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SHORT COMMUNICATION

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Frequency data for the STR loci HumFibra (FGA) and HumACTBP2 (SE33) in a population of Germans and Turks from South-West Germany

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Abstract Population studies were carried out on German and Turkish individuals from South-West Germany using the short tandem repeat (STR) systems HumFibra (n = 138 Turkish and 1161 German individuals) and HumACTBP2 (n = 202 Turkish and 1338 German individuals). After electrophoresis 19 alleles could be identified for HumFibra and 55 for HumACTBP2. No significant deviations from Hardy-Weinberg equilibrium were observed.

Key words Short tandem repeats · HumFibra (FGA) · HumACTBP2 (SE33) · Population studies

Introduction

An essential requisite for forensic case work is a reliable database of the population concerned which comprises data from different regions of Germany. Another aim of the present study is to describe the frequency distribution of the STR loci HumFibra (FGA) and HumACTBP2 (SE33) in Turks which are the most important group (35%) of foreign suspects in cases of violent crime from this region.

Material and methods

DNA was isolated from blood samples using either phenol-chloroform or chelex 100 (5%) extraction methods. DNA was amplified according to standard procedures using the published primer sequences for SE 33 and FGA (Mills et al. 1992; Polymeropoulos et al. 1992). Electrophoresis was performed either on 8% polyacrylamide gels followed by silver staining (FGA) or according to Kimpton et al. (1993) using fluorescent detection on ABI 377 (SE 33 and FGA). The allele designation was based on sequenced allelic ladders. The nomenclature used is in accordance with the recommendations of GEDNAP (Schneider et al. 1998). The distribution of the observed genotypes (cluster approach) is in good agreement with Hardy-Weinberg expectations (Guo and Thompson 1992).

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Results and discussion

In the system HumFibra 17 different alleles have been identified in S.-W. Germans (Table 1). The allele FGA 16 was found for the first time in the German population. Among Turks we found 14 different alleles. We observed 71 out of the 153 possible genotypes among Germans (Turks: 39 genotypes). Comparing the allele frequencies of the FGA system in the two populations in our study the longer alleles (> allele 23) were more frequent in the Turkish than in the German sample. Similar results could be obtained in a different Turkish sample (Rolf et al. 1998).

Table 1 HumFibra (FGA) alleles (%) in a population of 1161 South-West Germans and 138 Turks

Allele	S.-W. Germans Frequency (%)	Turks Frequency (%)
16	0.09	
17	0.22	
18	1.42	0.72
19	6.93	5.80
20	13.26	11.59
21	17.36	14.49
21.2	0.34	1.09
22	20.24	16.67
22.2	0.65	
23	13.65	19.93
23.2	0.52	
24	12.88	15.22
24.2	0.17	0.36
25	8.18	7.97
26	3.75	3.26
27	0.30	2.17
28	0.04	0.36
29		
30		0.36

Table 2 HumACTBP2 (SE 33) alleles (%) in a population of 1338 South-West Germans and 202 Turks. Additionally specified is the mean fragment size of the ladder alleles calculated from the size of the ladder alleles determined in 100–136 gels of 36 cm separation distance

Allele	Size window		S.-W. Germans Frequency (%)	Turks Frequency (%)
	bp	SD		
8			0.04	
9	218.20	0.14		0.25
10.2			0.04	
11				0.25
11.2			0.04	
12	230.02	0.17	0.26	0.74
12.2			0.07	
13	233.95	0.18	0.82	1.73
13.2			0.34	
14	237.88	0.18	3.33	1.98
14.2			0.30	
14.3			0.04	
15	241.80	0.19	4.07	3.47
15.2			0.26	
15.3			0.11	
16	245.72	0.19	3.74	4.46
16.2			0.22	
16.3			0.11	
17	249.61	0.20	6.88	13.61
17.2			0.30	0.25
17.3			0.04	
18	253.39	0.21	7.17	8.42
18.2			0.26	
18.3			0.04	
19	257.14	0.21	7.47	6.19
19.2			0.52	0.25
20	260.88	0.22	5.64	6.93
20.2			1.27	1.24
21	264.65	0.25	2.54	3.47
21.2	266.51	0.23	2.47	0.50
22			0.86	0.25
22.2	270.25	0.23	3.14	4.21
23			0.11	0.25
23.2	273.98	0.23	3.36	2.23
24.2	277.75	0.25	3.06	5.94
25			0.04	
25.2	281.47	0.24	3.51	1.98
26.2	285.19	0.23	5.61	3.71
27				
27.2	288.91	0.23	8.67	3.71
28				
28.2	292.62	0.23	6.65	5.20
29				
29.2	296.31	0.23	5.68	6.68
30.2	299.99	0.23	5.31	3.96
31			0.11	0.25
31.2	303.79	0.23	3.14	1.98
32			0.07	0.74
32.2	307.55	0.23	0.71	2.23
33			0.41	1.73
33.2	311.38	0.25	0.45	0.25
34			0.37	0.50
34.2			0.22	
35	317.07	0.26		0.50
36			0.11	

Likewise we found the rare shorter alleles 16 and 17 only in the German and the longer allele 30 only in the Turkish sample.

In the system HumACTBP2 we found 49 different alleles among Germans (Table 2) and 35 different alleles among Turks. Whether the dominant appearance of allele 17 in the Turkish population is due to the limited number of individuals will become clear when more Turks have been investigated. The allele SE33 14.3 was found in the German population for the first time. Concerning the genotype distribution, we observed 295 out of the 1225 possible genotypes in Germans and 134 genotypes could be observed in Turks. The results of this survey seem to be in accordance with data reported in other Caucasian populations (Alper et al. 1995; Bläß et al. 1996; Rolf et al. 1997) showing only minor differences in the frequency and the number of observed alleles. The population comparison test (RxC contingency table, G. Carmody) for pairwise comparisons revealed significant differences between German and Turkish samples in both STR systems (P value = 0).

In order to make our analysis of the system ACTBP2 comparable to other investigations and to define borderlines for automated genotyping, it is indispensable to define the precision of the fragment length measurement. The fragments of the allelic ladder were therefore mea-

Table 3 Differences of size measurement of 2 HumACTBP2 ladders on the same gel using ABI 377 and GS500 (ROX) internal standard. The mean measurement difference from 49–65 pairwise comparisons of ladder alleles is calculated

Allele	Fragment length (bp)	Measurement difference (bp)	SD	n
9	218.20	0.06	0.04	58
12	230.02	0.06	0.03	65
13	233.95	0.06	0.05	65
14	237.88	0.06	0.04	65
15	241.80	0.06	0.04	65
16	245.72	0.06	0.05	65
17	249.61	0.05	0.06	65
18	253.39	0.06	0.05	65
19	257.14	0.06	0.04	65
20	260.88	0.07	0.05	64
21	264.65	0.12	0.09	49
21.2	266.51	0.07	0.05	64
22.2	270.25	0.08	0.06	64
23.2	273.98	0.08	0.06	64
24.2	277.75	0.12	0.09	58
25.2	281.47	0.11	0.08	61
26.2	285.19	0.10	0.08	63
27.2	288.91	0.09	0.07	62
28.2	292.62	0.07	0.05	63
29.2	296.31	0.07	0.06	63
30.2	299.99	0.07	0.06	63
31.2	303.79	0.08	0.07	63
32.2	307.55	0.07	0.05	63
33.2	311.38	0.09	0.07	63
35	317.07	0.09	0.07	63

sured on more than 100 gels against the internal standard GS 500 (ROX) on the ABI 377. It is apparent that the size window for automated allele designation (Table 2) increases with greater fragment length from 0.7 to 1.2 bp (SD 0.14–0.26). Therefore routinely two allelic ladders are included on each gel and the allele designation was made in comparison to those fragments. Similar investigations are reported by Dupuy and Olaisen (1997) with comparable measurement differences. Additionally the measurement differences of equal fragments run on the same gel are given in Table 3. The mean differences ranged from 0.06 to 0.12 bp, the maximum values did not exceed 0.3 bp. As peak intensity and other interfering factors for example in stain analysis may be different, the difference between samples from normal casework (considerable number of mixed stains) and the ladder was also investigated. For the alleles SE 33 15 (mean difference = 0.05 bp; SD = 0.04; n = 64) SE 33 18 (mean difference = 0.05; SD = 0.05; n = 112) and SE 33 27.2 (mean difference = 0.07; SD = 0.05; n = 108) we found almost the same values as indicated in Table 3. Therefore it should be possible to type alleles differing in size by one basepair only.

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