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SHORT COMMUNICATION

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AMPFLP analysis of the VNTR loci D1S80 and ApoB in Hungary

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Abstract Population data studies for D1S80 and ApoB were carried out on a caucasian population sample from Hungary of 229 and 222 unrelated individuals, respectively. We observed 26 different alleles for D1S80 and 13 for ApoB. The allele frequencies found are similar to those reported in the literature for European caucasians. No evidence of significant deviations from Hardy-Weinberg equilibrium were observed for both AMPFLP systems.

Key words AMPFLP · D1S80 · ApoB · Allele frequencies · Hardy-Weinberg equilibrium

Introduction

AMPFLP technology is widely used for identity testing. Although there are numerous AMPFLP population data studies carried out on caucasians, up to now no data was available for individuals of Hungarian origin. In this report, we present genotype frequency data for D1S80 and ApoB in a population sample from Hungary of 229 and 222 unrelated individuals, respectively.

Materials and methods

DNA for PCR analysis was obtained from whole liquid blood or bloodstains of 229 unrelated individuals by previously described methods [1, 2]. The amplification and separation parameters for D1S80 and ApoB were as previously described [3, 6].

Results and discussion

The distribution of observed genotypes for D1S80 and ApoB in the Hungarian caucasian population sample are

Table 1 Distribution of D1S80 genotypes in 229 unrelated Hungarian caucasians

Genotype	Number observed	Genotype	Number observed
14–18	1	23–28	1
14–29	1	24–24	21
17–18	2	24–25	11
18–18	17	24–26	3
18–20	1	24–28	8
18–21	3	24–29	12
18–22	1	24–30	2
18–23	3	24–31	10
18–24	35	24–32	1
18–25	6	24–33	2
18–26	2	24–34	1
18–27	1	24–35	2
18–28	9	24–36	1
18–29	2	24–37	2
18–31	7	24–38	1
18–36	2	24–40	2
19–21	1	25–25	1
19–24	1	25–28	2
20–22	2	25–29	2
20–24	1	25–31	1
20–25	1	25–40	1
21–24	3	26–28	1
21–25	2	26–31	1
21–26	1	28–28	1
21–29	1	28–29	3
21–31	2	28–30	1
21–>40	1	28–31	1
22–24	10	28–36	1
22–25	1	29–30	1
22–28	1	29–31	1
22–31	1	29–36	1
22–34	1	31–31	1
23–24	2	31–36	1
23–25	2	31–39	1

Homozygosity ($n = 41$) = 0.179
Heterozygosity ($n = 188$) = 0.821
Expected heterozygosity h = 0.816 ± 0.026

PD = 0.95

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Table 2 Distribution of ApoB genotypes in 222 unrelated Hungarian caucasians

Genotype	Number observed	Genotype	Number observed
31–31	2	35–45	1
31–33	2	35–47	7
31–35	10	35–49	5
31–36	1	35–51	3
31–37	13	36–37	1
31–39	5	37–37	26
31–45	1	37–39	9
31–47	4	37–41	2
31–49	5	37–45	1
33–35	11	37–47	12
33–37	11	37–49	10
33–39	1	37–51	2
33–47	1	37–55	1
33–49	2	39–41	1
35–35	16	41–47	2
35–37	43	47–47	2
35–39	4	47–49	1
35–41	1	49–49	1
35–43	1	49–51	1

Homozygosity (n = 47) = 0.212
Heterozygosity (n = 175) = 0.788
Expected heterozygosity h = 0.781 ± 0.028

PD = 0.92

shown in Tables 1 and 2, respectively. For D1S80, a total of 26 different alleles was observed in 229 individuals. The most common alleles detected were those with 18 (f = 0.238) and 24 (f = 0.332) repeat units. In this population sample 68 out of 351 possible genotypes were encountered with the genotype 18–24 being the most frequent (f = 0.153). For ApoB 13 alleles were observed in 222 individuals. The most common alleles were 35 (f = 0.266) and 37 (f = 0.354). In this population study 38 out of the possible 91 genotypes were found with the genotype 35–37 being the most frequent (f = 0.194).

There is no significant deviation from Hardy-Weinberg expectations for both AMPFLPs based on the "allele binning strategy" [4] and the heterozygosity test [5].

The AMPFLP allele frequencies found in Hungary are similar to other caucasian population data [3, 6–8].

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