SUITABILITY OF THE HUMTH01, HUMCD4, AND HUMVWA STR POLYMORPHISMS FOR LEGAL MEDICINE INVESTIGATIONS IN THE POPULATION OF CATALONIA (NORTH-EAST SPAIN)

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Systems and loci: HUMTH01 (11p15.5), HUMCD4 (12p), HUMvWA (12p12-12pter)

Population and sample sizes: Catalonia (NE Spain). European Western Mediterranean population. HUMTC11 n=161. HUMCD4 n=117. HUMVWA n=122

Methods: Standard PCR amplifications were accomplished with fluorescein labelled primers. HUMTH01 primers (Edwards A 1992), HUMCD4 primers (Edwards MC 1991), HUMVWA primers (Kimpton 1992). Electrophoretic methods: 6% polyacrylamide denaturing gel electrophoresis. The gels were run for 4h. at 1450 V, 38 mA, 45W, 50°C and laser power at 3 mW on the ALF DNA Sequencer. The allelic ladders used were composed by a cocktail of samples with alleles of known size from each polymorphism.

Results:

Table 1. Observed genotypes.

HUMTH01		HUMCD4		HUMVWA31	
6/6	10	1/1	14	14/15	2
6/7	10	1/2	21	14/16	6
6/8	10	1/6	15	14/17	10
6/9	13	1/7	6	14/18	3
6/9.3	22	1/8	3	14/19	3
6/10	3	2/2	14	15/15	1
7/7	2	2/4	1	15/16	11
7/8	11	2/6	15	15/17	5
7/9	17	2/7	5	15/18	2
7/9.3	10	2/8	2	15/19	4
8/8	4	6/6	15	15/20	1
8/9	5	6/7	4	16/16	7
8/9.3	8	6/8	2	16/17	13
8/R1	1	16/18	8		
9/9	6	16/19	3		
9/9.3	16	17/17	10		
9/11	1	17/18	12		
9/R2	1	17/19	7		
9.3/9.3	11	18/18	9		
		18/19	5		
Chi^2=36.25 df= 36 $0.500 > p > 0.450$		Chi^2= 11.86 df= 15 $0.790 > p > 0.789$		Chi^2= 27.35 df= 21 $0.250 > p > 0.100$	

Table 2. Allele frequencies.

HUMTH01			HUMCD4			HUMVWA31		
n=161			n=117			n=122		
Allele	Freq.	bp.^{a}	Allele^b	Freq.	bp.^{a}	Allele	Freq.	bp.^{a}
6	0.2422	184	1	0.3119	86	14	0.0983	138
7	0.1614	188	2	0.3076	91	15	0.1106	142
8	0.1335	192	3	0		16	0.2254	146
9	0.2018	196	4	0.0042	101	17	0.2746	150
9.3	0.2422	199	5	0		18	0.1967	154
10	0.003	200	6	0.2820	112	19	0.0902	158
11	0.003	203	7	0.0641	117	20	0.0041	162
R1	0.003	209	8	0.0299	123			
R2	0.009	215						

(a) Fragment sizes determined automatically using Fragment Manager v.1.1 software Pharmacia

(b) Smallest allele in the HUMCD4 cocktail was therefore arbitrarily designated as "1" and the others were enumerated consecutively towards the cathode.

Table 3. Forensic diagnosis suitability results.

	HUMTH01	HUMCD4	HUMVWA31
Heterozygosity Index (HI)	79.50	63.25	77.87
Power discrimination (PD)	0.93	0.87	0.93
Chance Exclusion (CE)	0.59	0.47	0.61
Essen-Möller mean value (EM)	9.55	9.65	9.53

Comments: The high degree of variability of each PCR polymorphism makes these markers very useful in forensic genetics diagnosis.

References

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