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Announcement of Population Data

Autosomal microsatellite allele frequencies for 15 regionally defined Aboriginal Australian population datasets

Simon J. Walsh [a,b,*], John S. Buckleton [c]

[a] *Forensic and Technical Services, Australian Federal Police, GPO Box 401, Canberra, ACT 2601, Australia*
[b] *Centre for Forensic Science, University of Technology Sydney, Australia*
[c] *ESR Ltd., Private Bag 92-021, Auckland, New Zealand*

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Abstract

DNA profiling results presented in court must be accompanied by a statistical estimate of its evidential weight. In calculating such statistics, allele frequencies from the tested loci are required. These allele frequencies should be collected at a level that appropriately represents the genetic diversity that exists in the population. This paper reports allele frequencies and the results of population genetic testing of autosomal microsatellite profiles from indigenous Australian donors. In contrast to previous practice these data have been collated according to traditional regional boundaries rather than recently imposed State and Territory borders.

Keywords: DNA profiling; STR; Microsatelite; Population data; Aboriginal Australia

Population: Forensic Biology personnel from six of the Australian State and Territory Forensic Biology laboratories have compiled datasets from indigenous Australian donors. The total collection of samples numbers 6513 individuals. The aboriginality of each donor was assigned by self-declaration. Samples had been gathered during the course of routine forensic analyses, commonly in accordance with legislative regimes that govern the collection and analysis of DNA samples. All samples were associated with a geographic placeholder. This placeholder ascribed a contemporary geographical location, such as a State or Territory, and a city, town, or remote community centre. The placeholder was assigned through reference to either the place of residence of the donor or the location of the offence with which the donor was associated. With reference to the language map of Aboriginal Australia [1] these contemporary placeholders were assigned to a putative region and tribal territory as described elsewhere [2] (Table 1). In Northern Australia the North and Arnhem groups were altered from those described by Horton [1] into East Arnhem, West Arnhem and Tiwi groups. This follows the research of Walsh et al. [3].

DNA analysis: The extraction, amplification and detection of DNA samples were as earlier described [4–8].

Quality control: Contributing laboratories hold National Association of Testing Authorities, Australia (NATA) accreditation.

Results: The allele frequencies for the nine STR loci have been tabulated for 15 indigenous Australian regional populations. The data are represented in Tables 2–16.

Fisher's Exact test [9] for allelic association was undertaken with 10,000 shuffles using the Genetic Data Analysis [10] software provided courtesy of Dimitri Zaykin and Paul Lewis. Support for departure from Hardy–Weinberg equilibrium (HWE) was detected in at least one locus in 11 of the 15 datasets ($p < 0.05$, highlighted by bold typeface in Tables 2–7, 11, 13–16). These results are investigated in more detail elsewhere [2] and are not discussed here. In general they concur with observations from analysis of jurisdictionally defined datasets throughout Australia [4–8] and support the use of the sub-population model for the estimation of multi-locus genotype probabilities [11].

* Corresponding author at: Forensic and Technical Services, Australian Federal Police, GPO Box 401, Canberra, ACT 2601, Australia.
Tel.: +61 2 6223 3854; fax: +61 2 6223 3270.
E-mail address: simonjoseph.walsh@afp.gov.au (S.J. Walsh).

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Table 1
Summary of population samples analysed herein

Region	*N*
East Arnhem	240
West Arnhem	279
Desert	2516
Fitzmaurice	1073
Gulf	97
Kimberley	62
Northeast	74
Northwest	49
Rainforest	48
Riverine	1084
Southeast	817
Spencer	59
Tiwi	61
Torres Strait	21
West Cape	33

Four of the 15 datasets have fewer than 50 samples (Northwest, Rainforest, Torres Strait and West Cape) and a further five (Gulf, Kimberley, Northeast, Spencer and Tiwi) have between 50 and 100. The results of analysis of these datasets, in particular results of independence testing must be assessed with caution due to the smaller sample size.

Population data from 15 traditional regions of Aboriginal Australia has been collated and statistically examined to the level required by the international forensic community. We consider these databases appropriate to support the estimation of DNA match statistics in circumstances of disputed paternity or DNA-based forensic evidence involving indigenous Australian individuals.

This paper follows the specified approach outlined by Lincoln and Carracedo [12].

Table 2
Allele frequencies for the nine AmpF*l*STR® Profiler Plus™ STR loci for indigenous Australian donors from the East Arnhem Region

Allele	D3	vWA	FGA	D8	D21	D18	D5	D13	D7
7	–	–	–	–	–	–	–	–	0.0194
7.3	–	–	–	–	–	–	–	–	0.0012
8	–	–	–	–	–	–	–	0.2907	0.3753
9	–	–	–	0.0024	–	–	0.0706	0.0323	0.0133
10	–	–	–	0.0024	–	–	0.3074	0.0299	0.2760
11	0.0012	–	–	0.0990	–	0.0340	0.1722	0.3433	0.2264
12	–	–	–	0.1325	–	0.0279	0.2835	0.2213	0.0714
13	–	–	–	0.2864	–	0.3823	0.1280	0.0502	0.0169
14	0.0239	0.0453	–	0.1599	–	0.1978	0.0323	0.0323	–
15	0.3974	0.0239	–	0.2184	–	0.0740	0.0060	–	–
16	0.1778	0.2470	–	0.0788	–	0.0692	–	–	–
17	0.2554	0.3043	0.0060	0.0203	–	0.0400	–	–	–
18	0.1289	0.2458	0.0215	–	–	0.0667	–	–	–
19	0.0143	0.1229	0.0754	–	–	0.0667	–	–	–
20	0.0012	0.0095	0.1687	–	–	0.0303	–	–	–
21	–	0.0012	0.0969	–	–	0.0085	–	–	–
22	–	–	0.1842	–	–	0.0012	–	–	–
22.2	–	–	0.0096	–	–	–	–	–	–
23	–	–	0.0742	–	–	0.0012	–	–	–
23.2	–	–	0.0012	–	–	–	–	–	–
24	–	–	0.1364	–	–	–	–	–	–
24.2	–	–	0.0024	–	–	–	–	–	–
25	–	–	0.1376	–	–	–	–	–	–
26	–	–	0.0754	–	0.0156	–	–	–	–
27	–	–	0.0108	–	0.0036	–	–	–	–
28	–	–	–	–	0.1926	–	–	–	–
29	–	–	–	–	0.1423	–	–	–	–
30	–	–	–	–	0.1794	–	–	–	–
30.2	–	–	–	–	0.0335	–	–	–	–
31	–	–	–	–	0.0395	–	–	–	–
31.2	–	–	–	–	0.0921	–	–	–	–
32	–	–	–	–	0.0024	–	–	–	–
32.2	–	–	–	–	0.1400	–	–	–	–
33.2	–	–	–	–	0.0694	–	–	–	–
34.2	–	–	–	–	0.0084	–	–	–	–
35.2	–	–	–	–	0.0167	–	–	–	–
36.2	–	–	–	–	0.0072	–	–	–	–
37.2	–	–	–	–	0.0156	–	–	–	–
38.2	–	–	–	–	0.0167	–	–	–	–
39.2	–	–	–	–	0.0084	–	–	–	–
40.2	–	–	–	–	0.0144	–	–	–	–
41.2	–	–	–	–	0.0024	–	–	–	–