For the Record

Allelic Distribution for Two Short Tandem Repeat loci:
D10S2325 and D20S161

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Population: Western Germany, unrelated people $n = 102$ for D10S2325; $n = 100$ for D20S161

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DNA extraction from venous blood and DNA quantification was done as described previously (1).

The components of the PCR were 5 ng of genomic DNA, 1.5 U Taq polymerase, 10 mM Tris-HCl pH 9.0, 50 mM KCl, 1.5 mM $MgCl_2$, 200 µM of each dNTP (Ready-To-Go™PCR beads, Amersham Pharmacia Biotech), the final volume was brought to 25 µL with sterile double distilled water.

The primers were D10S2325 primer 1:5′-CTCACGAAA-GAAGCCTTCTG-3′, primer 2:5′-GAGCTGAGAGATCACG-CACT-3′ 2; amplification protocol: initial denaturation 94°C for 5min, 94°C for 1min, 61°C for 1min, 72°C for 2min; 30 cycles. D20S161 primer 1:5′-CCCCTTCAACTTGTCAGC-3′, primer 2: 5′-TCCTTCCAACTGGTATCTTG-3′, 3; amplification protocol: initial denaturation 94°C for 5min, 94°C for 1min, 58°C for 1 min, 72°C for 2min; 28 cycles. The PCR was carried out in a Trio-thermoblock (Biometra).

The PCR products were resolved by nondenaturating polyacrylamide gel electrophoresis with a discontinuous buffer system (4). Polyacrylamide gels (7.4% acrylamide) cast on Gelbond (Biozym),

were 0.75 mm thick with 0.08 M tris formiate in the gel and 0.28 M tris borate buffer in the agarose plugs. The electrophoresis was run up to 16 cm. Settings for power limitations were 1000 V, 40 mA, 15 W. The DNA fragments were visualized by silver staining.

The mean exclusion chance (ME) and the discrimination power (DP) was calculated according to Jones (5). Exact tests were performed using the DNA-view software (C. Brenner, Berkeley, CA) for checking the Hardy-Weinberg expectations.

The distribution of observed genotypes and allelic frequencies in our German population sample for D10S2325 is shown in Table 1, and for D20S161 in Table 2.

Acknowledgments

References

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TABLE 1—*Observed allele frequencies and genotype values for D10S2325 in 102 unrelated German individuals.*

Allele Frequencies		
6	1	0.005
7	28	0.137
8	9	0.044
9	17	0.083
10	29	0.142
11	39	0.191
12	29	0.142
13	29	0.142
14	14	0.069
15	5	0.025
16	3	0.015
18	1	0.005

Genotype Frequencies					
Genotypes	Number	Proportion	Genotypes	Number	Proportion
6–9	1	0.01	10–10	1	0.01
7–7	3	0.029	10–11	8	0.078
7–8	2	0.02	10–12	6	0.059
7–9	3	0.029	10–13	2	0.02
7–10	2	0.02	10–14	2	0.02
7–11	4	0.039	10–15	1	0.01
7–12	1	0.01	10–16	1	0.01
7–13	6	0.059	10–18	1	0.01
7–14	2	0.02	11–11	5	0.049
7–15	1	0.01	11–12	5	0.049
7–16	1	0.01	11–13	4	0.039
8–10	2	0.02	11–14	2	0.02
8–11	1	0.01	12–12	2	0.02
8–12	1	0.01	12–13	7	0.069
8–13	1	0.01	12–14	1	0.01
8–14	1	0.01	12–15	1	0.01
8–15	1	0.01	13–13	2	0.02
9–10	2	0.02	13–14	3	0.029
9–11	5	0.049	14–14	1	0.01
9–12	3	0.029	14–16	1	0.01
9–13	2	0.02			
9–15	1				

Heterozygosity: 0.87.
Mean exclusion chance (ME): 0.736.
Discrimination power (DP): 0.969.
P-value (exact test): 0.80483.

TABLE 2—*Observed allele frequencies and genotype values for D20S161 in 100 unrelated German individuals.*

Allele	Frequencies	
14	1	0.05
15	1	0.05
16	4	0.02
17	41	0.205
18	94	0.47
19	40	0.2
20	11	0.055
21	8	0.04

Genotype Frequencies		
Genotypes	Number	Proportion
14–21	1	0.01
15–16	1	0.01
16–17	1	0.01
16–18	2	0.02
17–17	7	0.07
17–18	16	0.16
17–19	5	0.05
17–20	4	0.04
17–21	1	0.01
18–18	21	0.21
18–19	25	0.25
18–20	5	0.05
18–21	4	0.04
19–19	3	0.03
19–20	2	0.02
19–21	2	0.02

Heterozygosity: 0.692.
Mean exclusion chance (ME:) 0.46.
Discrimination power (DP): 0.862.
P-value (exact test): 0.16094.