

FOR THE RECORD

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Allele Frequencies for Nine STR Loci in African American and Caucasian Populations from Marion County, Indiana, USA

KEYWORDS: forensic science, DNA typing, short tandem repeat, polymerase chain reaction, population genetics, Marion County Indiana, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820

POPULATIONS: African American (*n* = 190) Caucasians (*n* = 170).

Whole blood obtained by venipuncture was collected in EDTA vacutainer tubes from individuals residing in Marion County, Indiana. The DNA was extracted by phenol chloroform method (1) and purified by ethanol precipitation and/or by Centricon® concentrators (Amicon Corporation-Beverly, MA). The quantity of extracted DNA was estimated using the slot-blot procedure using commercial kits (Gibco-BRL, Gaithersburg, MD). PCR amplification was

performed using the AmpF/STR Profiler Plus™ PCR amplification kit (PE-Biosystems, Foster City, CA) following the manufacturer's protocol. The amplified products were separated and detected using the ABI Prism™ 377 DNA sequencer (PE-Biosystems, Foster City, CA). The data were analyzed using a program written by Chakraborty and Zhong.

The complete data are available to any interested researcher upon request.

Reference

1. Comey CT, Koons BW, Presley KW, Smerick JB, Sobieralski CA, Stanley DM, et al. DNA extraction strategies for amplified fragment length polymorphism analysis. *J Forensic Sci* 1994;39:1254-69.

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TABLE 1—STR allele frequency data for African American population (*n* = 190).

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D6S818	D13S317	D7S820
6	—	—	—	—	—	—	—	—	0.0026
7	—	—	—	—	—	—	0.0026	—	0.0105
8	—	—	—	0.0026	—	—	0.0632	0.0263	0.2079
9	—	—	—	0.0026	—	nd	0.0237	0.0368	0.1447
10	—	—	—	0.0368	—	0.0053	0.0605	0.0395	0.3132
11	—	0.0079	—	0.0447	—	0.0026	0.2737	0.2842	0.1895
<12	0.0026	—	—	—	—	—	—	—	—
12	0.0105	nd	—	0.1211	—	0.0737	0.3421	0.4053	0.1184
13	0.0026	0.0053	—	0.2053	—	0.0632	0.2184	0.1553	0.0105
13.2	—	—	—	—	—	0.0079	—	—	—
14	0.1079	0.0447	—	0.3474	—	0.0868	0.0079	0.0526	0.0026
14.2	—	—	—	—	—	0.0026	—	—	—
15	0.3000	0.2447	—	0.1842	—	0.1605	0.0053	nd	nd
16	0.2974	0.2526	—	0.0421	—	0.1658	nd	—	—
>16	—	—	—	—	—	—	0.0026	—	—
17	0.2000	0.2079	—	0.0132	—	0.1684	—	—	—
<18	—	—	0.0026	—	—	—	—	—	—
18	0.0658	0.1447	0.0079	nd	—	0.1000	—	—	—
18.2	—	—	0.0079	—	—	—	—	—	—

continues

TABLE 1—Continued.

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D6S818	D13S317	D7S820
19	0.0131	0.0474	0.0868	nd	—	0.0895	—	—	—
19.2	—	—	0.0053	—	—	—	—	—	—
20	—	0.0342	0.0684	—	—	0.0553	—	—	—
21	—	0.0053	0.0947	—	—	0.0053	—	—	—
>21	—	0.0052	—	—	—	—	—	—	—
22	—	—	0.1395	—	—	0.0132	—	—	—
22.2	—	—	0.0026	—	—	—	—	—	—
23	—	—	0.1816	—	—	nd	—	—	—
24	—	—	0.1737	—	—	nd	—	—	—
25	—	—	0.1000	—	0.0026	nd	—	—	—
26	—	—	0.0605	—	0.0026	nd	—	—	—
27	—	—	0.0368	—	0.0579	—	—	—	—
28	—	—	0.0105	—	0.2632	—	—	—	—
29	—	—	0.0053	—	0.1290	—	—	—	—
29.3	—	—	—	—	0.0026	—	—	—	—
30	—	—	0.0053	—	0.1790	—	—	—	—
30.2	—	—	—	—	0.0079	—	—	—	—
>30	—	—	0.0053	—	—	—	—	—	—
31	—	—	—	—	0.1000	—	—	—	—
31.2	—	—	—	—	0.0579	—	—	—	—
32	—	—	—	—	0.0053	—	—	—	—
32.2	—	—	—	—	0.0711	—	—	—	—
33	—	—	—	—	0.0053	—	—	—	—
33.1	—	—	—	—	0.0026	—	—	—	—
33.2	—	—	—	—	0.0553	—	—	—	—
34	—	—	—	—	0.0079	—	—	—	—
34.2	—	—	—	—	0.0026	—	—	—	—
35	—	—	—	—	0.0368	—	—	—	—
36	—	—	—	—	0.0105	—	—	—	—
<i>p</i> *	0.525	0.643	0.09	0.021	0.306	0.918	0.305	0.931	0.99

* Exact test based on 2000 shufflings.

Interclass correlations yielding $p < 0.05$ for pairwise comparisons: D3S1358/D21S11, D8S1179/D18S51.

— means that allele not applicable to that locus.

nd—allele not detected in this study.

TABLE 2—STR allele frequency data for Caucasian population (n = 170).

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
7	—	—	—	—	—	—	nd	—	0.0235
8	—	—	—	0.0265	—	—	0.0029	0.1000	0.1677
8.1	—	—	—	—	—	—	—	—	0.0029
9	—	—	—	0.0177	—	nd	0.0382	0.1059	0.1677
10	—	—	—	0.0882	—	0.0147	0.0382	0.0618	0.2324
11	0.0059	nd	—	0.0706	—	0.0147	0.3765	0.2941	0.2353
12	nd	0.0029	—	0.1529	—	0.1412	0.3853	0.2677	0.1353
13	nd	nd	—	0.3471	—	0.1500	0.1471	0.1177	0.0324
14	0.1382	0.1029	—	0.1882	—	0.1618	0.0088	0.0500	0.0029
15	0.2618	0.1088	—	0.0765	—	0.1265	0.0029	0.0029	nd
16	0.2765	0.2382	—	0.0324	—	0.1029	nd	—	—
17	0.1912	0.2735	—	nd	—	0.1441	—	—	—
18	0.1265	0.1647	0.0059	nd	—	0.0941	—	—	—
19	nd	0.0941	0.0882	nd	—	0.0235	—	—	—
20	—	0.0118	0.1235	—	—	0.0147	—	—	—
21	—	0.0029	0.1824	—	—	0.0029	—	—	—
21.2	—	—	0.0029	—	—	—	—	—	—
22	—	—	0.1794	—	—	0.0058	—	—	—
22.2	—	—	0.0059	—	—	—	—	—	—
23	—	—	0.1206	—	—	0.0029	—	—	—
23.2	—	—	0.0059	—	—	—	—	—	—
24	—	—	0.1618	—	—	nd	—	—	—
24.2	—	—	0.0029	—	nd	—	—	—	—
25	—	—	0.0706	—	nd	nd	—	—	—
26	—	—	0.0382	—	nd	nd	—	—	—
27	—	—	0.0088	—	0.0471	—	—	—	—
28	—	—	0.0029	—	0.1441	—	—	—	—
29	—	—	nd	—	0.2147	—	—	—	—
30	—	—	nd	—	0.2353	—	—	—	—
30.2	—	—	—	—	0.0412	—	—	—	—

TABLE 2—Continued.

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
31	—	—	—	—	0.0618	—	—	—	—
31.2	—	—	—	—	0.1147	—	—	—	—
32	—	—	—	—	0.0265	—	—	—	—
32.2	—	—	—	—	0.0794	—	—	—	—
33.2	—	—	—	—	0.0265	—	—	—	—
34.2	—	—	—	—	0.0088	—	—	—	—
<i>p</i> *	0.9	0.008	0.949	0.426	0.743	0.356	0.365	0.973	0.692

* Exact test based on 2000 shufflings.

Interclass correlations yielding $p < 0.05$ for pairwise comparisons: D3S1358/D7S820.

— means that allele not applicable to that locus.

nd—allele not detected in this study.