

GERMAN DATA ON THE PCR BASED LOCI HUMVWA31, HUMTH01, HUMFES/FPS, HUMF13B AND D1S80

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Summary

To create a preliminary data base for the PCR based loci HUMVWA31, HUMTH01, HUMFES/FPS, HUMF13B AND D1S80 population data from Germany were collected and additional population studies have been carried out on ethnic Germans living in Northrhine Westphalia. With exception of the D1S80 system no deviations from the Hardy-Weinberg-equilibrium have been detected. The German samples have been pooled by calculating the weighted arithmetical means to be useful as preliminary data base for forensic purposes.

Material and Methods

DNA was isolated from ethnic Germans living in Northrhine Westphalia. Isolation was carried out using a commercially available kit (Qiagen, Germany). The samples were typed according to Kimpton et al, 1994. AVACH values have been calculated according to Krüger et al, 1968.

Results and Discussion

The German gene frequencies for the loci HUMVWA31, HUMTH01, HUMFES/FPS, HUMF13B and D1S80 are presented in table 1 - table 5. For the Northrhine Westphalian samples no deviations from the Hardy-Weinberg-equilibrium were found: HUMVWA31 ($\chi^2 = 8.17$, $df = 10$, $50 > p > 70$); HUMTH01 ($\chi^2=15.64$, $df=9$, $5 > p > 10$); HUMFES/FPS ($\chi^2=5.09$, $df=4$, $20 > p > 30$).

The German AVACH values (samples pooled by calculating weighted arithmetical means) are HUMVW31 (0.6163), HUMTH01 (0.5645), HUMFES/FPS (0.4136), HUMF13B (0.4328) and D1S80 (0.6425).

Locus HUMVWA31

Population	n	Ref.	12	13	14	15	16	17	18	19	20	21
Düsseldorf	608	(1)	0.0000	0.0049	0.0477	0.1118	0.2385	0.2714	0.2105	0.1020	0.0115	0.0016
NRW	488		0.0020	0.0000	0.1086	0.0963	0.1947	0.3053	0.2111	0.0738	0.0082	0.0000
Münster	642	(2)	0.0000	0.0047	0.1100	0.0980	0.2100	0.2700	0.2100	0.0770	0.0170	0.0016
Germany	1738		0.0006	0.0035	0.0878	0.1024	0.2157	0.2804	0.2105	0.0848	0.0126	0.0012

Table 1 HUMVWA31A system: allele frequencies in Germany; *Germany* pooled by calculating the weighted arithmetical means of the allele frequencies; n = number of examined genomes; Ref. = references: (1) Huckenbeck et al 1996^a, (2) Möller et al. 1994.

Locus HUMTH01

Population	n	Ref.	5	6	7	8	9	9.3/10	11
Düsseldorf	604	(1)	0.0166	0.1722	0.1705	0.1291	0.1639	0.3377	0.0099
NRW	546		0.0092	0.2234	0.1429	0.1044	0.1648	0.3553	0.0000
Münster	220	(2)	0.0020	0.2310	0.1630	0.1120	0.1920	0.2890	0.0100
North Germany	536	(3)	0.0000	0.2180	0.1600	0.1030	0.1720	0.3470	0.0000
Germany	1906		0.0081	0.2065	0.1588	0.1127	0.1697	0.3397	0.0043

Table 2 HumTH01 system: allele frequencies in Germany; **Germany** calculated by weighted arithmetical means (n=numbers of genomes; Ref=references: (1) Huckenbeck et al 1996^b, (2) Wiegand et al 1993, (3) Berschick et al 1994).

Locus HUMF13B

Population	n	Ref.	6	7	8	9	10	11
Düsseldorf	602	(1)	0.0648	0.0017	0.2691	0.2342	0.4302	0.0000
Münster	524	(2)	0.0878	0.0030	0.2443	0.2557	0.4084	0.0038
Germany	1126		0.0755	0.0023	0.2576	0.2442	0.4201	0.0018

Table 3 HumF13B system: allele frequencies in Germany; **Germany** calculated by weighted arithmetical means (n=number of genomes; Ref=references: (1) Huckenbeck et al 1996^c, (2) Serac 1995)

Locus HUMFES/FPS

Population	n	Ref.	8	9	10	11	12	13	14
Düsseldorf	600	(1)	0.0033	0.0033	0.2850	0.4667	0.2033	0.0383	0.0000
Northrhine Westphalia	446		0.0157	0.0000	0.2960	0.3991	0.2242	0.0628	0.0022
Münster	266	(2)	0.0075	0.0075	0.2854	0.4624	0.1842	0.0526	0.0052
Germany	1312		0.0084	0.0030	0.2888	0.4428	0.2065	0.0495	0.0018

Table 4 HumFES/FPS system: allele frequencies in Germany; **Germany** calculated by weighted arithmetical means (n=genomes; Ref= references:(1) Huckenbeck et al 1996^d (2) according to Serac (1994).

Locus D1S80

Alleles			14	15	16	17	18	19	20	21	22	23	24	25	26
Population	Ref.	n													
Germany Düsseldorf	(1)	756			0.003	0.005	0.253	0.013	0.024	0.029	0.033	0.017	0.343	0.046	0.012
Germany Bonn	(2)	308			0.003		0.279	0.006	0.042	0.026	0.032	0.010	0.341	0.039	0.010
Germany Northwest	(3)	436			0.002	0.009	0.245	0.002	0.037	0.018	0.035	0.021	0.378	0.052	0.007
Germany	(4)	500			0.006		0.198	0.002	0.028	0.032	0.050	0.018	0.346	0.044	0.030
<i>Germany</i>		<i>2000</i>			<i>0.004</i>	<i>0.004</i>	<i>0.242</i>	<i>0.007</i>	<i>0.031</i>	<i>0.027</i>	<i>0.038</i>	<i>0.017</i>	<i>0.351</i>	<i>0.046</i>	<i>0.015</i>

Alleles			27	28	29	30	31	32	33	34	35	36	37	38	39	40+
Population	Ref.	n														
Germany Düsseldorf	(1)	756	0.005	0.042	0.081	0.012	0.057	0.007	0.005	0.005		0.001	0.007			
Germany Bonn	(2)	308	0.020	0.020	0.055	0.003	0.087	0.010	0.010		0.006					
Germany Northwest	(3)	436	0.007	0.060	0.039	0.007	0.048		0.002	0.009		0.002	0.009		0.002	0.002
Germany	(4)	500	0.006	0.060	0.058	0.010	0.058	0.012	0.004	0.008		0.010	0.016			0.004
<i>Germany</i>		<i>2000</i>	<i>0.008</i>	<i>0.047</i>	<i>0.062</i>	<i>0.009</i>	<i>0.060</i>	<i>0.007</i>	<i>0.005</i>	<i>0.006</i>		<i>0.004</i>	<i>0.009</i>		<i>0.004</i>	<i>0.001</i>

Table 5 D1S80 system: allele frequencies in Germany; *Germany* pooled by calculating the weighted arithmetical mean (n=genomes; Ref.=references; allele 40 (includes alleles >40), all numbers of alleles include anodal and cathodal variants; (1) Huckenbeck et al 1996^e, (2) Huber & Holtz 1994, (3) Skowasch et al. 1992, (4) Schnee-Griese et al. 1993.

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