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SHORT COMMUNICATION

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Hungarian population data for the STR systems TH01 and VWA

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Abstract Population data studies for TH01 and VWA were carried out on a Hungarian caucasian population sample of 244 unrelated individuals. We found 7 and 8 different alleles for TH01 and VWA, respectively. Using a high resolution/non-denaturing horizontal PAGE system no variations in the mobility of alleles were detected except for the allele 14 in VWA. The allele frequencies observed are similar to those reported in the literature for European caucasians. The genotype distributions meet Hardy-Weinberg expectations for both STR systems.

Key words STR · TH01 · VWA · Allele frequencies · Hardy-Weinberg equilibrium

Introduction

The PCR amplified short tandem repeats (STRs) consist of relatively small DNA fragments and are therefore very promising polymorphic markers for the forensic practice, especially for degraded biological materials occurring in criminal cases [1–4]. Before, introducing the two STR systems (TH01, VWA) into casework in Hungary, population surveys were needed. In this report, we present data for TH01 and VWA in a population sample of 244 unrelated caucasians from Hungary.

Materials and methods

DNA for PCR analysis was obtained from whole liquid blood samples from 244 unrelated individuals as previously described [5]. The amplification and separation conditions for TH01 and VWA were as previously described [2, 3].

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Results and discussion

The distributions of observed genotypes and allele frequencies for TH01 and VWA in a Hungarian caucasian population sample of 244 unrelated persons are shown in Tables 1 and 2, respectively. We found 7 different alleles for the TH01 system. The most common alleles were the allele 6 (f = 0.207) and the non-consensus allele 9.3 (f = 0.326). In this population sample 21 out of 28 possible genotypes were encountered with the genotype 6–9.3 being the most frequent (f = 0.139). For VWA 8 alleles were detected. The most common alleles were 16 (f = 0.195) and 17 (f = 0.277). We found 27 out of the possible 36 genotypes with the genotype 16–17 being the most frequent (f = 0.123).

By using high resolution/non-denaturing gel system for both STRs we obtained no variant electrophoretic mo-

Table 1 Observed allele frequency and genotype values for TH01 in 244 unrelated Hungarian caucasians

Genotypes	Observed	Genotypes	Observed
5– 9	1	7– 9.3	26
5– 9.3	1	7–10	1
6– 6	7	8– 8	3
6– 7	19	8– 9	11
6– 8	19	8– 9.3	18
6– 9	14	8–10	1
6– 9.3	34	9– 9	11
6–10	1	9– 9.3	24
7– 7	6	9–10	1
7– 8	7	9.3–9.3	28
7– 9	11		

Obs. homozygosity (n = 55)	= 0.225
Obs. heterozygosity (n = 189)	= 0.775
Exp. heterozygosity (h)	= 0.782 ± 0.026
Power of discrimination (PD)	= 0.92

Allele frequencies (f) 5: 0.004; 6: 0.207; 7: 0.156; 8: 0.127; 9: 0.172; 9.3: 0.326; 10: 0.008

Table 2 Observed allele frequency and genotype values for VWA in 244 unrelated Hungarian caucasians

Genotypes	Observed	Genotypes	Observed
14–14	4	16–18	21
14–15	6	16–19	5
14–16	11	16–20	2
14–17	19	16–21	1
14–18	8	17–17	18
14–19	3	17–18	16
14–20	1	17–19	14
15–15	4	17–20	2
15–16	13	18–18	10
15–17	18	18–19	11
15–18	14	18–20	1
15–19	2	19–19	3
16–16	6	19–20	1
16–17	30		

Obs. homozygosity ($n = 55$)	= 0.184
Obs. heterozygosity ($n = 189$)	= 0.816
Exp. heterozygosity (h)	= 0.816 ± 0.025
Power of discrimination (PD)	= 0.94

Allele frequencies (f) 14: 0.115; 15: 0.125; 16: 0.195; 17: 0.277; 18: 0.186; 19: 0.086; 20: 0.014; 21: 0.002

bilities for the alleles except a microheterogeneity of the allele 14 in VWA [6].

Based on the "allele binning strategy" [7] and heterozygosity test [8] no significant deviations from Hardy-Weinberg expectations were found for both STRs. In the chi-square analysis we used a 6-allele-group-model, where the alleles 5 and 10 in TH01 and the alleles 19, 20, and 21 in VWA were grouped together (TH01: $\chi^2 = 11.16$, df = 15, $0.7 < P < 0.8$; VWA: $\chi^2 = 14.05$, df = 15, $0.5 < P < 0.6$). TH01 and VWA allele frequencies found in Hungary are similar to other caucasian population data [2–4].

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