manufacturer's guidelines, but using reduced volume reactions.

Typing: PCR products were analysed by capillary gel electrophoresis using the ABI 310 DNA Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) and analysed with both GeneScan® version 3.1.2 (Applied Biosystems) and GeneMapper® *ID* version 3.2 (Applied Biosystems). The alleles from all loci reported here were called according to the published nomenclatures and the ISFG guidelines for performing STR analyses [1].

Analysis of data: Allele frequencies, power of discrimination, power of exclusion, polymorphism information content, match probability and typical paternity index were calculated using the Excel PowerStats spreadsheet (Promega Corporation, Madison, WI, USA) [2]. Expected heterozygosity, observed heterozygosity, an exact test for Hardy–Weinberg equilibrium and pairwise F_{ST} were estimated using Arlequin version 3.1 [3] (Tables 1 and 2).

Access to data: Available upon request. Please contact whgoodwin@uclan.ac.uk.

Other remarks: The most discriminating marker in the Indian Gujurati and Pakistani populations is D2S1338, with a power of discrimination of 0.967 and 0.968, respectively. Deviation from Hardy–Weinberg equilibrium was observed at two loci, D19S442 and FGA, in the Indian dataset, where p was observed to be <0.05 (Table 1). However, after Bonferroni correction was applied, which based on the number of loci examined tolerated p values to 0.005 ($0.05/10 = 0.005$), all loci were in equilibrium.

An exact test of population differentiation was also conducted between our datasets and allele frequency datasets from Bangladeshi [4], Iraqi [5], Iranian [6] and Malaysian [7] populations (Table 3). Little differentiation can be seen between the Indian and Pakistani populations – an observation supported by the low F_{ST} estimate of 0.00146. While there is little differentiation between populations with similar geographic ancestral history, e.g. India, Pakistan and Bangladesh; populations farther towards Persia and Southeast Asia, show greater differentiation, as expected.

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Table 1
Observed Gujarati allele frequencies (*n* = 172)

Allele	D3S1385	vWA	D16S539	D2S1338	D8S1179	D21S11	D18S51	D19S443	TH01	FGA
6	–	–	–	–	–	–	–	–	0.2471	–
7	–	–	–	–	–	–	–	–	0.1890	–
7.3	–	–	–	–	–	–	–	–	–	–
8	–	–	0.0552	–	0.0087	–	–	–	0.1221	–
8.3	–	–	–	–	–	–	–	–	–	–
9	–	–	0.1483	–	0.0174	–	–	0.0029	0.2762	–
9.3	–	–	–	–	–	–	–	–	0.1599	–
10	–	–	0.0843	–	0.1686	–	0.0087	–	0.0058	–
10.2	–	–	–	–	–	–	–	–	–	–
11	–	–	0.3459	–	0.0756	–	0.0087	–	–	–
12	–	–	0.2035	–	0.1308	–	0.0930	0.1163	–	–
12.2	–	–	–	–	–	–	–	0.0116	–	–
13	0.0058	0.0029	0.1424	–	0.2500	–	0.1279	0.2907	–	–
13.2	–	–	–	–	–	–	–	0.0116	–	–
14	0.0785	0.1337	0.0174	–	0.1628	–	0.2820	0.2471	–	–
14.2	–	–	–	–	–	–	–	0.0436	–	–
15	0.2820	0.0581	0.0029	–	0.1308	–	0.1802	0.1366	–	–
15.2	–	–	–	–	–	–	–	0.0698	–	–
16	0.2733	0.2558	–	0.0087	0.0436	0.0029	0.1192	0.0349	–	–
16.2	–	–	–	–	–	–	–	0.0174	–	–
17	0.2529	0.2820	–	0.0465	0.0116	–	0.0872	0.0145	–	–
17.2	–	–	–	–	–	–	–	–	–	–
18	0.1076	0.1860	–	0.1919	–	–	0.0291	–	–	0.0029
18.2	–	–	–	–	–	–	–	0.0029	–	–
19	–	0.0698	–	0.1599	–	–	0.0291	–	–	0.1047
20	–	0.0087	–	0.1221	–	0.0058	0.0145	–	–	0.0988
21	–	0.0029	–	0.0291	–	–	0.0087	–	–	0.1076
21.2	–	–	–	–	–	–	–	–	–	0.0029
22	–	–	–	0.0959	–	–	–	–	–	0.1221
22.2	–	–	–	–	–	–	–	–	–	0.0233
23	–	–	–	0.1715	–	–	0.0087	–	–	0.1541
23.2	–	–	–	–	–	–	–	–	–	0.0029
24	–	–	–	0.0814	–	–	0.0029	–	–	0.2006
24.2	–	–	–	–	–	–	–	–	–	0.0029
25	–	–	–	0.0669	–	–	–	–	–	0.1047
26	–	–	–	0.0233	–	–	–	–	–	0.0523
26.2	–	–	–	–	–	–	–	–	–	0.0058
27	–	–	–	0.0029	–	0.0116	–	–	–	0.0087
28	–	–	–	–	–	0.1279	–	–	–	0.0058
29	–	–	–	–	–	0.2122	–	–	–	–
29.2	–	–	–	–	–	0.0029	–	–	–	–
30	–	–	–	–	–	0.1890	–	–	–	–
30.2	–	–	–	–	–	0.0262	–	–	–	–
31	–	–	–	–	–	0.0262	–	–	–	–
31.2	–	–	–	–	–	0.1308	–	–	–	–
32	–	–	–	–	–	0.0058	–	–	–	–
32.2	–	–	–	–	–	0.1599	–	–	–	–
33.2	–	–	–	–	–	0.0843	–	–	–	–
34.2	–	–	–	–	–	0.0116	–	–	–	–
35.2	–	–	–	–	–	0.0029	–	–	–	–
Ho	0.744	0.855	0.791	0.814	0.872	0.837	0.837	0.756	0.703	0.890
He	0.766	0.797	0.788	0.872	0.843	0.834	0.841	0.764	0.700	0.868
PD	0.905	0.908	0.921	0.967	0.952	0.957	0.954	0.933	0.915	0.963
PE	0.500	0.704	0.582	0.625	0.739	0.704	0.670	0.625	0.571	0.774
p	0.821	0.073	0.878	0.312	0.987	0.966	0.932	0.023[a]	0.364	0.024[a]
PIC	0.725	0.764	0.757	0.856	0.821	0.830	0.821	0.790	0.750	0.860
MP	0.095	0.092	0.079	0.033	0.048	0.043	0.046	0.067	0.085	0.037
TPI	1.950	3.440	2.390	2.690	3.910	3.440	3.070	2.690	2.320	4.530

Ho, observed heterozygosity; He, expected heterozygosity; PD, power of discrimination; PE, power of exclusion; p, exact test of Hardy–Weinberg; PIC, polymorphic information content; MP, match probability; TPI, typical paternity index.

[a] Bonferroni correction (0.05/10 = 0.005).