

SHORT COMMUNICATION

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The STR systems HumVWA and HumACTBP2 in a Hungarian population

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Abstract Allele frequencies of the Short tandem repeat systems HumVWA and HumACTBP2 were determined from 105 unrelated individuals from the area of Szeged, Hungary. A total of 8 alleles was detected for VWA, and 23 alleles were found for ACTBP2. In both systems no deviations from Hardy-Weinberg equilibrium were observed. A comparison of the Hungarian and German frequency profiles revealed significant differences at both STR loci.

Key words Short tandem repeats · HumVWA · HumACTBP2 · Population studies · Hungary

Introduction

To obtain a database of the population living in the Szeged area, the systems HumACTBP2 (Moos and Gallwitz 1983; Polymeropoulos et al. 1992) and HumVWA (Mercier et al. 1991; Kimpton et al. 1992) were examined.

Materials and methods

DNA was extracted with the chelex method (Walsh et al. 1991) from air-dried blood on cotton fabric from 105 unrelated adults from the population of Southern Hungary. PCR and electrophoresis were done according to Möller et al. (1994). Allele designation was carried out by side-to-side comparison with allelic ladders (Möller and Brinkmann 1994; Wiegand et al. 1993).

The statistical analyses were performed using the HWE-Analyses program (C. Puers, Münster, Germany). Among others, we cal-

culated the observed and expected numbers of heterozygotes (Nei 1978), the mean exclusion chance (Krueger et al. 1968), the discrimination index (Jones 1972) and the Hardy-Weinberg equilibrium (Guo and Thompson 1992).

Table 1 Allele frequency distribution for HumVWA and HumACTBP2 in a Hungarian population ($n = 105$ unrelated individuals) and a German population ($n = 755$ unrelated individuals for HumVWA, $n = 630$ for HumACTBP2)

HumVWA			ACTBP2		
Allele	Hungarians ($n = 105$)	Germans ($n = 755$)	Allele	Hungarians ($n = 105$)	Germans ($n = 630$)
13	–	0.001	11A	–	0.008
14	0.119	0.095	11	–	0.007
15	0.081	0.099	12	0.019	0.024
16	0.152	0.204	13	0.052	0.035
17	0.296	0.280	14	0.043	0.048
18	0.171	0.220	15	0.043	0.063
19	0.129	0.085	16	0.090	0.071
20	0.033	0.013	17	0.038	0.065
21	0.019	0.002	18	0.033	0.059
22	–	0.001	19	0.038	0.050
			20	0.024	0.031
			21	0.010	0.022
			22	0.014	0.016
			23	0.024	0.031
			24	0.010	0.014
			25	0.038	0.036
			26	0.086	0.039
			27	0.057	0.045
			28	0.086	0.054
			29	0.062	0.074
			30	0.105	0.065
			31	–	0.032
			32	0.048	0.055
			33	0.033	0.025
			34	0.033	0.016
			35	–	0.004
			36	0.014	0.009
			37	–	0.002

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Table 2 Statistical parameters for the STR systems HumVWA and ACTBP2 in a Hungarian population (H_{obs} observed heterozygosity, H_{exp} expected heterozygosity, MEC mean exclusion chance, DI discrimination indices)

	HumVWA	HumACTBP2
H_{obs}	0.8667	0.9619
H_{exp}	0.8254 ± 0.0726	0.9451 ± 0.0436
MEC	0.65012	0.87980
DI	0.94041	0.98376
P-Values for HWE-hypothesis:		
Simulated exact test	0.8382	0.244
G-test	0.3074	0.9532
Chi-square-test	0.5632	0.1262
Heterozygosity test	0.2649	0.4501

The frequency profile comparison between the Hungarian and German populations was carried out using a test for genetic heterogeneity (RxC contingency table; G. Carmody, Ottawa, Canada).

Results and discussion

For the HumVWA system 8 alleles and for the HumACTBP2 system 23 alleles were observed.

In the Hungarian population, HumVWA alleles 13 and 22 and HumACTBP2 alleles 11A, 11 31,35 and 37 were not found. The allele distribution for the Hungarian and German populations are similar although minor differences exist (Table 1). The use of the Carmody test for heterogeneity revealed significant differences between the Hungarian and German populations ($P < 0.05$). This is due to individual pairwise differences up to 5.2% for HumVWA (allele 16) and 4.7% for HumACTBP2 (allele 30). However, larger population samples and more STR systems will be necessary to further elucidate possible reasons.

The population data for Hungarians showed no significant deviation from the Hardy-Weinberg equilibrium (Table 2).

References

- Guo SW, Thompson E (1992) Performing the exact test of Hardy-Weinberg proportion for multiple alleles. *Biometrics* 48: 361–372
- Jones DA (1972) Blood samples: probabilities of discriminations. *J Forensic Sci Soc* 12: 355–359
- Kimpton CP, Walton A, Gill P (1992) A further tetranucleotide repeat polymorphism in the vWF gene. *Hum Mol Genet* 1:28
- Krueger J, Fuhrmann W, Lichte KH, Steffens C (1968) Zur Verwendung des Polymorphismus der sauren Erythrozytenphosphatase bei der Vaterschaftsbegutachtung. *Dtsch Z Gerichtl Med* 64: 127–146
- Mercier B, Gaucher C, Mazurier C (1991) Characterisation of 98 alleles in 105 unrelated individuals in the F8vWF gene. *Nucleic Acids Res* 19: 4800
- Moos M, Gallwitz D (1983) Structure of the two β -actin related processed genes one of which is located next to a simple repetitive sequence. *EMBO J* 2: 757–761
- Möller A, Brinkmann B (1994) Locus ACTBP2 (SE33) Sequencing data reveal considerable polymorphism. *Int J Legal Med* 106: 262–267
- Möller A, Wiegand P, Grischow C, Seuchter SA, Baur MP, Brinkmann B (1994) Population data and forensic efficiency values for the STR systems HumVWA, HumMBP and HumFABP. *Int J Legal Med* 106: 183–189
- Nei KM (1978) Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics* 89: 583–590
- Polymeropoulos MH, Rath DS, Xiao H, Merrill CR (1992) Tetranucleotide repeat polymorphism at the human beta-actin-related pseudogene H-beta-AC-psi-2 (ACTBP2). *Nucleic Acids Res* 20:1432
- Walsh PS, Metzger DA, Higuchi R (1991) Chelex-100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *Biotechniques* 10:506–513
- Wiegand P, Budowle B, Rand S, Brinkmann B (1993) Forensic validation of the STR systems SE33 and TC11. *Int J Legal Med* 105:315–320