

FOR THE RECORD

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Allele Frequency Data for Profiler Plus Loci in Australia

POPULATION: Data from over 12,000 Profiler Plus™ profiles collected from eight Australian forensic agencies have been combined to give samples for three major groups: Asian ($N = 721$), Aboriginal ($N = 3515$) and Caucasian ($N = 8261$).

KEYWORDS: forensic science, population genetics, Australia, D3S135, vWA, FGA, D8S117, D21S11, D18S51, D5S818, D13S31, D7S820, CSF1PO, TPOX, TH01, D16S53

The data reported here are from Australian Federal Police (419 Caucasian), New South Wales (358 Caucasian), Queensland (75 Asian, 480 Aboriginal, 1411 Caucasian), Northern Territory (119 Asian, 560 Full-blooded Aboriginal plus 1697 Declared Aboriginal, 2130 Caucasian), South Australia (119 Aboriginal, 412 Caucasian), Tasmania (600 Caucasian), Victoria (115 Asian, 286 Caucasian), Western Australia (115 Asian, 659 Aboriginal, 2644 Caucasian). These data form a larger set than those previously reported for Australia (1–3).

Allele frequencies are shown in Tables 1–9, and these tables reflect some minor differences among laboratories in allele designations: at D21S11, for example, one laboratory does not size alleles above 39, and uses the >39 notation. Other laboratories report allele sizes of 39.2, 40.2 and 41.2.

An exact test for Hardy-Weinberg (4) was performed for each locus in each of the three combined samples. The p -values (PE) based on 10,000 permutations are shown in Tables 1–9. There are more

values below the conventional 5% significance level than are usually reported in this journal, which may be due to the sample sizes being larger than usual. It is helpful to combine p -values over both loci and samples, and the combined values from Fisher's procedure (5) are shown in Table 10. The generally low values for the Aboriginal data are likely due to some of those data being from an admixed population. Low values were also found when the Aboriginal samples were considered separately. Because Australian forensic agencies use (conditional) match probabilities with appropriate values of θ (6), the observed departures from Hardy-Weinberg are not relevant. Unpublished results confirm that multi-locus matching probabilities are conservatively estimated by θ values of 0.01 or higher.

The complete dataset is available upon request from B. S. Weir via email: weir@stat.ncsu.edu.

TABLE 1—Sample allele frequencies for D3S1358.

Allele	Asian $N:711$	Aboriginal $N:3515$	Caucasian $N:8197$
11	.0014	.0009	.0016
12	.0014	.0021	.0010
13	.0021	.0026	.0027
14	.0387	.0516	.1213
15	.3481	.3711	.2691
16	.3186	.2488	.2561
17	.2145	.2026	.1940
18	.0668	.1064	.1415
19	.0056	.0127	.0121
20	.0028	.0010	.0006
21	.0000	.0003	.0000
21.1	.0000	.0000	.0001
PE:	0.112	0.674	0.985

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TABLE 2—Sample allele frequencies for vWA.

Allele	Asian N:716	Aboriginal N:3515	Caucasian N:8202
11	.0007	.0000	.0001
12	.0000	.0000	.0002
13	.0000	.0004	.0010
14	.2430	.0458	.1080
15	.0377	.0674	.0978
16	.1522	.2293	.2140
17	.2521	.2910	.2719
18	.2109	.2179	.2032
19	.0831	.1260	.0868
20	.0189	.0209	.0157
21	.0014	.0011	.0013
22	.0000	.0000	.0001
PE:	0.128	0.006	0.767

TABLE 3—Sample allele frequencies for FGA.

Allele	Asian N:718	Aboriginal N:3515	Caucasian N:8230
15	.0000	.0000	.0002
16	.0014	.0013	.0001
16.1	.0000	.0000	.0001
17	.0014	.0047	.0011
18	.0265	.0256	.0166
18.2	.0007	.0000	.0000
19	.0787	.0688	.0605
19.2	.0000	.0000	.0002
20	.0474	.1041	.1394
20.2	.0007	.0016	.0016
21	.1226	.1149	.1787
21.2	.0077	.0040	.0026
22	.1831	.1775	.1855
22.2	.0097	.0065	.0098
23	.1636	.1553	.1423
23.2	.0132	.0034	.0047
24	.1671	.1578	.1352
24.2	.0077	.0028	.0010
24.3	.0000	.0000	.0001
25	.0794	.1185	.0804
25.2	.0063	.0003	.0004
25.3	.0000	.0000	.0001
26	.0682	.0398	.0317
26.1	.0000	.0000	.0001
26.2	.0007	.0001	.0001
27	.0132	.0114	.0068
27.1	.0000	.0001	.0000
28	.0007	.0010	.0009
29	.0000	.0003	.0001
PE:	0.574	0.141	0.452

TABLE 4—Sample allele frequencies for D8S1179.

Allele	Asian N:719	Aboriginal N:3515	Caucasian N:8198
6	.0007	.0000	.0000
8	.0021	.0047	.0198
9	.0021	.0048	.0121
10	.1391	.0384	.0934
11	.1015	.0821	.0780
12	.1342	.1543	.1427
13	.2114	.2371	.3156
14	.1669	.1809	.1971
15	.1572	.1885	.1072
15.3	.0000	.0009	.0000
16	.0647	.0792	.0303
17	.0139	.0256	.0036
18	.0063	.0033	.0002
19	.0000	.0001	.0000
PE:	0.761	0.323	0.002

TABLE 5—Sample allele frequencies for D21S11.

Allele	Asian N:718	Aboriginal N:3513	Caucasian N:8220
12	.0000	.0004	.0000
20	.0007	.0000	.0000
24.2	.0000	.0000	.0010
25	.0000	.0000	.0001
25.2	.0000	.0023	.0009
26	.0007	.0038	.0015
26.2	.0000	.0000	.0004
27	.0049	.0151	.0372
27.2	.0000	.0000	.0001
28	.0703	.1116	.1504
28.2	.0042	.0000	.0001
29	.2702	.2327	.2134
29.2	.0007	.0017	.0008
29.3	.0000	.0000	.0001
30	.2284	.1966	.2472
30.2	.0160	.0411	.0338
30.3	.0014	.0000	.0000
31	.0759	.0475	.0718
31.2	.0703	.1083	.1017
32	.0299	.0114	.0131
32.1	.0007	.0000	.0000
32.2	.1623	.1019	.0890
33	.0049	.0011	.0016
33.1	.0000	.0003	.0005
33.2	.0481	.0490	.0291
34	.0007	.0000	.0000
34.1	.0000	.0001	.0000
34.2	.0063	.0077	.0032
35	.0000	.0000	.0003
35.2	.0021	.0158	.0009
36	.0000	.0000	.0001
36.2	.0014	.0168	.0006
37	.0000	.0001	.0000
37.2	.0000	.0131	.0003
38	.0000	.0001	.0000
38.2	.0000	.0115	.0004
39	.0000	.0006	.0000
39.2	.0000	.0064	.0002
40.2	.0000	.0020	.0001
41.2	.0000	.0009	.0000
PE:	0.899	0.008	0.045

TABLE 6—Sample allele frequencies for D18S51.

Allele	Asian N:712	Aboriginal N:3512	Caucasian N:8188
8	.0007	.0000	.0000
9	.0014	.0003	.0003
10	.0014	.0031	.0089
11	.0070	.0483	.0147
12	.0604	.0592	.1465
12.2	.0000	.0001	.0000
13	.1327	.1980	.1238
13.2	.0000	.0006	.0000
14	.1896	.1690	.1582
14.2	.0000	.0001	.0001
15	.2135	.1231	.1495
15.2	.0000	.0000	.0001
16	.1594	.1247	.1329
16.2	.0000	.0000	.0001
17	.0829	.0823	.1154
18	.0527	.0789	.0776
18.2	.0000	.0001	.0000
19	.0358	.0550	.0399
19.1	.0000	.0003	.0000
19.2	.0000	.0001	.0000
20	.0197	.0262	.0173
20.2	.0000	.0000	.0001
21	.0197	.0196	.0079
21.3	.0000	.0001	.0000

TABLE 6—Continued.

Allele	Asian N:712	Aboriginal N:3512	Caucasian N:8188
22	.0133	.0090	.0048
23	.0049	.0011	.0013
24	.0021	.0004	.0005
25	.0014	.0001	.0002
26	.0007	.0000	.0000
27	.0007	.0000	.0000
PE:	0.121	0.000	0.952

TABLE 7—Sample allele frequencies for D5S818.

Allele	Asian N:717	Aboriginal N:3515	Caucasian N:8210
7	.0244	.0010	.0010
8	.0014	.0016	.0021
9	.0551	.0683	.0364
10	.2252	.2107	.0644
11	.2999	.2903	.3739
12	.2343	.2862	.3547
13	.1499	.1267	.1552
14	.0091	.0139	.0104
15	.0007	.0013	.0019
PE:	0.800	0.001	0.069

TABLE 8—Sample allele frequencies for D13S317.

Allele	Asian N:719	Aboriginal N:3513	Caucasian N:8205
6	.0000	.0003	.0000
7	.0014	.0024	.0004
8	.2816	.2975	.1259
9	.1391	.0562	.0734
10	.1314	.0423	.0655
11	.2330	.3190	.3026
12	.1648	.2082	.2811
13	.0382	.0548	.1031
14	.0097	.0191	.0466
15	.0007	.0003	.0012
16	.0000	.0000	.0001
PE:	0.531	0.005	0.802

TABLE 9—Sample allele frequencies for D7S870.

Allele	Asian N:715	Aboriginal N:3509	Caucasian N:8161
5	.0000	.0000	.0001
7	.0070	.0077	.0180
7.3	.0000	.0006	.0001
8	.1552	.3398	.1643
9	.0573	.0895	.1543
9.1	.0035	.0000	.0001
10	.1706	.1985	.2631
11	.3462	.2241	.2084
11.3	.0000	.0000	.0000
12	.2140	.1188	.1543
13	.0420	.0190	.0309
14	.0042	.0019	.0059
15	.0000	.0001	.0005
16	.0000	.0000	.0001
21	.0000	.0000	.0001
PE:	0.205	0.004	0.020

TABLE 10—Combined p-values for Hardy-Weinberg tests.

Sample	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S870	Total
Asian	.112	.128	.574	.761	.899	.121	.800	.531	.205	.364
Aboriginal	.674	.006	.141	.323	.008	.000	.001	.005	.004	.000
Caucasian	.985	.767	.452	.002	.045	.952	.069	.802	.020	.010
Total	.518	.021	.358	.016	.013	.002	.003	.053	.001	1.000

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