

HPRTB

In X-linked polymorphisms it is not convenient to calculate combined allele frequencies for males and females. In most of the published data there is no hint for the portion of males and females. In contrast to the other tables, "n" in the following table means the number of alleles, not the number of individuals (*except for the data from South Germany).

	Europe				
Population	Europe (Basques, Catalans, Northern Italians, Northern Europeans)	Basques (Females)	Basques (Males)	Belgium (Flanders)	Germany (South)
Ref.	(1)	(2)	(2)	(9)	(7)
n	340	372	140	315	661*
Alleles					
6	0.0000	0.0000	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0000	0.0000
8	0.0000	0.0108	0.0000	0.0000	0.0000
9	0.0020	0.0000	0.0000	0.0090	0.0050
10	0.0020	0.0108	0.0143	0.0030	0.0140
11/11A	0.0110	0.1478	0.1929	0.1280	0.1310
12/12A	0.1200	0.3925	0.3929	0.3670	0.2880
13	0.3670	0.2419	0.2571	0.2840	0.3220
14	0.2730	0.1452	0.0929	0.1650	0.1520
15	0.1470	0.0512	0.0357	0.0430	0.0730
16	0.0700	0.0000	0.0071	0.0090	0.0160
17	0.0020	0.0000	0.0071	0.0000	0.0000
18	0.0000	0.0000	0.0000	0.0000	0.0000
S	0.9940	1.0002	1.0000	1.0080	1.0010

	Europe				America
Population	Hungary	Poland (Southeast, Females)	Poland (Southeast, Males)	United Kingdom	America (Mayas, Surui, Karitiana)
Ref.	(3)	(10)	(10)	(4)	(1)
n	242	114*	100*	364	50
Alleles					
6	0.0000	0.0000	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0000	0.0000
8	0.0050	0.0090	0.0000	0.0000	0.0000
9	0.0200	0.0170	0.0100	0.0030	0.0000
10	0.0100	0.0090	0.0000	0.0230	0.0000
11	0.1320	0.1100	0.1100	0.1600	0.0000
12	0.3530	0.4080	0.3100	0.3380	0.1190
13	0.2840	0.2760	0.4000	0.2820	0.2800
14	0.1370	0.1360	0.1500	0.1370	0.3790
15	0.0540	0.0350	0.0200	0.0530	0.1590
16	0.0050	0.0000	0.0000	0.0050	0.0590
17	0.0000	0.0000	0.0000	0.0000	0.0000
18	0.0000	0.0000	0.0000	0.0000	0.0000
S	1.0000	1.0000	1.0000	1.0010	0.9960

	America, North				
Population	USA (Afro- Americans)	USA (Afro- Americans)	USA (Asiatics)	USA (Caucasoids)	USA (Caucasoids)
Ref.	(5)	(6)	(6)	(5)	(6)
n	218	276	98	214	417
Alleles					
6	0.0000	0.0040	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0050	0.0020
8	0.0000	0.0000	0.0000	0.0000	0.0000
9	0.0230	0.0180	0.0000	0.0280	0.0050

10	0.0180	0.0150	0.0000	0.0510	0.0100
11	0.1060	0.0690	0.0710	0.1360	0.1340
12	0.3490	0.2570	0.0000	0.3410	0.3430
13	0.2110	0.3040	0.2040	0.2290	0.2950
14	0.2020	0.2460	0.5100	0.1500	0.1560
15	0.0730	0.0830	0.1220	0.0470	0.0430
16	0.0180	0.0040	0.0820	0.0140	0.0120
17	0.0000	0.0000	0.0100	0.0000	0.0000
18	0.0000	0.0000	0.0000	0.0000	0.0000
S	1.0000	1.0000	0.9990	1.0010	1.0000

	America, North		America, Central	America, South	
Population	USA (Hispanics)	USA (Hispanics)	Mexico (Jalisco)	Argentina (Caucasoids, Buenos Aires)	Argentina (Mapuche, Rio Negro Province)
Ref.	(5)	(6)	(11)	(8)	(8)
n	214	210	233	278	62
Alleles					
6	0.0000	0.0000	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0000	0.0000
8	0.0000	0.0000	0.0043	0.0000	0.0000
9	0.0000	0.0050	0.0043	0.0000	0.0000
10	0.0050	0.0000	0.0086	0.0320	0.0000
11	0.0650	0.0620	0.0730	0.1790	0.0320
12	0.2760	0.3000	0.2790	0.3160	0.3220
13	0.3690	0.3710	0.3047	0.2840	0.4000
14	0.2100	0.2000	0.2017	0.1370	0.2410
15	0.0560	0.0620	0.1116	0.0470	0.0000
16	0.0190	0.0000	0.0129	0.0030	0.0000
17	0.0000	0.0000	0.0000	0.0000	0.0000
18	0.0000	0.0000	0.0000	0.0000	0.0000

S	<i>1.0000</i>	<i>1.0000</i>	<i>1.0001</i>	<i>0.9980</i>	<i>0.9950</i>
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	America, South				Asia
Population	Argentina (Tehuelche, Chubut Province)	Argentina (Wichi, Salta Province)	Brazil (Pernam-buco)	Brazil (Rio de Janeiro)	Asia (Chinese, Japanese, Cambodian)
Ref.	(8)	(8)	(14)	(13)	(1)
n	22	42	254	140	46
Alleles					
6	0.0000	0.0000	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0000	0.0000
8	0.0000	0.0000	0.0000	0.0000	0.0000
9	0.0000	0.0000	0.0160	0.0140	0.0000
10	0.0000	0.0000	0.0200	0.0140	0.0000
11	0.0900	0.0000	0.1460	0.0770	0.0000
12	0.2200	0.3500	0.2950	0.2950	0.1660
13	0.5900	0.1600	0.3190	0.3480	0.1250
14	0.0900	0.3500	0.1650	0.1880	0.3330
15	0.0000	0.1100	0.0240	0.0580	0.1450
16	0.0000	0.0000	0.0160	0.0050	0.2080
17	0.0000	0.0000	0.0000	0.0000	0.0200
18	0.0000	0.0000	0.0000	0.0000	0.0000
S	<i>0.9900</i>	<i>0.9700</i>	<i>1.0010</i>	<i>0.9990</i>	<i>0.9970</i>

	Asia, Far East			
Population	China (Han, Shanghai, Female)	China (Han, Shanghai, Male)	China (Han, Guangzhou, Female)	China (Han, Guangzhou, Male)
Ref.	(12)	(12)	(12)	(12)
n	98	49	70	47

Alleles				
6	0.0000	0.0000	0.0000	0.0000
7	0.0000	0.0000	0.0000	0.0000
8	0.0000	0.0000	0.0000	0.0000
9	0.0000	0.0000	0.0000	0.0000
10	0.0000	0.0000	0.0000	0.0000
11	0.0000	0.0000	0.0000	0.0000
12	0.0610	0.0410	0.0570	0.1060
13	0.2450	0.2860	0.2710	0.2980
14	0.5610	0.4690	0.4860	0.3620
15	0.0820	0.1840	0.1140	0.1700
16	0.0410	0.0000	0.0720	0.0430
17	0.0000	0.0200	0.0000	0.0000
18	0.0100	0.0000	0.0000	0.0210
S	1.0000	1.0000	1.0000	1.0000

	Oceania: Australia, Melanesia, Polynesia	Africa
Population	Pacific (Australian Aborigines, Papua New Guinea, Naisoi Melanesians)	Africa (Mbuti and Biaka, Lisongo)
Ref.	(1)	(1)
n	47	44
Alleles		
6	0.0000	0.0000
7	0.0000	0.0000
8	0.0000	0.0000
9	0.0000	0.0000
10	0.0000	0.0000

11	0.0000	0.0220
12	0.1060	0.1130
13	0.3610	0.2040
14	0.2120	0.2720
15	0.1700	0.2270
16	0.0850	0.1360
17	0.0630	0.0220
18	0.0000	0.0000
S	0.9970	0.9960

References

- (1) **Pérez-Lezaun, A., Calafell, F., Mateu, E., Comas, D., Bosch, E., Bertranpetit, J.** (1997) Allele frequencies for 20 microsatellites in a worldwide population survey. *Hum. Hered.* 47: 189-196
- (2) **Iriondo, M., Barbero, M. C., Izagirre, N., Manzano, C.** (1997) Data on six short-tandem repeat polymorphisms in an autochthonous Basque population. *Hum. Hered.* 47: 131-137
- (3) **Füredi, S., Budowle, B., Woller, J., Pádár, Z.** (1996) Hungarian population data on six STR loci - HUMVWFA31, HUMTH01, HUMCSF1PO, HUMFES/FPS, HUMTPOX, and HUMHPRTB - derived using multiplex PCR amplification and manual typing. *Int. J. Legal Med.* 109: 100-101
- (4) **Pai, A. P., Jackson, T., Pritchard, D. J., Papiha, S. S.** (1994) Population genetic studies of short tandem repeat loci (STRs): efficiency in paternity testing. *Adv. Forens. Haemogenet.* 5: 184-186
- (5) **Promega Corp.** (1996) Gene Print™ STR systems, Technical Manual
- (6) **Edwards, A., Hammond, H. A., Jin, L., Caskey, T., Chakraborty, R.** (1992) Genetic variation at five trimeric and tetrameric tandem repeat loci in four human population groups. *Genomics* 12: 241-253
- (7) **Bender, K., Beller, G., Lautsch, S.** (1998) Tetranucleotide short tandem repeat polymorphisms and their possible mode of origin. *Cytogenet. Cell Genet.* 80: 34-36
- (8) **Sala, A., Penacino, G., Corach, D.** (1998) Comparison of allele frequencies of eight STR loci from Argentinian Amerindian and European populations. *Hum. Biol.* 70: 937-947
- (9) **Mertens, G., Mommers, N., Heylen, H., Gielis, M., Muylle, L., Vandenberghe, A.** (1997) Allele frequencies of nine STR systems in the Flemish population and application in parentage testing. *Int. J. Legal Med.* 110: 177-180
- (10) **Koziol, P., Czerski, T., Madro, R.** (1999) Population genetic data for HumF13B, HumLPL and HumHPRTB in southeast Poland. *Int. J. Legal Med.* 113: 55-57
- (11) **Rangel-Villalobos, H., Rivas, F., Torres-Rodríguez, M., Jaloma-Cruz, A.R., Gallegos-Arreola, M.P., López-Satow, J., Cantú, J.M., Figuera, L.E.** (1999) Allele frequency distributions of six Amp-FLPS (D1S80, APO-B, VWA, TH01, CSF1PO and HPRTB) in a Mexican population. *Forensic Sci. Int.* 105: 125-129
- (12) **Xiao, F.-X., Gilissen, A., Gu, X.-X., Cassiman, J.-J., Decorte, R.** (1998) Genetic data obtained for two Chinese Han populations with a quadruplex fluorescent STR typing system (HUMVWA, HUMTH01, D21S11 and HPRT). *Int. J. Legal Med.* 111: 343-345
- (13) **Barros de Castro, I.A., Rinzler, C.M.C., Rumjanek, F.D.** (2000) Allele frequency distributions for twelve STR loci in a Brazilian population. *J. Forensic Sci.* 45: 941
- (14) **Mauricio da Silva, L., Silva, R.S., Dellalibera, E., Donadi, E.A.** (2000) Population genetics of HPRTB, F13B, and LPL in Pernambuco, Northeast Brazil. *J. Forensic Sci.* 45: 684-686

Recalculated data and misprints of the book (correct data in red)

(1) Pérez-Lezaun, A., Calafell, F., Mateu, E., Comas, D., **Bosch, E., Bertranpetit, J. (1997) Allele frequencies for 20 microsatellites in a worldwide population survey. Hum. Hered. 47: 189-196**