Int J Legal Med (1995) 108:93–95

ORIGINAL ARTICLE

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HumFES/FPS and HumF13B: Turkish and German population data

Received: 5 April 1995 / Accepted: 3 July 1995

Abstract The allele distribution of two STRs has been investigated in two populations, i.e. Turks (n = 203/200) and Germans (n = 414/402). The Turkish population showed 11 alleles in HumFES/FPS and 6 alleles in HumF13B while the German population had 9 (FES) and 8 (F13B) alleles respectively. Although the frequency profiles looked quite similiar in both populations, there exist significant differences mainly due to alleles 8 and 10 (F13B) and allele 12 (FES). Four variant alleles have been sequenced and are described. Investigation of 368 (FES)/372 (F13B) meioses revealed no new mutations.

Key words Short tandem repeat · HumFES/FPS · HumF13B · Turks/Germans · Meioses

Introduction

The short tandem repeat (STR) loci HumFES/FPS (Polymeropoulos et al. 1991) and HumF13B (Nishimura and Murray 1992), both containing tetrameric repeats, were examined in population samples from southern Turkey and northwest Germany.

Material and methods

Two population samples, each consisting of healthy unrelated Caucasians were investigated: n = 203 Turks from the Adana area (Southern Turkey), n = 414 Germans from the Münster area (North West Germany). The Turkish samples consisted of dried blood stains and therefore the extraction was done using Chelex 100 and Proteinase K (Wiegand et al. 1993) while the German blood samples were extracted as described (Brinkmann et al. 1991). The FES-alleles were processed and detected as described among others with a sequenced allelic ladder (Möller et al. 1994). – The assay for F13B contained: 5 ng template DNA, 1 U Taq DNA polymerase, 2 µl reaction buffer (500 mM KCL, 100 mM Tris/HCl pH 8.8, 1% Triton X-100), 25 mM $MgCl_2$, 200 mM each dNTP, 1 mM each primer (primer sequence according to Nishimura and Murray 1992).

Cycle conditions

a) 10 cycles: 96°C, 60 s; 60°C, 60 s; 70°C, 90 s
b) 20 cycles: 90°C, 60 s; 60°C, 60 s; 70°C, 90 s.

Table 1 Allele frequencies for HumFES/FPS and HumF13B in Turkish and German populations. The nomenclature of alleles is according to the number of repeats (*C* cathodal, *A* anodal; *n* number of individuals typed)

HumFES/FPS			HumF13B		
Allele	Turks (n = 203)	Germans (n = 414)	Allele	Turks (n = 200)	Germans (n = 402)
7	0.003	–	6	0.075	0.103
8	0.007	0.012	7	0.030	0.012
9	0.005	0.006	8	0.315	0.224
10A	0.209	0.248	9	0.243	0.225
10	0.037	0.056	9C	–	0.001
11A	0.017	0.030	10	0.335	0.432
11	0.372	0.413	10C	–	0.001
12A	0.003	–	11	0.003	0.001
12	0.296	0.188			
13	0.044	0.045			
14	0.007	0.002			

Table 2 Heterozygosity rate (H), mean exclusion chance (MEC) and discrimination indices (DI) for HumFES/FPS and HumF13B in a Turkish and a German population survey. (*Tur.* Turks, *Ger.* Germans)

	H		MEC		DI	
	Tur.	Ger.	Tur.	Ger.	Tur.	Ger.
HumFES	0.67	0.69	0.49	0.50	0.88	0.88
HumF13B	0.73	0.69	0.47	0.46	0.87	0.87

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Table 3 Population comparison test (R X C contingency table, G. Carmody, Ottawa, Canada) for pairwise comparisons. The *P*-values for a Chi-square test and a G-test are given. (*SE* standard error)

System	Comparison	Chi-square	P-value	G statistics	P-value
HumFES	Tur.-Ger.	26.88	0.0020 ± 0.0014 (SE)	26.82	0.0040 ± 0.0020 (SE)
HumF13B	Tur.-Ger.	23.34	0.0010 ± 0.0010 (SE)	23.64	0.0010 ± 0.0010 (SE)

Electrophoresis of HumF13B was performed in 6% non-denaturing polyacrylamide gels, all other conditions were as described for HumFES/FPS (Möller et al. 1994). For F13B we have also established an allelic ladder composed of sequenced alleles (Fig. 1 nomenclature according to ISFH DNA recommendations 1992). – Isolation of silver stained fragments, subsequent Taq-cycle-sequencing and sequence analysis was performed as described (Möller and Brinkmann 1994).

In addition, we have also analysed allele segregation in 368 mother/father – offspring pairs (FES) and 372 pairs (F13B) respectively.

Statistical analysis

Test for heterogeneity between populations: R X C contingency table; G. Carmody, Ottawa, Canada. Discrimination indices and heterozygosity rates: Jones et al. (1972); Hardy-Weinberg equilibrium: exact test (Guo and Thompson 1992; Software from C. Puers, Münster, Germany).

Results and discussion

Both populations were in Hardy-Weinberg equilibrium ($P > 0.05$) for both systems. Although the frequency profiles in both populations appeared very similar (Table 1, Fig. 2), the statistical analysis revealed significant differences (Table 3) mainly due to allele 12 (FES) and allele 8 and 10 (F13B). – The forensic efficency data (heterozygosity, mean exclusion chance, discrimination index) were very similar in both populations (Table 2).

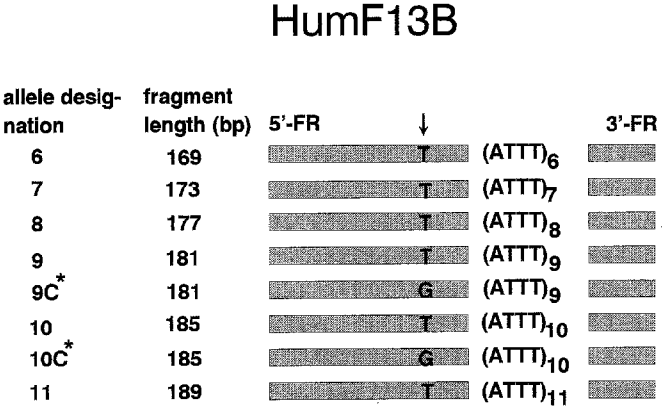

Fig. 1 Sequence structure of the short tandem repeat system HumF13B. The allele designation is according to the number of repeats; the variant alleles 9C and 10C are denominated with respect to their slower electrophoretic mobilities relative to the regular alleles 9 and 10 (*C* = cathodal). Fragment lengths are given in base pairs (*bp*); *asterisks*: alleles not included into the allelic ladder; *arrow*: sequence variation at position 89 of the 5′- flanking region (*FR*)

In 368 meioses (HumFES, Germans) and 372 meioses (HumF13B, Germans) respectively, no mutations affecting fragment length or mobility in a native gel system occurred. Since this separation resolves length differences of 1 bp and also many structural variants of the same length (Möller et. al 1994) we assume that new mutations did not occur in this survey.

We have also observed 4 new variants, all confirmed by sequencing: allele 7 (FES; with 7 repeats only) in Turks, allele 12A in Turks with an A to C base substitution at positon 34 of the 5' flanking region. The substitution was identical to that of variants 10A and 11A (Möller et al. 1994). Furthermore, at HumF13B (Fig. 1) 2 variant alleles, i.e. 9C, 10C (C stands for cathodal) were observed in Germans, where a T to G base transition in position 89 of in the 5′ flanking region effected a reduced electrophoretic mobility in non-denaturing gels (Fig. 1).

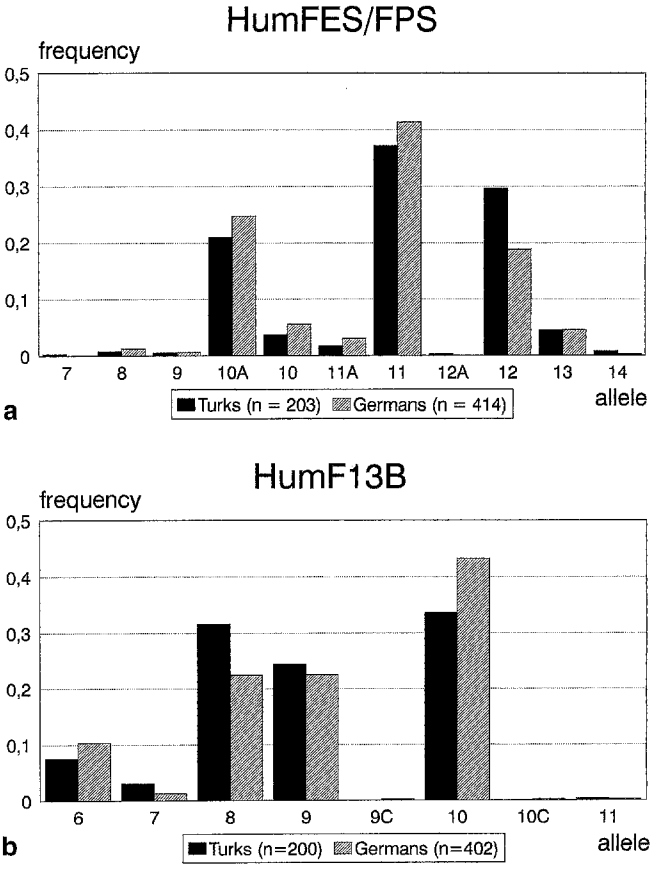

Fig. 2a, b Comparison of allele frequency distributions in Turks and Germans. **a** HumFES/FPS; **b** HumF13B

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