

## FOR THE RECORD

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# Population data for the AMPF $\ell$ STR<sup>®</sup> Profiler Plus<sup>™</sup> STR Loci from Residents of the Australian Capital Territory (ACT)

**POPULATIONS:** Profiler Plus—Resident donors (N = 620) from the Australian Capital Territory (ACT). Although the ethnicity of the donors was not recorded the population of the ACT is largely homogeneous, with over 96% of respondents declaring their ancestry as Caucasian in the 2002 National Census (1).

**KEYWORDS:** Forensic science, DNA typing, short tandem repeats, population genetics, Profiler Plus, polymerase chain reaction, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, Australian Capital Territory, Australian Federal Police

Allele frequencies were determined for each of the AMPF $\ell$ STR<sup>®</sup> Profiler Plus<sup>™</sup> STR loci from individuals representing the general population of the Australian Capital Territory (ACT), one of the eight States and Territories of Australia. Blood samples were collected from unrelated healthy volunteers or individuals randomly selected from the ACT Red Cross Blood Bank.

DNA was extracted with Chelex (2) and quantitated using the Quantiblot<sup>®</sup> system (Applied Biosystems, Foster City, CA) according to the manufacturer's recommendations. DNA amplification was performed by PCR on an (ABI 9700) thermal cycler, using approximately 1 ng of DNA and the AMPF $\ell$ STR<sup>®</sup> Profiler Plus<sup>™</sup> multiplex systems (Applied Biosystems, Foster City, CA). All amplifications were undertaken using quarter reactions as per the manufacturer's directions. Analysis of the PCR products was performed on a ABI310. Assignment of alleles was undertaken using Genescan<sup>®</sup> Analysis 3.1 and Genotyper<sup>®</sup> 2.5 software applications (ABI).

See Table 1 (the abbreviated form of locus nomenclature has been used). The complete data set is available to any interested researcher upon request.

Analysis of Data—Fischer's Exact test (3), expected ( $H_E$ ) and observed ( $H_O$ ) heterozygosity were calculated using the Genetic Data Analysis software (4). A departure from Hardy-Weinberg equilibrium ( $p < 0.05$ ) was detected at the D8S1179 locus in the general population. This was identified as originating from an over-representation of 16,16 homozygotes (4 observed against 0 expected). A  $p$ - $p$  plot (Fig. 1) was constructed following the approach of Buckleton (5). As the data falls within the boundaries of 95% CI envelope it implies no significant departures from HWE have been

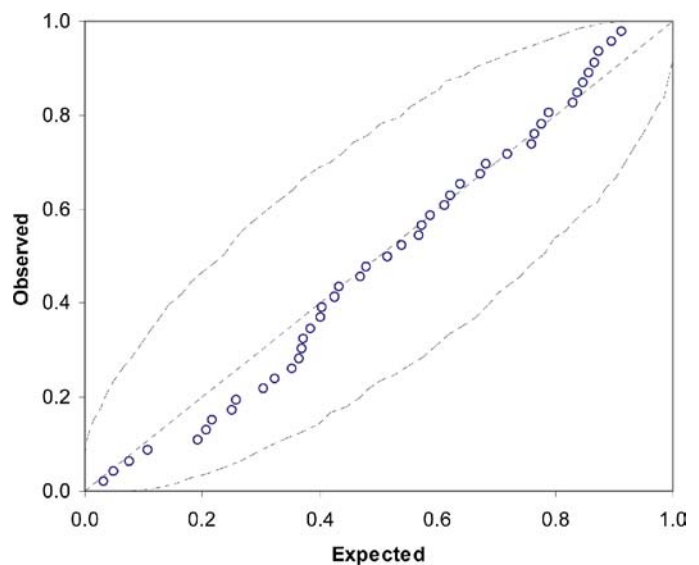


FIG. 1— $p$ - $p$  plot showing the results of Fischer's Exact test on the AFP data. The  $x = y$  trend-line represents HWE and deviations from that trend-line can be seen as mild departures from equilibrium. The 95% confidence limit is also displayed as the region within the two curved lines. As the data falls within the boundaries of this envelope it implies no significant departures from HWE have been observed.

observed, however the moderate size of the dataset and its effect on the power of the Fisher's exact test must be taken into account.

Population data from the general population of the ACT at the nine STR loci of the AMPF $\ell$ STR<sup>®</sup> Profiler Plus<sup>™</sup> multiplex system has been statistically examined to the level required by the international forensic community. We consider this database suitable for use in matters of disputed paternity or DNA-based forensic evidence within the Australian Capital Territory.

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TABLE 1—Allele frequencies for the nine Profiler Plus loci from individuals from the general population of the Australian Capital Territory.

Allele	D3	vWA	FGA	D8	D21	D18	D5	D13	D7
7	...	...	...	...	...	...	...	...	0.0185
8	...	...	...	0.0234	...	...	0.0032	0.1323	0.1597
9	...	...	...	0.0137	...	...	0.0387	0.0702	0.1895
10	...	...	...	0.0879	...	0.0113	0.0581	0.0548	0.2532
11	0.0008	...	...	0.0766	...	0.0145	0.3847	0.2960	0.1952
12	0.0008	...	...	0.1573	...	0.1589	0.3444	0.2895	0.1379
13	0.0073	0.0008	...	0.3234	...	0.1266	0.1573	0.1016	0.0355
14	0.1234	0.1121	...	0.1935	...	0.1492	0.0113	0.0548	0.0097
15	0.2661	0.1129	...	0.0960	...	0.1516	0.0024	0.0008	0.0008
16	0.2323	0.2032	...	0.0266	...	0.1234	...	...	...
17	0.2000	0.2565	...	0.0016	...	0.1137	...	...	...
18	0.1524	0.2226	0.0202	...	...	0.0702	...	...	...
19	0.0137	0.0758	0.0581	...	...	0.0468	...	...	...
20	0.0032	0.0137	0.1524	...	...	0.0169	...	...	...
20.2	...	...	0.0016	...	...	...	...	...	...
21	...	0.0024	0.1726	...	...	0.0097	...	...	...
21.2	...	...	0.0032	...	...	...	...	...	...
22	...	...	0.1806	...	...	0.0065	...	...	...
22.2	...	...	0.0089	...	...	...	...	...	...
23	...	...	0.1484	...	...	0.0008	...	...	...
23.2	...	...	0.0024	...	...	...	...	...	...
24	...	...	0.1444	...	...	...	...	...	...
24.2	...	...	...	...	0.0016	...	...	...	...
25	...	...	0.0782	...	...	...	...	...	...
25.2	...	...	...	...	0.0024	...	...	...	...
26	...	...	0.0258	...	0.0016	...	...	...	...
27	...	...	0.0032	...	0.0435	...	...	...	...
28	...	...	...	...	0.1661	...	...	...	...
29	...	...	...	...	0.1823	...	...	...	...
29.2	...	...	...	...	0.0008	...	...	...	...
30	...	...	...	...	0.2637	...	...	...	...
30.2	...	...	...	...	0.0274	...	...	...	...
31	...	...	...	...	0.0766	...	...	...	...
31.2	...	...	...	...	0.0944	...	...	...	...
32	...	...	...	...	0.0161	...	...	...	...
32.2	...	...	...	...	0.0847	...	...	...	...
33	...	...	...	...	0.0008	...	...	...	...
33.2	...	...	...	...	0.0347	...	...	...	...
34.2	...	...	...	...	0.0024	...	...	...	...
35.2	...	...	...	...	0.0008	...	...	...	...
<i>n</i>	1240	1240	1240	1240	1240	1240	1240	1240	1240
<i>p</i> -value	0.1926	0.5725	0.4778	<b>0.0318</b>	0.6212	0.5881	0.5381	0.2065	0.4028
<i>H</i> <sub>O</sub>	0.7972	0.8128	0.8615	0.8096	0.8442	0.8782	0.7043	0.7905	0.8163
<i>H</i> <sub>E</sub>	0.8000	0.7952	0.8645	0.8113	0.8629	0.8887	0.7242	0.7887	0.8290

*n* (number of alleles), *H*<sub>O</sub> (observed heterozygosity), *H*<sub>E</sub> (expected heterozygosity), *p*-value (Hardy-Weinberg equilibrium—Fisher's exact test based on 10,000 shufflings).

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