SHORT COMMUNICATION

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TNFa and b microsatellites in Germany

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Abstract Allele frequencies of TNFa and TNFb microsatellites were determined from 315 healthy unrelated Germans (mothers and putative fathers) by means of PCR. They were stably inherited and segregated in a Mendelian way. New mutations were not observed.

Key words Microsatellites \cdot TNFa \cdot TNFb \cdot Population study

Introduction

The genes for the tumor necrosis factor (TNF α) and lymphotoxin (LT α and LT β) are arranged within a 7 kb region in the MHC class III region (Nedospasov et al. 1991; Jongeneel et al. 1991). The TNFa and b microsatellites are located 3.5 kb upstream of the TNF α gene.

Materials and methods

Blood samples were obtained from 315 healthy unrelated individuals. The DNA extraction was performed as previously described (Miller et al. 1988). For the TNFa and TNFb microsatellite typing the method of Jongeneel et al. (1991) was used with minor modifications. The allele distributions of TNFa and b were identified according to the length of the VNTRs.

Results and discussion

The VNTR loci of TNFa and b are informative genetic markers (Table 1) for individual identification and can be

Dedicated to Prof. Dr. Werner Göhler on the occasion of his 70th birthday

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Table 1 Observed allele frequencies of TNFa and TNFb	Allele	TNFa	TNFb
microsatellites	1	0.021	0.152
	2	0.249	0
	3	0.016	0.097
	4	0.087	0.44
	5	0.056	0.294
	6	0.111	0
Mean exclusion chance TNFa: 72.4%, TNFb 43.7% Exact HW test for locus TNFa: $\chi^2 = 87$; df = 78; 0.178 0.199; PD = 0.96 Exact HW test for locus TNFb: $\chi^2 = 48$; df = 10; 0.006 0.0028; PD = 0.84	7	0.103	0.017
	8	0.003	
	9	0.025	
	10	0.144	
	11	0.141	
	12	0.006	
	13	0.037	

used in forensic casework of crime and paternity (Brinkmann 1996; Takeshita et al. 1997). Of the TNFa alleles 85.4 % (86.1_{exp}) were found to be heterozygous. The most frequently observed TNFa allele combinations were a 2–10 and a 2–11 each accounting for more than 8%. The most common genotype of TNFb was b 4–5 (28.6%).The rate of heterozygosity was 72.4 % (68.8_{exp}).

References

- Brinkmann B (1996) The STR approach. In: Carracedo A, Brinkmann B, Bär W (eds) Advances in forensic haemogenetics 6. Springer, Berlin Heidelberg New York, pp 41–51
- Jongeneel CV, Briant L, Udalova IA, Sevin A, Nedospasov SA, Cambon-Thomsen A (1991) Extensive genetic polymorphism in the human tumor necrosis factor region and relation to extended HLA haplotypes. Proc Natl Acad Sci USA 88:9717– 9721
- Miller SA, Dykes DD, Polesky HF (1988) A simple salting out procedure for extracting DNA from human nucleated cells. Nucleic Acids Res16 (3):1215
- Nedospasov SA, Udalova IA, Kuprash DV, Turetskaya R (1991) DNA sequence polymorphism at the human tumor necrosis factor (TNF) locus. J Immunol 147 (3):1053–1059
- Takeshita H, Meyer E, Brinkmann B (1997) The STR loci HumTPO and HumLPL: population genetic data in eight populations. Int J Legal Med 110:331–333