

FOR THE RECORD

Aleksander Bagdonavicius,¹ B. Appl. Sci.; Gavin R. Turbett,¹ Ph.D.; John S. Buckleton,² Ph.D.; and Simon J. Walsh,³ B.Sc. (Hons)

Western Australian Sub-Population Data for the Thirteen AMPFISTR[®] Profiler Plus[™] and COfiler[™] STR Loci

POPULATIONS: Profiler Plus: Caucasians ($n = 2645$), Aboriginals ($n = 659$) and South East Asians ($n = 115$) from Western Australia. COfiler: Caucasians ($n = 205$), Aboriginals ($n = 203$) and South East Asians ($n = 103$) from Western Australia.

KEYWORDS: forensic science, DNA typing, short tandem repeats, population genetics, Profiler Plus, COfiler, polymerase chain reaction, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, CSF1P0, D16S539, Th01, TP0X, amelogenin, Western Australia, Caucasian, Aboriginal, South East Asian

Allele frequencies were determined for each of the AMPFISTR[®] Profiler Plus[™] and COfiler[™] STR loci from individuals representing the three major sub-populations of Western Australia, a state of Australia.

Blood or buccal swabs were collected from unrelated healthy volunteers or individuals randomly selected from criminal cases. Ethnicity was based on self-declaration, either by the individual or their family. South East Asia in this instance is defined as persons originating from Singapore, Malaysia, Southern China, Cambodia, Philippines, Indonesia, Vietnam and Laos.

DNA was extracted with Chelex according to methods published previously (1). DNA was quantitated using the Quantiblot[®] system (Applied Biosystems, Foster City, Ca, USA) according to the manufacturers recommendations. DNA amplification was performed by PCR on an ABI Prism 9700[™] thermal cycler, using 1–2 ng of DNA and the AMPFISTR[®] Profiler Plus[™] and COfiler[™] multiplex systems (Applied Biosystems). All amplifications were undertaken as per the manufacturers directions, except that the total PCR reaction volume was reduced to 25 μ L. Analysis of the PCR products was performed by capillary electrophoresis using ABI Prism 310 Genetic Analysers. Assignment of alleles was undertaken using Genescan[®] Analysis 3.1 and Genotyper[®] 2.5 software applications (ABI) and confirmed by manual independent inspection by two scientists. Concordance of the results at the D3S1358 and D7S820 loci, which are present in both kits, was a prerequisite for inclusion in the study and was reviewed in all cases.

¹ Forensic Biology Laboratory, Forensic Services, PathCentre. Hospital Avenue, Nedlands, Perth, Western Australia, 6009, Australia.

² United Kingdom Forensic Science Service, Research and Development Unit, Birmingham, United Kingdom.

³ Science and Justice Consulting, PO Box 83, Surry Hills, NSW, 2010, Australia.

Results

See Tables 1–3. The abbreviated form of locus nomenclature has been used.

Analysis of Data

Fischer's Exact test (2), expected (H_E) and observed (H_o) heterozygosity were calculated using the Genetic Data Analysis software (3) provided courtesy of Paul Lewis (Department of Ecology and Evolutionary Biology, The University of Connecticut).

Departures from Hardy-Weinberg equilibrium ($p < 0.05$) were detected at the D8S1179 and D7S820 loci in the Caucasian sub-population. Departures were also detected at the D21S11 and D13S317 loci in the Aboriginal sub-population and at the D13S317 locus in the South East Asian sub-population.

The probability of obtaining a match between two distinct and unrelated people (PM) was calculated for each sub-population at each of the thirteen AMPFISTR[®] Profiler Plus[™] and COfiler[™] STR loci. Multiplication of these values gives an estimate of the discriminating power of the combined DNA profiling systems. For the three sub-populations, the exclusion probability (PE) was calculated at the thirteen tested loci, according to Evett and Weir (4).

Population data from the major sub-populations of Western Australia at the thirteen STR loci of the AMPFISTR[®] Profiler Plus[™] and COfiler[™] STR multiplex systems has been statistically examined to the level required by the international forensic community. We consider these databases suitable for use in matters of disputed paternity or DNA-based forensic evidence.

The complete data set is available upon request via e-mail at gavin.turbett@health.wa.gov.au.

TABLE 1—Allele frequencies for the 13 Profiler Plus and COfiler loci from individuals of Caucasian descent.

Allele	D3	VWA	FGA	D8	D21	D18	D5	D13	D7	CSF	D16	TH01	TPOX
6	—	—	—	—	—	—	—	—	—	—	—	0.2366	—
7	—	—	—	—	—	—	0.0009	0.0002	0.0161	—	—	0.1805	—
8	—	—	—	0.0200	—	—	0.0021	0.1253	0.1662	—	0.0220	0.1146	0.5415
9	—	—	—	0.0127	—	—	0.0393	0.0733	0.1584	0.0171	0.1220	0.1390	0.1024
9.3	—	—	—	—	—	—	—	—	—	—	—	0.3195	—
10	—	—	—	0.0951	—	0.0098	0.0624	0.0656	0.2635	0.2854	0.0610	0.0098	0.0561
11	0.0030	0.0004	—	0.0811	—	0.0155	0.3766	0.3053	0.2068	0.3000	0.2976	—	0.2610
12	0.0009	—	—	0.1448	—	0.1471	0.3505	0.2730	0.1505	0.3220	0.2683	—	0.0390
13	0.0025	0.0008	—	0.3153	—	0.1257	0.1543	0.1108	0.0318	0.0537	0.1902	—	—
14	0.1231	0.1019	—	0.1911	—	0.1558	0.0112	0.0456	0.0060	0.0171	0.0366	—	—
15	0.2718	0.0996	0.0004	0.1042	—	0.1531	0.0028	0.0009	0.0008	0.0049	0.0024	—	—
15.2	—	—	—	—	—	0.0002	—	—	—	—	—	—	—
16	0.2556	0.2204	0.0002	0.0321	—	0.1312	—	—	—	—	—	—	—
17	0.1932	0.2724	0.0009	0.0036	—	0.1119	—	—	—	—	—	—	—
18	0.1361	0.2030	0.0140	—	—	0.0832	—	—	—	—	—	—	—
19	0.0130	0.0860	0.0601	—	—	0.0369	—	—	—	—	—	—	—
19.2	—	—	0.0004	—	—	—	—	—	—	—	—	—	—
20	0.0008	0.0146	0.1431	—	—	0.0157	—	—	—	—	—	—	—
20.2	—	—	0.0019	—	—	—	—	—	—	—	—	—	—
21	—	0.0009	0.1733	—	—	0.0078	—	—	—	—	—	—	—
21.2	—	—	0.0021	—	—	—	—	—	—	—	—	—	—
22	—	—	0.1794	—	—	0.0045	—	—	—	—	—	—	—
22.2	—	—	0.0096	—	—	—	—	—	—	—	—	—	—
23	—	—	0.1482	—	—	0.0011	—	—	—	—	—	—	—
23.2	—	—	0.0043	—	—	—	—	—	—	—	—	—	—
24	—	—	0.1393	—	—	0.0006	—	—	—	—	—	—	—
24.2	—	—	0.0008	—	0.0013	—	—	—	—	—	—	—	—
25	0.355	0.2556	0.0794	—	0.0002	—	—	0.529	—	—	—	—	—
25.2	0.7898	0.8082	0.0008	0.0013	0.0013	—	—	0.529	—	—	410	410	410
26	0.7769	0.8049	0.0344	0.0017	0.0004	—	—	0.529	5290	—	410	410	410
26.2	0.795	0.064	—	0.0004	0.0004	—	—	0.529	5290	—	410	410	410
27	0.077	—	0.0060	0.0367	0.0367	—	—	0.529	5290	—	410	410	410
28	—	—	0.0013	0.1537	0.1537	—	—	0.529	5290	—	410	410	410
29	—	—	—	0.2057	0.2057	—	—	0.529	5290	—	410	410	410
29.2	—	—	—	0.0006	0.0006	—	—	0.529	5290	—	410	410	410
30	—	—	—	0.2476	0.2476	—	—	0.529	5290	—	410	410	410
30.2	—	—	—	0.0425	0.0425	—	—	0.529	5290	—	410	410	410
31	—	—	—	0.0711	0.0711	—	—	0.529	5290	—	410	410	410
31.2	—	—	—	0.0947	0.0947	—	—	0.529	5290	—	410	410	410
32	—	—	—	0.0136	0.0136	—	—	0.529	5290	—	410	410	410
32.2	—	—	—	0.0915	0.0915	—	—	0.529	5290	—	410	410	410
33	—	—	—	0.0013	0.0013	—	—	0.529	5290	—	410	410	410
33.1	—	—	—	0.0002	0.0002	—	—	0.529	5290	—	410	410	410
33.2	—	—	—	0.0312	0.0312	—	—	0.529	5290	—	410	410	410
34.2	—	—	—	0.0032	0.0032	—	—	0.529	5290	—	410	410	410
35	—	—	—	0.0002	0.0002	—	—	0.529	5290	—	410	410	410
35.2	—	—	—	0.0006	0.0006	—	—	0.529	5290	—	410	410	410
36.2	—	—	—	0.0006	0.0006	—	—	0.529	5290	—	410	410	410
37.2	—	—	—	0.0002	0.0002	—	—	0.529	5290	—	410	410	410
N	5290	5290	5290	5290	5290	5290	5290	5290	5290	410	410	410	410
p	0.355	0.988	0.199	0.043	0.496	0.392	0.335	0.529	0.038	0.249	0.864	0.676	0.413
H _E	0.7898	0.8082	0.8646	0.8152	0.8462	0.8763	0.7061	0.7927	0.8113	0.7232	0.7848	0.7787	0.6251
H _O	0.7769	0.8049	0.8681	0.8098	0.8476	0.8635	0.7221	0.7917	0.8091	0.7366	0.7463	0.8049	0.6439
PE	0.795	0.795	0.903	0.795	0.912	0.872	0.772	0.772	0.772	0.707	0.743	0.660	0.595
PM	0.077	0.064	0.033	0.057	0.041	0.028	0.137	0.071	0.063	0.130	0.080	0.084	0.193

N: (number of alleles), H_E: (expected heterozygosity), H_O: (observed heterozygosity), p: (Hardy-Weinberg equilibrium – exact test based on 10,000 shufflings), PE: (probability of exclusion) and PM: (random match probability). Of this database 2645 individuals were typed using AMPF/STR[®] Profiler Plus[™] and 205 individuals were typed using AMPF/STR[®] COfiler[™].

TABLE 2—Allele frequencies for the thirteen Profiler Plus and COfiler loci from individuals of Aboriginal descent.

Allele	D3	VWA	FGA	D8	D21	D18	D5	D13	D7	CSF	D16	TH01	TPOX
5	—	—	—	—	—	—	—	—	—	—	—	0.0025	—
6	—	—	—	—	—	—	—	—	—	—	—	0.3522	—
7	—	—	—	—	—	—	0.0008	0.0008	0.0061	0.0025	—	0.2808	—
8	—	—	—	0.0061	—	—	—	0.3005	0.2876	0.0172	0.0099	0.0788	0.3227
9	—	—	—	0.0152	—	0.0008	—	0.0683	0.1123	0.0123	0.0640	0.1453	0.3325
9.3	—	—	—	—	—	—	—	—	—	—	—	0.1355	—
10	—	—	—	0.0569	—	—	—	—	0.1737	0.1872	0.0887	0.0049	0.0567
11	—	—	—	0.0744	—	0.0038	0.1328	0.0410	0.2086	0.3325	0.3399	—	0.2537
12	0.0099	—	—	0.1419	—	0.0501	0.3536	0.3080	0.1775	0.3325	0.3227	—	0.0345
13	0.0008	0.0015	—	0.2709	—	0.1836	0.1366	0.0531	0.0303	0.1084	0.1453	—	—
13.2	—	—	—	—	—	0.0023	—	—	—	—	—	—	—
14	0.0751	0.0493	—	0.1684	—	0.1282	0.0182	0.0167	0.0038	0.0049	0.0271	—	—
15	0.3520	0.0675	—	0.1555	—	0.1343	0.0008	0.0023	—	0.0025	0.0025	—	—
16	0.2436	0.2208	—	0.0774	—	0.1267	—	—	—	—	—	—	—
17	0.1897	0.3323	0.0091	0.0326	—	0.0918	—	—	—	—	—	—	—
18	0.1222	0.2071	0.0152	0.0008	—	0.0766	—	—	—	—	—	—	—
19	0.0068	0.1024	0.0561	—	—	0.0470	—	—	—	—	—	—	—
20	—	0.0190	0.0880	—	—	0.0243	—	—	—	—	—	—	—
21	—	—	0.1062	—	—	0.0228	—	—	—	—	—	—	—
21.2	—	—	0.0023	—	—	—	—	—	—	—	—	—	—
22	—	—	0.1935	—	—	0.0190	—	—	—	—	—	—	—
22.2	—	—	0.0099	—	—	—	—	—	—	—	—	—	—
23	—	—	0.1571	—	—	0.0030	—	—	—	—	—	—	—
23.2	—	—	0.0038	—	—	—	—	—	—	—	—	—	—
24	—	—	0.1624	—	—	—	—	—	—	—	—	—	—
24.2	—	—	0.0008	—	—	—	—	—	—	—	—	—	—
25	—	—	0.1442	—	—	—	—	—	—	—	—	—	—
26	—	—	0.0417	—	—	—	—	—	—	—	—	—	—
27	—	—	0.0076	—	0.0008	—	—	—	—	—	—	—	—
28	—	—	0.0008	—	0.0281	—	—	—	—	—	—	—	—
29	—	—	0.0015	—	0.1093	—	—	—	—	—	—	—	—
29.2	—	—	—	—	0.2627	—	—	—	—	—	—	—	—
30	—	—	—	—	0.0008	—	—	—	—	—	—	—	—
30.2	—	—	—	—	0.1959	—	—	—	—	—	—	—	—
31	—	—	—	—	0.0387	—	—	—	—	—	—	—	—
31.2	—	—	—	—	0.0843	—	—	—	—	—	—	—	—
32	—	—	—	—	0.0782	—	—	—	—	—	—	—	—
32.2	—	—	—	—	0.0159	—	—	—	—	—	—	—	—
33.1	—	—	—	—	0.1025	—	—	—	—	—	—	—	—
33.2	—	—	—	—	0.0015	—	—	—	—	—	—	—	—
34.2	—	—	—	—	0.0357	—	—	—	—	—	—	—	—
35.2	—	—	—	—	0.0046	—	—	—	—	—	—	—	—
36.2	—	—	—	—	0.0068	—	—	—	—	—	—	—	—
37.2	—	—	—	—	0.0243	—	—	—	—	—	—	—	—
38.2	—	—	—	—	0.0046	—	—	—	—	—	—	—	—
39.2	—	—	—	—	0.0023	—	—	—	—	—	—	—	—
41.2	—	—	—	—	0.0030	—	—	—	—	—	—	—	—
N	1318	1318	1318	1318	1318	1318	1318	1318	1318	406	406	406	406
p	0.440	0.101	0.631	0.513	0.019	0.159	0.068	0.003	0.340	0.163	0.363	0.706	0.683
H _E	0.7612	0.7807	0.8670	0.8385	0.8533	0.8886	0.7337	0.7621	0.7991	0.7334	0.7483	0.7532	0.7183
H _o	0.7527	0.7633	0.8558	0.8558	0.8316	0.8786	0.7178	0.7344	0.7891	0.6897	0.7833	0.6897	0.6995
PE	0.772	0.743	0.880	0.813	0.893	0.872	0.743	0.772	0.743	0.772	0.743	0.707	0.595
PM	0.095	0.080	0.032	0.045	0.037	0.023	0.115	0.095	0.070	0.118	0.104	0.101	0.133

N: (number of alleles), H_E: (expected heterozygosity), H_o: (observed heterozygosity), p: (Hardy-Weinberg equilibrium — exact test based on 10,000 shufflings), PE: (probability of exclusion) and PM: (random match probability). Of this database 659 individuals were typed using AMPF/STR[®] Profiler Plus[™] and 203 individuals were typed using AMPF/STR[®] COfiler[™].

TABLE 3—Allele frequencies for the thirteen Profiler Plus and Cofiler loci from individuals of South East Asian descent.

Allele	D3	VWA	FGA	D8	D21	D18	D5	D13	D7	CSF	D16	TH01	TPOX
6	—	—	—	—	—	—	—	—	—	—	—	0.1262	—
7	—	—	—	—	—	—	0.0174	—	0.0043	0.0097	—	0.2573	—
8	—	—	—	—	—	—	0.0043	0.3000	0.1478	—	0.0049	0.0340	0.5583
9	—	—	—	—	—	—	0.0391	0.1913	0.0913	0.0437	0.2379	0.4320	0.1262
9,3	—	—	—	—	—	—	—	—	—	—	—	0.0874	—
10	—	—	—	0.1565	—	0.0043	0.2043	0.1391	0.1652	0.1699	0.1359	0.0534	0.0097
11	—	—	—	0.0870	—	0.0130	0.3391	0.1565	0.3522	0.2670	0.2282	0.0049	0.2816
12	—	—	—	0.1391	—	0.0609	0.2435	0.1348	0.1913	0.4078	0.2621	0.0049	0.0243
13	—	—	—	0.2000	—	0.1478	0.1522	0.0652	0.0391	0.0874	0.1019	—	—
14	0.0043	0.2391	—	0.1217	—	0.1652	—	0.0130	0.0087	0.0097	0.0291	—	—
15	0.0696	0.0391	—	0.2304	—	0.2087	—	—	—	0.0049	—	—	—
16	0.3391	0.1913	—	0.0435	—	0.1174	—	—	—	—	—	—	—
17	0.2043	0.2391	—	0.0130	—	0.0826	—	—	—	—	—	—	—
18	0.0652	0.1783	0.0522	0.0087	—	0.0565	—	—	—	—	—	—	—
19	0.0087	0.0870	0.0565	—	—	0.0565	—	—	—	—	—	—	—
20	0.0043	0.0217	0.0652	—	—	0.0304	—	—	—	—	—	—	—
20,2	—	—	0.0043	—	—	—	—	—	—	—	—	—	—
21	—	0.0043	0.1217	—	—	0.0261	—	—	—	—	—	—	—
22	—	—	0.1391	—	—	0.0174	—	—	—	—	—	—	—
22,2	—	—	0.0087	—	—	—	—	—	—	—	—	—	—
23	—	—	0.1826	—	—	0.0043	—	—	—	—	—	—	—
23,2	—	—	0.0174	—	—	—	—	—	—	—	—	—	—
24	—	—	0.1826	—	—	—	—	—	—	—	—	—	—
25	—	—	0.0957	—	—	0.0043	—	—	—	—	—	—	—
25,2	—	—	0.0043	—	0.0043	—	—	—	—	—	—	—	—
26	—	—	0.0478	—	—	—	—	—	—	—	—	—	—
27	—	—	0.0217	—	—	0.0043	—	—	—	—	—	—	—
28	—	—	—	—	0.0652	—	—	—	—	—	—	—	—
28,2	—	—	—	—	0.0087	—	—	—	—	—	—	—	—
29	—	—	—	—	0.2478	—	—	—	—	—	—	—	—
29,2	—	—	—	—	0.0043	—	—	—	—	—	—	—	—
30	—	—	—	—	0.2652	—	—	—	—	—	—	—	—
30,2	—	—	—	—	0.0130	—	—	—	—	—	—	—	—
31	—	—	—	—	0.0565	—	—	—	—	—	—	—	—
31,2	—	—	—	—	0.0565	—	—	—	—	—	—	—	—
32	—	—	—	—	0.0391	—	—	—	—	—	—	—	—
32,2	—	—	—	—	0.1652	—	—	—	—	—	—	—	—
33,2	—	—	—	—	0.0565	—	—	—	—	—	—	—	—
34,2	—	—	—	—	0.0130	—	—	—	—	—	—	—	—
35,2	—	—	—	—	0.0043	—	—	—	—	—	—	—	—
N	230	230	230	230	230	230	230	230	230	206	206	206	206
p	0.529	0.964	0.610	0.306	0.883	0.691	0.669	0.048	0.388	0.694	0.562	0.983	0.906
H _E	0.7446	0.8112	0.8805	0.8422	0.8287	0.8783	0.7623	0.8105	0.7837	0.7274	0.7968	0.7230	0.5954
H _o	0.6957	0.8174	0.8870	0.7826	0.8261	0.8870	0.7304	0.7913	0.7826	0.7184	0.8447	0.7184	0.5728
PE	0.743	0.743	0.854	0.772	0.854	0.872	0.707	0.707	0.743	0.743	0.707	0.743	0.595
PM	0.110	0.065	0.027	0.046	0.052	0.028	0.097	0.064	0.079	0.119	0.075	0.118	0.229

N: (number of alleles), H_E: (expected heterozygosity), H_o: (observed heterozygosity), p: (Hardy-Weinberg equilibrium – exact test based on 10,000 shufflings), PE: (probability of exclusion) and PM: (random match probability). Of this database 115 individuals were typed using AMPF/STR® Profiler Plus™ and 103 individuals were typed using AMPF/STR® Cofiler™.

Acknowledgments

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Additional information and reprint requests:

Dr. Gavin R Turbett, Ph.D.

Forensic Biology Laboratory

PathCentre

Hospital Avenue, Nedlands

Western Australia 6009

E-mail: gavin.turbett@health.wa.gov.au