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SHORT COMMUNICATION

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Frequency profiles of 3 STRs in a Turkish population

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Abstract Population genetic studies were carried out on Caucasians from southern Turkey (n = 204 individuals) using the short tandem repeat (STR) systems HumTHO1, HumVWA and HumACTBP2. After electrophoresis in polyacrylamide gels, 6 alleles could be identified for HumTHO1, 7 alleles for VWA and 26 alleles for ACTBP2. No significant deviations from Hardy-Weinberg equilibrium could be observed.

Key words Short tandem repeats · HumTHO1 · HumVWA · HumACTBP2 · Population studies · Southern Turkey

Introduction

Three STR (short tandem repeat) loci all containing 4 bp as basic repeat motif were selected for PCR typing of a population survey from southern Turkey as follows: HumTH01 (TH01): Edwards et al. (1992), Puers et al. (1993), Pfitzinger et al. (1995), HumVWA (VWA): Kimpton et al. (1992), Sajantila et al. (1994): HumACTBP2 (ACTBP2): Polymeropoulos et al. (1992), Cabrero et al. (1995).

Various systematic studies have already been performed on population genetics, applicability, sensitivity and structure using these STRs (Kimpton et al. 1993; Möller and Brinkmann 1994; Möller et al. 1994). For ACTBP2 an improved allelic ladder containing 26 sequenced alleles was used (Möller et. al. 1995).

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Table 1 Frequency values for HumTHO1 (n = 203) HumVWA (n = 203) and HumACTBP2 (n = 204) in a Turkish population. For HumACTBP2 the „interalleles" were assigned to the next anodal allele in the ladder [a]

Allele		Frequency
HumTHO1		
6		0.298
7		0.204
8		0.103
9		0.219
9.3		0.145
10		0.030
HumVWA		
14		0.079
15		0.096
16		0.237
17		0.315
18		0.185
19		0.071
20		0.017
HumACTBP2		
<N12	(12)	0.012
N12	(12)	0.002
N13	(14–2)	0.012
N14	(14)	0.034
N15	(15)	0.027
N16	(16)	0.034
N17	(17)	0.081
N18	(18)	0.096
N19	(19)	0.088
N20	(20)	0.056
N21	(21)	0.037
N22	(22)	0.022
N23	(22*)	0.020
N24	(22**)	0.032
N25	(23)	0.037
N26	(26)	0.027
N27	(25)	0.033
N28	(27)	0.042
N29	(27*)	0.096
N30	(28)	0.079
N31	(29)	0.032
N32	(30)	0.034
N33	(34–4)	0.037
N34	–	0.007
N35	(33)	0.010
N36	(35)	0.015

[a] The HumACTBP2 allelic ladder (<N12 – N36; N = new) is composed of 26 sequenced alleles (Möller et al. 1995), which were differentiated in a non-denaturating, horizontal discontinuous gel system. This nomenclature containing the letter „N" is arbitrary and at position „N34" the ladder has a gap, which was also used for typing. In comparison the nomenclature in brakets shows the number of repeats. The alleles with the same repeat number (e.g. 22, 22* and 22**) cannot be separated in denaturing gel systems. The alleles 14(–2) and 34(–4) have a 2-bp and a 4-bp deletion in the 5′ flanking region, respectively

Table 2 Heterozygosity rates (*H-obs* observed heterozygosity, *H-exp* expected heterozygosity, *SE* standard error) mean exclusion chance (*MEC*) and discrimination indices (*DI*) for HumTHO1, HumVWA and HumACTBP2 in a Turkish survey from Adana

STR	H-obs	H-exp (± SE)	MEC	DI
HumTHO1	0.81	(0.79 ± 0.055)	0.59	0.92
HumVWA	0.75	(0.79 ± 0.057)	0.59	0.93
HumACTBP2	0.91	(0.94 ± 0.031)	0.89	0.99

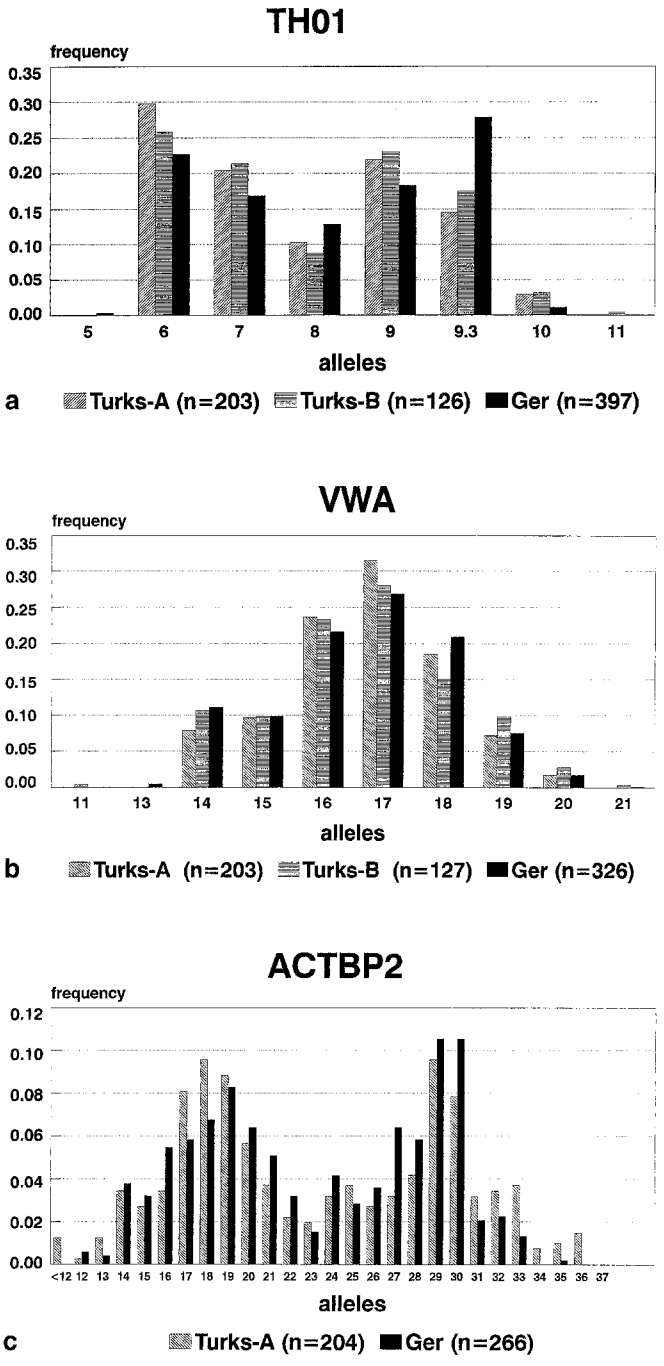

Fig. 1 a–c Comparison of the allele frequencies in different population studies. *Ger* Germans from Münster area, *Turks-A* Turks from Adana area, *Turks-B* Turks from Brussels. **a** HumTHO1; **b** HumVWA; **c** HumACTBP2.

Material and methods

DNA was extracted from 200 µl blood, air dried on filter paper, from 204 healthy unrelated Caucasians living in the Adana area of Turkey using 150 µl Chelex 100 (5%)(Bio-Rad, Germany) with the addition of 50 µl Proteinase K (2 mg/ml) (Wiegand et al. 1993a). The three loci were amplified using published primer sequences (HumTHO1: Gill et al. 1992; HumVWA: Kimpton et al. 1992; HumACTBP2: Polymeropoulos et al. 1992). The reaction assay and electrophoresis were carried out as previously described (Wiegand et al. 1993b; Möller et al. 1994).

The nomenclatures for the allelic ladders used are based on the number of repeats (Brinkmann and Wiegand 1993; Möller and Brinkmann 1994). For ACTBP2 a new ladder and allele designation was applied as previously described (Möller and Brinkmann 1994), with the modification that 5 additional alleles were included (Möller et al. 1995).

The population genetic comparisons were carried out using a test for heterogeneity (R × C contingency table; G. Carmody, Ottawa, Canada).

Results and discussion

The results of this survey (Table 1) are in good accordance with those recorded in other Caucasian populations showing only minor differences in the number of observed alleles and heterozygosity rates (Tables 1, 2; Fig. 1a-c). Some alleles were not found in this study in comparison to a survey from northwest Germany (Brinkmann and Wiegand 1993; Möller et al. 1994; Möller et al. 1995) e.g. THO1 alleles 5 and 11, VWA alleles 13 and 21 and ACTBP2 allele 37. On the other hand one variant allele (<12) was observed in ACTBP2 with a frequency of 1.2%.

The efficiency data are shown in Table 2. The single discrimination indices were > 90% and the combined mean probability of exclusion 98%. Hardy-Weinberg calculations showed no significant deviation from equilibrium for any of the three systems when a cluster approach (Rand et al. 1992) was applied (Table 3).

A comparison of the frequency profiles for HumTHO1 (Fig. 1a) showed good agreement with another Turkish population sample – a subpopulation living in Brussels since approximately 1960 (Brinkmann and Wiegand 1994) – but significant differences from a Caucasian population

Table 3 Chi-square test for Hardy-Weinberg calculations (allele-group model according to Rand et al. 1992)

STR	HumTHO1	HumVWA	HumACTBP2
Alleles (groups)	5 Allele-model	5 Allele-model	4 Allele-model
I	Allele 6	Allele 14,15	Allele <12–17
II	Allele 7	Allele 16	Allele 18–21
III	Allele 8	Allele 17	Allele 22–28
IV	Allele 9	Allele 18	Allele 29–36
V	Allele 9.3,10	Allele 19,20	
Chi-square	11.51	15.54	7.32
P	0.6–0.7	0.3–0.4	0.6–0.7
df	14	14	9

Table 4 Population comparison test (R × C contingency table, G. Carmody, Ottawa, Canada) for pairwise comparisons. The *P*-values for a Chi-square test (*Chi*) and a G-test (*G*) are given. (*Tur-A* Turkish survey from Adana, *Tur-B* Turkish survey from Brussels, *Ger* Germans)

STR	Population comparisons	Chi-square	P value	G statistic	P value
HumTH01	Tur-A: Tur-B	3.944	0.700 / 0.0145 (SE)	4.257	0.706 / 0.0144 (SE)
	Tur-A: Ger	38.542	0.00	40.325	0.00
HumVWA	Tur-A: Tur-B	8.501	0.383 / 0.0154 (SE)	9.076	0.391 / 0.0154 (SE)
	Tur-A: Ger	43.313	0.411 / 0.0156 (SE)	22.890	0.346 / 0.0150 (SE)
HumACTBP2	Tur-A: Ger	49.9	0.001 / 0.001 (SE)	55.459	0.00

in northwest Germany (Table 4). Good homogeneity was found for HumVWA when all three populations were compared (Fig. 1b; $P > 0.05$). Some minor differences were found for HumACTBP2 (Fig. 1c, Table 4) compared with the German data (e.g. alleles <12, 17, 18, 27, 28) which resulted in a low *P*-value.

Neither Turkish subpopulation showed any significant differences in their allele frequencies for any of the three STRs, indicating that the time of geographical separation was too short to have had an influence on the allele frequencies.

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