

SWISS POPULATION DATA FOR THE STR SYSTEMS HUMVWA HUMF13A1 AND HUMFES

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Systems and loci: HUMVWA (12p12-12pter), HUMF13A1 (6p25-p24) and HUMFES (15q25-qter).

Population and sample size: Swiss population sample, N = 386 for HUMVWA, N = 425 for HUMF13A1 and N = 370 for HUMFES.

Methods:

HUMVWA Primers (Kimpton et al. 1992), HUMF13A1 Primers (Polymeropoulos et al. 1991), HUMFES Primers (Polymeropoulos et al. 1991).

Amplification conditions (Thermocycler: Biometra Triothermoblock): 94°C - 45 sec., 55°C - 30 sec., 72°C - 30 sec.; 30 cycles. HUMVWA and HUMF13A1 were coamplified.

Analysis and fluorescent detection: The PCR-products were analyzed and detected on an ABI 373A automated DNA sequencer (ABI GeneScan 672). The electrophoresis was carried out on 6 % de-naturing polyacrylamide gels according to the ABI protocol (running conditions: 1600 V, 24mA, 8hs). Allele designations were determined by comparison with an allelic ladder.

HWE-Analysis: The Hardy-Weinberg equilibrium hypothesis was tested using the software HWEANA17.EXE (HWE-Analysis, Version 3.0) developed and refined by Puers (1994/95).

Results:

HUMVWA: Observed genotypes

Gen.	Obs.	Gen.	Obs.	Gen.	Obs.	Gen.	Obs.
13-14	1	15-15	1	16-18	36	18-19	18
14-14	3	15-16	17	16-19	11	18-20	2
14-15	6	15-17	16	16-20	1	19-19	3
14-16	16	15-18	18	17-17	21	19-20	4
14-17	21	15-19	4	17-18	48	19-21	1
14-18	13	15-20	2	17-19	26		
14-19	2	16-16	16	17-20	2		
14-20	1	16-17	57	18-18	19		

HUMVWA: Allele frequencies

Allele	Frequency	Allele	Frequency	Allele	Frequency
13	0.001	16	0.220	19	0.093
14	0.085	17	0.275	20	0.016
15	0.084	18	0.224	21	0.001

HUMF13A1: Observed genotypes

Gen.	Obs.	Gen.	Obs.	Gen.	Obs.	Gen.	Obs.
3-3	2	4-7	7	5-15	4	6-19	1
3-4	2	4-8	1	5-16	3	7-7	48
3-5	13	4-12	1	6-6	44	7-13	1
3-6	19	4-14	1	6-7	91	7-15	7
3-7	27	4-15	1	6-8	1	7-16	4
3-15	3	5-5	8	6-12	1	15-15	1
3-16	2	5-6	48	6-13	1	15-17	1
4-4	1	5-7	57	6-14	2		
4-5	5	5-12	1	6-15	4		
4-6	9	5-13	1	6-16	2		

HUMF13A1: Allele frequencies

Allele	Frequency	Allele	Frequency	Allele	Frequency
3	0.082	8	0.002	16	0.013
4	0.034	12	0.004	17	0.001
5	0.174	13	0.004	19	0.001
6	0.314	14	0.004		
7	0.341	15	0.026		

HUMFES: Observed genotypes

Gen.	Obs.	Gen.	Obs.	Gen.	Obs.	Gen.	Obs.
8-9	1	9-11	1	10-13	9	12-13	6
8-10	1	9-12	1	11-11	53	12-14	1
8-11	7	10-10	35	11-12	66		
8-12	1	10-11	103	11-13	9		
9-10	1	10-12	59	12-12	16		

HUMFES: Allele frequencies

Allele	Frequency	Allele	Frequency	Allele	Frequency
8	0.014	11	0.396	14	0.001
9	0.005	12	0.224		
10	0.327	13	0.032		

Forensic efficiency

	VWA	F13A1	FES
Mean paternity exclusion chance (MEC)	0.6117	0.5223	0.4165
Mean exclusion probability (MEP)	0.6057	0.5041	0.4066
Polymorphism information content (PIC)	0.7743	0.7054	0.6240
Probability of match (pM)	0.0730	0.1091	0.1679
Discrimination power (D)	0.9271	0.8909	0.8321

Comments:

A Swiss population database has been established for the 3 PCR based STR loci HUMVWA, HUMF13A1 and HUMFES. For all 3 systems the Hardy-Weinberg equilibrium was tested using the HWE-Analysis computer program of Puers (1994/95) which performs the following HWE-analyses: the exact test, chi-square and logarithmic likelihood ratio test, test of HWE hypothesis by comparison of the observed heterozygosity/homozygosity with the unbiased estimate of the expected heterozygosity/homozygosity, the Random-shuffling-exact-, the chi-square- and G-Test. All 3 loci showed no significant deviations from assumed Hardy-Weinberg equilibria.

The distributions of allele frequencies in the Swiss population sample are similar to those observed in other Caucasians, e.g. in Germany (Möller et al. 1994), in Italy (Buscemi et al. 1995), in the UK (Kimpton et al. 1993) and in France (Pfitzinger et al. 1995).

The 3 investigated polymorphic STR systems HUMVWA, HUMF13A1 and HUMFES are reliable and sensitive marker systems that are well suited for use in forensic casework.

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