Population data of the VNTR loci D10S28, D4S139, D16S309 and D5S110 in German Caucasians

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INTRODUCTION

Variable number of tandem repeat (VNTR) loci are highly polymorphic markers that are commonly used for paternity and forensic testing. The allele distribution of these markers however differs between ethnic groups. Therefore, proper calculation of paternity probability (PP) can only be conducted with frequencies obtained from population samples of the same ethnic origin as the individual tested. We have studied the allele distribution of four VNTR loci, D10S28, D4S139, D16S309 and D5S110 in a population sample of German Caucasians.

PROBE AND LOCUS:

TBQ7	(D10S28)	(Bragg 1987)
PH30	(D4S139)	(Milner 1989)
MS205	(D16S309)	(Royle 1992)
LH1	(D5S110)	(Armour 1990)

POPULATION AND SAMPLE SIZE:

Hesse (Germany)
N: 201 Individuals, (D10S28)
N: 133 Individuals, (D4S139)
N: 221 Individuals, (D16S309)
N: 147 Individuals, (D5S110)

METHODS

Restriction enzyme HAEIII : D10S28 (TBQ7), D4S139 (PH30), D5S110 (LH1)
HINF I : D16S309 (MS205)

Electrophoretic methods: Fragments were separated by agarose gelelectrophoresis (24-26 hours at 0.8-1.0 V/cm). Electrophoresis conditions were chosen depending on the range of fragment sizes detected by the various DNA probes. Hybridisation, southern blot transfer to nylon membrans (Qiabrane from Qiagen Inc, Chatsworth, CA, USA) and chemiluminescence detection of probes was performed as recommended by the manufacturers (NICE™ MS205 ICI/CELLMARK, GenePrint Light™ TBQ7 Promega and ACES™ LH1/pH30 Gibco BRL). Fragments were analysed by an semiautomatic computerized system (DNA-Auswertungssystem Version 2.40 from Muche M. Immucor Medizinische Diagnostik GmbH, Rödermark, Germany).

RESULTS

MS205 Allele sizes and frequencies (0,1 kb Intervals)

Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency
0,8	0,0045	1,7	0,0068	2,4	0,0566	3,1	0,0362	3,8	0,0158
1,1	0,0023	1,8	0,0091	2,5	0,0543	3,2	0,0566	3,9	0,0136
1,2	0,0045	1,9	0,0226	2,6	0,0452	3,3	0,0362	4,0	0,0091
1,3	0,0045	2,0	0,0339	2,7	0,0566	3,4	0,0204	4,1	0,0023
1,4	0,0091	2,1	0,0249	2,8	0,1041	3,5	0,0249	4,2	0,0023
1,5	0,0045	2,2	0,0498	2,9	0,0973	3,6	0,0317	4,3	0,0023
1,6	0,0158	2,3	0,0543	3,0	0,0520	3,7	0,0271	4,4	0,0091

PH30 Allele sizes and frequencies (0,1 kb Intervals)

Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency
2,8	0,005	5,8	0,02	7,8	0,02	10,2	0,005	13,2	0,005
3,5	0,01	5,9	0,025	7,9	0,005	10,3	0,005	13,4	0,005
3,6	0,02	6,1	0,03	8,0	0,015	10,4	0,01	13,8	0,005
3,8	0,01	6,2	0,03	8,2	0,005	10,5	0,01	13,9	0,005
3,9	0,005	6,3	0,02	8,3	0,005	10,6	0,005	14,3	0,005
4,0	0,005	6,4	0,015	8,4	0,015	10,7	0,005	14,4	0,005
4,1	0,005	6,5	0,025	8,6	0,025	10,8	0,005	15,2	0,005
4,3	0,005	6,6	0,025	8,7	0,005	10,9	0,01	15,7	0,005
4,4	0,005	6,7	0,015	8,8	0,02	11,0	0,005	16,2	0,005
4,5	0,025	6,8	0,01	9,0	0,005	11,1	0,005	16,3	0,005
4,7	0,015	6,9	0,015	9,2	0,005	11,3	0,005	16,8	0,005
4,8	0,03	7,0	0,03	9,4	0,005	11,6	0,005	17,6	0,005
5,0	0,01	7,1	0,015	9,5	0,01	11,7	0,005	17,8	0,005
5,1	0,02	7,2	0,02	9,6	0,005	11,9	0,01	17,9	0,005
5,2	0,005	7,4	0,01	9,8	0,025	12,3	0,01	18,2	0,005
5,3	0,01	7,5	0,02	9,9	0,015	12,5	0,005	21,5	0,005
5,5	0,015	7,6	0,015	10,0	0,005	13,0	0,01	22,7	0,005
5,7	0,015	7,7	0,005	10,1	0,01	13,1	0,005		

TBQ7 Allele sizes and frequencies (0,1 kb Intervals)

Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency
1,0	0,005	2,1	0,0473	3,2	0,00995	4,3	0,00746	5,5	0,00746
1,1	0,017	2,2	0,0423	3,3	0,0149	4,4	0,0124	5,6	0,0025
1,2	0,015	2,3	0,0124	3,4	0,00746	4,5	0,0174	5,7	0,0025
1,3	0,015	2,4	0,0249	3,5	0,0274	4,6	0,00498	5,9	0,005
1,4	0,0075	2,5	0,0149	3,6	0,0249	4,7	0,00995	6,0	0,00746
1,5	0,0522	2,6	0,0174	3,7	0,0174	4,8	0,0174	6,1	0,0025
1,6	0,0597	2,7	0,00995	3,8	0,00746	4,9	0,0174	6,5	0,005
1,7	0,0547	2,8	0,0398	3,9	0,0124	5,0	0,0025	7,1	0,0025
1,8	0,0547	2,9	0,0249	4,0	0,0249	5,1	0,00746	9,2	0,0025
1,9	0,0771	3,0	0,0448	4,1	0,0174	5,3	0,0025		
2,0	0,0323	3,1	0,0149	4,2	0,0124	5,4	0,0025		

LH1 Allele sizes and frequencies (0,1 kb Intervals)

Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency
1,2	0,0102	2,4	0,0272	3,5	0,0442	4,6	0,0102	5,9	0,017
1,4	0,0034	2,5	0,0238	3,6	0,0544	4,7	0,0102	6,0	0,0068
1,5	0,0102	2,6	0,034	3,7	0,017	4,8	0,0102	6,1	0,0068
1,6	0,017	2,7	0,0204	3,8	0,0102	4,9	0,0034	6,5	0,0034
1,7	0,0238	2,8	0,0442	3,9	0,0306	5,0	0,0102	7,0	0,0102
1,8	0,0136	2,9	0,0578	4,0	0,0068	5,1	0,0068	7,2	0,0034
1,9	0,0272	3,0	0,0306	4,1	0,0204	5,2	0,0136	7,6	0,0034
2,0	0,0204	3,1	0,0374	4,2	0,0136	5,3	0,0068	7,7	0,0034
2,1	0,0442	3,2	0,0306	4,3	0,0136	5,4	0,0102	7,8	0,0034
2,2	0,034	3,3	0,0238	4,4	0,0204	5,7	0,0034	8,1	0,0034
2,3	0,0204	3,4	0,0442	4,5	0,0204	5,8	0,0034		

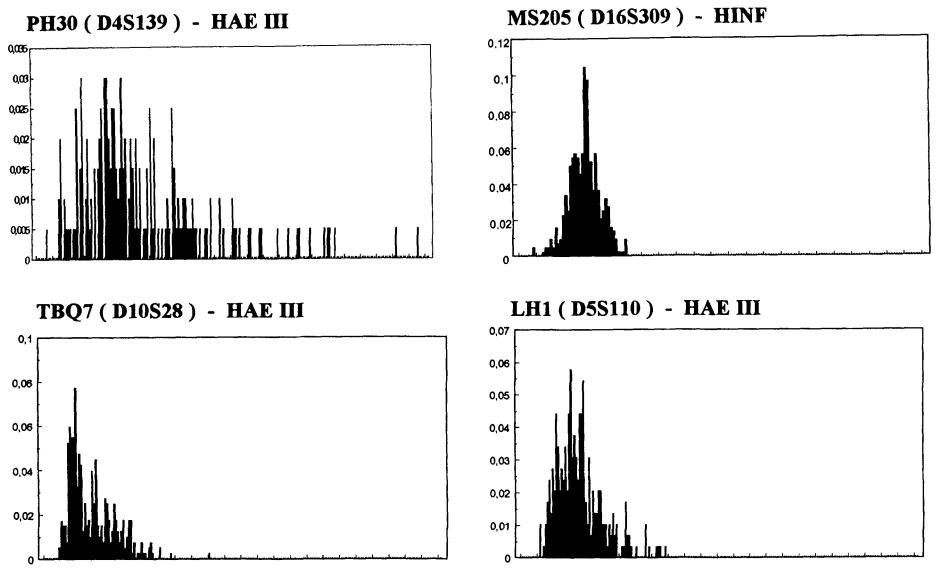

Figure 1: Allele sizes and frequencies of VNTR SLP polymorphisms in German Caucasians

COMMENTS

Chemiluninescence detection of these probes could be easily performed. Reproducibility of size measurement was performed by examining control DNA (K 562) on every gel. The allele distribution observed with the SLP's TBQ7, LH1 and MS205 did reveal frequent fragments lying close together in the lower kb region, whereas the SLP PH30 exhibited a more irregular distribution with 19,8% of fragments lying above 10 kb (Fig.1). Size determination of fragments above 10 kb is very often limited due to the reduced electrophoretic separation of these fragments. The range of the fragment size of individual alleles in this high molecular region can increase to more than $\pm$5% and thus the precise determination of identical fragments between to individuals is limited. In this respect, the information content of loci with wide spread allelic size ranges is reduced. Nevertheless, in cases of clear differences in the fragment sizes of alleles between two individuals these high molecular fragments can be very informative. In conclusion, the high heterozygosity rates and the extensive polymorphism of these SLP's are ideal for human identification testing.

VNTR loci	HR	VNTR loci	HR
D10S28 (TBQ7) - HAEIII	0,90	D16S309 (MS205) - HINFI	0,98
D4S139 (PH30) - HAEIII	0,97	D5S110 (LH1) - HAEIII	0,96

REFERENCES

Armour JA, Povey S, Jeremiah S, Jeffreys AJ (1990) Systematic cloning of human minisattelites from ordered array charomid libraries. Genomics, Vol. 8: 501-512

Bragg T, Nakamura Y, Jones C, White R (1987) Isolation and mapping of a polymorphic DNA sequence (cTBQ7) on chromosome 10 (D10S28). Nucleic Acids Research, Vol 16 (233): 11395

Milner ECB, Lotshaw CL, van Dijk KW, Concannon P, Schroeder HW (1989) Isolation and mapping of a polymorphic DNA sequence pH30 on chromosome 4 [HGM provisional no. D4S139] Nucl Acids Res, Vol 17 : 4002

Royle NJ, Armour JA, Webb M, Thomas A, Jeffreys AJ (1992) A hypervariable locus D16S309 located at the distal end of 16p. Nucl Acids Res, Vol 20 : 1164