

FOR THE RECORD

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Minnesota Population Data on 15 STR Loci Using the Identifiler[®] Kit

POPULATION: Six hundred and seventy-one unrelated individuals from Minnesota, USA.

KEYWORDS: forensic science, population genetics, short tandem repeat, Identifiler, D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA

Samples: The population samples, obtained from the Minneapolis Memorial Blood Center, are comprised of four groups: Native Americans (203), Hispanic (151), Caucasian (160), and African American (157). Population affiliation was assigned based on self-declaration. The DNA was extracted using the method described by Dykes (1).

Amplification: *c.* 1 ng of each sample was amplified using the commercially available Identifiler kit (Applied Biosystems, Foster City, CA). Amplification was carried out in a Geneamp 9700 thermal cycler (Applied Biosystems) according to the manufacturer's recommended protocol (2).

Typing: Amplified product was analyzed on either an ABI 310 Genetic Analyzer or an ABI 3100 Genetic Analyzer (Applied Biosystems) following the manufacturer's recommendations (2). GeneScan and Genotyper software were used for allele designations.

QC: Ten percent of all samples were re-amplified and typed by a second analyst. All results were concordant between the two analyses.

Data analysis: Allele frequencies were determined for each sample population group by the direct counting method (Table 1). Standard population genetic tests (Table 2) were performed on these data (3–7). Based on the exact test and 2000 shuffling experiments, there were no detectable departures from Hardy–Weinberg expectations (HWE) in the African American and Hispanic samples. One departure from HWE was detected in the Caucasian population sample (CSF1PO, $p = 0.004$), and one departure from HWE was observed in the Native American database (D5S818, $p = 0.049$). Observing only one departure out of 15 loci is no more than would be expected by chance. Furthermore, after applying the Bonferroni correction (8), when multiple tests are performed on a dataset, there is little evidence of departures from HWE in the four Minnesota population samples. An inter-class correlation test analysis was performed to detect any correlations between alleles at any of the pair-wise comparisons of the 15 loci in each of the population databases. For each sample population, a total of 105 pair-wise comparisons were performed. The number of significant departures is two observations (1.9%) for the African American

TABLE 1—Allele frequencies (in percent) for 15 STR loci in four sample populations residing in Minnesota.

	African American (N = 157*)	Caucasian (N = 160)	Hispanic (N = 151)	Native American (N = 203)
D8S1179				
8	0.637	2.813	0.331	0.493
9	1.592	2.188	0.331	0.246
10	2.548	8.438	6.623	4.680
11	6.369	8.125	5.298	3.448
12	8.280	11.563	12.583	11.084
13	14.968	30.938	33.113	37.438
14	35.669	21.563	28.146	30.542
15	22.611	11.250	12.252	9.606
16	6.369	2.813	1.325	1.970
17	0.318	0.313	—	0.493
18	0.637	—	—	—
D21S11				
25.2	—	—	0.331	—
26	—	—	0.331	—
27	6.688	3.438	1.656	0.739
28	26.115	16.250	9.272	5.911
29	17.516	18.125	20.861	16.256
29.2	0.318	0.625	0.662	0.246
29.3	—	0.625	—	—
30	17.516	27.188	29.470	34.236
30.2	1.274	2.500	2.318	1.970
31	8.917	7.188	6.291	5.911
31.2	4.777	8.125	8.609	19.458
32	2.548	0.938	1.325	0.739
32.2	7.643	9.688	12.914	9.606
33	—	0.625	—	0.739
33.1	0.318	—	—	—
33.2	1.592	4.375	4.305	3.448
34	0.318	—	—	—
34.2	0.637	0.313	0.993	0.739
35	3.822	—	0.662	—
D7S820				
6	0.318	—	—	—
7	1.274	1.563	1.325	0.493
8	19.108	16.875	11.921	13.054
8.1	0.318	—	—	—
9	13.376	5.313	7.616	8.374
10	29.618	28.125	24.834	22.167
11	21.019	16.875	29.801	28.818
12	12.102	16.563	20.861	23.892
13	2.229	3.750	3.311	3.202
14	0.637	0.938	0.331	—
CSF1PO				
7	6.688	—	0.662	—
8	5.732	0.625	0.331	0.493

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TABLE 1—Continued.

	African American (N = 157*)	Caucasian (N = 160)	Hispanic (N = 151)	Native American (N = 203)
9	2.229	5.000	0.662	7.882
10	24.522	27.188	21.523	31.773
11	27.070	29.688	29.470	22.906
12	26.752	30.625	41.722	31.527
13	5.096	6.875	5.298	4.680
14	1.274	—	0.331	0.739
15	0.637	—	—	—
D3S1358				
11	—	—	—	0.246
12	—	—	0.331	—
13	0.955	—	—	—
14	8.917	13.438	7.616	6.404
15	23.885	27.500	35.099	41.626
16	28.662	24.688	26.490	32.512
17	26.752	20.313	19.205	10.099
18	10.191	12.813	10.265	8.374
19	0.637	1.250	0.662	0.739
20	—	—	0.331	—
THO1				
5	0.318	—	—	—
6	15.924	23.750	22.185	20.443
7	37.580	20.625	33.444	45.320
8	21.975	10.938	9.603	5.172
9	12.102	15.625	14.901	6.158
9.3	11.465	28.438	18.874	22.660
10	0.637	0.625	0.993	0.246
D13S317				
8	4.459	14.375	11.921	4.926
9	3.185	7.188	19.205	18.227
10	3.185	5.625	6.291	13.547
11	27.707	28.438	26.159	24.631
12	40.446	30.938	23.179	22.906
13	15.924	9.375	8.609	7.635
14	5.096	4.063	4.636	7.882
15	—	—	—	0.246
D16S539				
8	0.955	1.250	1.325	0.739
9	19.108	8.125	10.265	12.069
10	12.420	6.875	15.232	16.010
11	34.713	35.000	27.815	30.788
12	16.879	30.313	28.808	28.325
13	12.420	15.625	14.901	10.099
14	3.503	2.813	1.656	1.970
D2S1338				
16	4.459	5.313	3.311	2.463
17	11.783	19.063	20.199	9.606
18	6.688	10.000	3.974	7.143
19	19.427	9.688	19.536	29.064
20	11.146	13.438	13.245	9.606
21	8.599	4.375	3.974	2.463
22	10.191	2.813	7.616	15.517
23	10.828	9.063	10.596	11.823
23.3	—	0.313	—	—
24	7.962	9.063	10.596	8.621
25	5.732	13.750	6.291	2.956
26	1.911	3.125	0.662	0.739
27	0.955	—	—	—
28	0.318	—	—	—
D192433				
10	0.637	—	—	—
11	7.962	0.313	0.662	0.493
11.2	—	—	0.331	—
12	9.236	5.313	6.623	3.448
12.2	2.548	—	1.656	—
13	30.255	21.250	16.556	18.227
13.2	5.096	1.250	6.291	16.010
14	22.930	36.563	31.126	24.138
14.2	3.503	1.563	5.298	3.695
15	6.688	22.188	14.901	13.054
15.2	6.369	3.750	9.603	10.591
16	1.274	5.000	4.305	4.187
16.2	3.185	1.250	2.318	1.724
17	—	—	0.331	0.739
17.2	0.318	0.938	—	2.709
18.2	—	0.625	—	0.985
vWA				
11	0.955	—	—	—

TABLE 1—Continued.

	African American (N = 157*)	Caucasian (N = 160)	Hispanic (N = 151)	Native American (N = 203)
12	0.637	—	—	0.246
13	2.866	—	—	0.246
14	6.051	7.813	7.616	4.680
15	22.611	8.438	12.252	6.897
16	25.478	23.438	30.132	33.005
17	18.471	25.625	22.185	33.005
18	14.013	22.500	19.868	15.271
19	7.325	10.000	5.960	5.172
20	1.274	2.188	1.656	1.232
21	0.318	—	0.331	0.246
TPOX				
6	8.333	—	0.662	—
7	2.244	—	—	0.246
8	32.372	56.563	43.377	38.670
9	21.474	9.063	10.927	4.187
10	8.333	4.688	6.291	3.202
11	25.321	25.313	28.146	39.163
12	1.923	4.375	10.596	14.532
D18S51				
10	0.637	0.938	0.662	0.739
10.2	0.637	—	—	—
11	0.637	0.938	0.993	—
12	5.414	13.750	8.278	14.532
13	5.414	10.313	13.907	9.852
13.2	1.592	—	—	—
14	7.962	18.125	15.563	26.847
14.2	0.318	—	—	—
15	16.879	15.313	18.543	12.069
15.2	0.318	—	—	—
16	18.790	11.875	11.589	10.591
16.2	0.318	—	—	—
17	16.879	13.750	14.238	14.286
18	9.873	8.125	7.285	2.709
19	9.236	3.750	3.974	4.187
20	2.866	1.563	3.311	1.724
21	1.592	0.313	0.331	1.478
22	0.637	0.938	0.993	0.739
23	—	—	0.331	0.246
24	—	0.313	—	—
D5S818				
7	0.637	1.250	6.623	16.010
8	5.732	—	1.325	0.246
9	2.866	3.750	3.642	5.911
10	6.369	6.563	3.311	4.680
11	25.478	37.500	39.073	40.640
12	36.624	34.688	30.464	22.660
13	19.745	15.000	14.901	9.606
14	2.229	1.250	0.662	0.246
15	0.318	—	—	—
FGA				
17	0.318	—	0.331	—
17.2	0.318	—	—	—
18	0.955	2.188	0.993	1.232
18.2	0.637	—	—	—
19	6.688	7.188	6.623	9.852
19.2	0.318	—	—	—
20	3.503	13.125	8.278	12.562
21	17.516	17.813	15.232	12.808
21.2	—	—	0.331	—
22	19.108	16.563	15.232	11.084
22.2	—	1.875	—	0.246
23	13.376	14.063	11.921	15.764
23.2	0.318	—	0.662	0.246
24	18.153	15.625	18.543	15.764
24.2	—	—	0.331	—
24.3	0.318	—	—	—
25	9.873	8.750	12.583	13.300
26	4.459	1.563	6.291	5.172
26.2	—	—	—	0.493
27	2.229	0.625	1.656	0.739
28	1.592	0.313	0.993	0.493
29	0.318	0.313	—	—
> 30	—	—	—	0.246

*One sample was excluded from the frequency calculations for the African American population group for the TPOX locus because it was tri-allelic.

TABLE 2—Population statistic analyses for 15 STR loci in four sample populations residing in Minnesota.

	D8S1179	D21S11	D7S820	CSF1P0	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
Minnesota African Americans															
Observed homozygosity (%)	26.10	15.30	19.10	16.60	26.10	24.20	31.80	15.30	10.20	19.70	25.50	20.50	10.20	22.90	10.80
Expected homozygosity (%)	21.40	15.00	19.90	21.40	22.70	24.00	27.00	21.50	10.70	17.10	17.70	22.70	12.10	24.40	13.40
Homozygosity test (<i>p</i> value)	0.152	0.920	0.801	0.143	0.304	0.959	0.171	0.057	0.828	0.371	0.011	0.509	0.453	0.661	0.350
Exact test (<i>p</i> value)	0.355	0.150	0.970	0.340	0.330	0.908	0.945	0.140	0.241	0.396	0.159	0.081	0.749	0.725	0.064
Power of discrimination (Obs)	0.924	0.952	0.927	0.912	0.911	0.906	0.891	0.912	0.972	0.947	0.942	0.902	0.968	0.900	0.957
Probability of exclusion	0.593	0.701	0.604	0.581	0.553	0.542	0.503	0.583	0.778	0.670	0.645	0.558	0.751	0.537	0.727
Minnesota Caucasians															
Observed homozygosity (%)	13.10	11.90	15.00	25.60	24.40	22.50	20.60	26.90	10.00	25.00	19.40	42.50	10.00	25.60	17.50
Expected homozygosity (%)	18.10	15.60	18.60	26.10	21.40	21.40	21.40	24.90	11.30	23.30	19.20	39.40	12.50	28.70	13.20
Homozygosity test	0.099	0.198	0.240	0.896	0.294	0.729	0.822	0.558	0.607	0.613	0.965	0.429	0.345	0.386	0.106
Exact test	0.424	0.150	0.425	0.004*	0.345	0.725	0.114	0.411	0.743	0.747	0.639	0.084	0.536	0.566	0.432
Power of discrimination (Obs)	0.934	0.954	0.931	0.869	0.920	0.915	0.916	0.896	0.971	0.913	0.933	0.782	0.964	0.850	0.964
Probability of exclusion	0.646	0.690	0.626	0.495	0.579	0.572	0.587	0.529	0.767	0.559	0.616	0.363	0.742	0.469	0.728
Minnesota Hispanics															
Observed homozygosity (%)	21.20	21.20	19.90	29.80	24.50	16.60	18.50	19.90	15.90	16.60	17.20	26.50	11.30	26.50	12.60
Expected homozygosity (%)	22.50	16.70	21.30	30.80	24.40	22.60	18.40	21.40	13.00	16.70	20.10	29.20	12.40	27.20	12.40
Homozygosity test	0.710	0.142	0.674	0.793	0.980	0.077	0.965	0.643	0.293	0.966	0.369	0.461	0.674	0.838	0.936
Exact test	0.203	0.596	0.893	0.920	0.986	0.373	0.154	0.055	0.033	0.644	0.401	0.575	0.976	0.601	0.149
Power of discrimination (Obs)	0.904	0.951	0.920	0.848	0.899	0.901	0.931	0.911	0.963	0.950	0.922	0.862	0.968	0.875	0.965
Probability of exclusion	0.569	0.672	0.580	0.430	0.530	0.558	0.631	0.577	0.734	0.675	0.602	0.471	0.744	0.496	0.744
Minnesota Native Americans															
Observed homozygosity (%)	32.00	19.20	25.10	21.20	28.10	35.50	18.20	21.70	20.20	16.70	26.10	38.40	16.70	30.50	15.80
Expected homozygosity (%)	25.80	19.80	21.20	25.90	28.90	30.30	17.70	22.40	15.40	14.90	24.90	32.50	15.00	25.50	12.20
Homozygosity test	0.039	0.846	0.177	0.121	0.579	0.111	0.849	0.806	0.056	0.454	0.694	0.072	0.488	0.101	0.127
Exact test	0.087	0.070	0.169	0.539	0.107	0.189	0.658	0.998	0.567	0.480	0.814	0.060	0.061	0.049*	0.776
Power of discrimination (Obs)	0.896	0.925	0.920	0.877	0.846	0.863	0.943	0.915	0.957	0.956	0.897	0.838	0.954	0.896	0.970
Probability of exclusion	0.524	0.623	0.579	0.501	0.459	0.455	0.644	0.564	0.698	0.701	0.530	0.411	0.700	0.529	0.747

*Departure from Hardy-Weinberg equilibrium (HWE).

data set, four observations (3.8%) for the Caucasian data set, three observations (2.9%) for the Hispanic data set, and four observations (3.8%) for the Native American data set. The number of observed departures for each dataset is no more than would be expected by chance. These observations support the use of the allele frequencies in the Minnesota population data for estimating the rarity of a DNA profile based on standard calculations. These standard calculations include the use of a minimum allele frequency (i.e., $5/2N$, where N is the size of the database) and population genetic approaches to correct for the departures from HWE (i.e., the use of $\ominus$ with the modified product rule) (9).

The complete dataset is available to any interested researcher upon request from the corresponding author Ann Marie Gross at ann.gross@state.mn.us.

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