

Haptoglobin (Hp) subtypes in the German Rhine-Ruhr area

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INTRODUCTION

The two allelic polymorphism of the haptoglobin (Hp) system was detected by means of starch gel electrophoresis (SGE) more than 30 years ago (Smithies 1955). With an exclusion chance of 18% the Hp system has become a regular part of paternity testing since many years. Although Hp subtypes were discovered already in 1962 by Smithies et al., technical problems in producing unequivocal Hp pherograms of all five subtypes Hp*1F, 1S, 2FF, 2FS and 2SS hindered its common use in paternity testing. Only after application of isoelectric focusing (IEF) technique and after description of practicable techniques for purification of the Hp molecule (Oleisen et al. 1981, Santoro et al. 1982, Shibata et al. 1982, Patzelt and Schröder 1985) and after application of immunoblotting to Hp subtyping as well (Teige et al. 1983, 1986) all conditions for large scale routine Hp subtyping are given.

We present here Hp subtype frequencies determined in a large population from Western Germany (Rhine-Ruhr area) according to the method published by Patzelt and Schröder (1985), who worked out the technique of IEF of haptoglobin cleavage products. This method was developed by Shibata et al. (1982) and meanwhile investigated also by Zischler et al. (1987) in a Southwestern German population.

GENES AND PROTEINS

A short comment should be given to the rare and interesting phenomena of duplication of genes as well as confirmation and polymerization of gene products existing in the Hp system. The Hp molecules are composed of two kinds of polypeptide chains, α and β chains. The individual differences (genetic polymorphism) are based on variations in the α chain, with the β chain being everywhere the same. Three alleles at the Hp locus on chromosome 16 are responsible for three main kinds of α chains in all mammals. Two of the alleles, Hp*1F and Hp*1S, control α chains that differ from each other only by a single specific replacement of one amino acid (α 1 chains). The third allele, Hp*2, differs from both Hp*1 alleles in a much more striking way. It is nearly twice as long as the Hp*1 gene and its gene product (α 2 chain) shows to be a combination of two nearly complete α 1 chains arranged in tandem sequence. The formation of the Hp*2 allele obviously was the result of a genetic "accident" (Smithies et al. 1962, Nance and Smithies 1962), in which an ancestral Hp gene of normal length underwent an unequal crossing over with its allele in the homologous chromosome but at a non homologous site. Since two Hp*1 alleles exist, Hp*1S and Hp*1F, three different Hp*2 alleles

resulted from the unequal crossing over, Hp*2FF, *2FS and *2SS. Accordingly altogether five Hp alleles can be identified by IEF techniques.

The confirmation and polymerization of Hp gene products (α_1, α_2 and β chains) is another point which has to be explained for a better understanding of the Hp system. After transcription and processing the Hp m-RNA initiates the translation of one large polypeptide chain, which contains the α and β parts of the Hp molecule. These chains are cleaved by limited proteolysis to form an α - β dimer. An individual, being homozygous for the Hp*1 gene, forms tetrameric molecules with two β chains and two α_1 chains. According to the alleles Hp*1F and *1S, both α_1 chains carry the same or both allotypes. An individual being homozygous for the duplicated H*2 gene produces dimers with the larger α_2 chains. Each of these chains carry Hp subtypes according to the composition of the Hp*1 genes (1F, 1S), which had produced the Hp*2 gene by unequal crossing over, Hp*2FF, *2FS or *2SS. An individual being heterozygous for the Hp*1 and Hp*2 genes forms tetramers out of different dimers with short α_1 and long α_2 chains. According to free cysteine residues of the α_2 chains Hp2 homozygote and Hp 2-1 heterozygote molecules tend to polymerize according to following formulas. Hp 2-2: $(\alpha_2\beta) \cdot n, n=3, 4, 5, \dots$; Hp 2-1: $(\alpha_1\beta) \cdot 2 \times (\alpha_2\beta) \cdot n, n=0, 1, 2, \dots$. Multiple Hp bands seen in SGE are indicators of different degrees of polymerization (Yang and Prybylska 1983, Pastewka et al. 1985).

MATERIAL AND METHODS*

Sera

Non hemolytic sera from 1035 normal, unrelated Caucasian blood donors of the German Rhine-Ruhr area.

Hp purification

100 (200 μ l) of non hemolytic serum was added to 2ml (4ml) DEAE suspension which was prepared by mixing one part of a 1% aqueous DEAE stock solution with two parts of a 10mM sodium acetic buffer (pH 4.7). After centrifugation at 5000g for 5min. the clear supernatant was sucked off. To elute the hemoglobin molecules the pellet was washed with 2ml of the sodium acetic buffer and resuspended with 100 μ l (200 μ l) of a 0.125M ammonium acetic solution. After additional centrifugation for 10min. 40 μ l of the clear haptoglobin containing supernatant was transferred to a second tube for reductive cleavage.

Reductive cleavage

40 μ l Hp containing supernatant was mixed with 40 μ l of a reductive reagent, which was prepared by dissolution of 1g urea in 1.2ml borate buffer of pH 8.8 (0.1M boric acid, 0.04M NaOH) plus 20 μ l of β -mercaptoethanol. The mixture was incubated for 30min. and 8 μ l of an iodacetamide solution (92mg iodacetamide in 1ml of aqua dest.) was added to prevent refolding of the separated α and β chains of the Hp molecule.

Isoelectric focusing and staining

IEF of the cleavage products was performed in polyacrylamide gels (T=5.5%, C=3%; 260x125x0,5mm) on gel bond films using the LKB

*A very detailed description of the method is available at request.

equipment (Ultraphor, Macrodrive 5, Multitemp II). Before polymerization an ampholine mixture (Ampholine LKB, two parts pH 3.5-10, two parts pH 5-7, one part pH 6-8) is added in 5% proportion of the total gel (0.8ml carrier ampholytes for a 16ml gel). Gels can be stored at 4-6°C up to a fortnight. Electrode paper strips for prefocusing and focusing were soaked with 0.5M NaOH for the cathode and with 0.5M H₃PO₄ for the anode. After prefocusing of the gel for 30min. at 5-10°C samples were applied on to the gel by applicator pieces (Whatman No1, 5x10mm). IEF was performed for 150min. Applicator pieces were removed after 30min. Maximum electric values for prefocusing and focusing were 1600V, 10mA and 10W. Fixation, staining and decolorization of the gels were performed according to Steck et al. (1980).

RESULTS

Hp subtype patterns obtained by IEF of purified and cleaved Hp proteins are presented in Fig.1. According to an isoelectric point of pI=6.52 the major band of Hp 2FF appears in our technique in the very cathodal region of the gel near the sample application area.

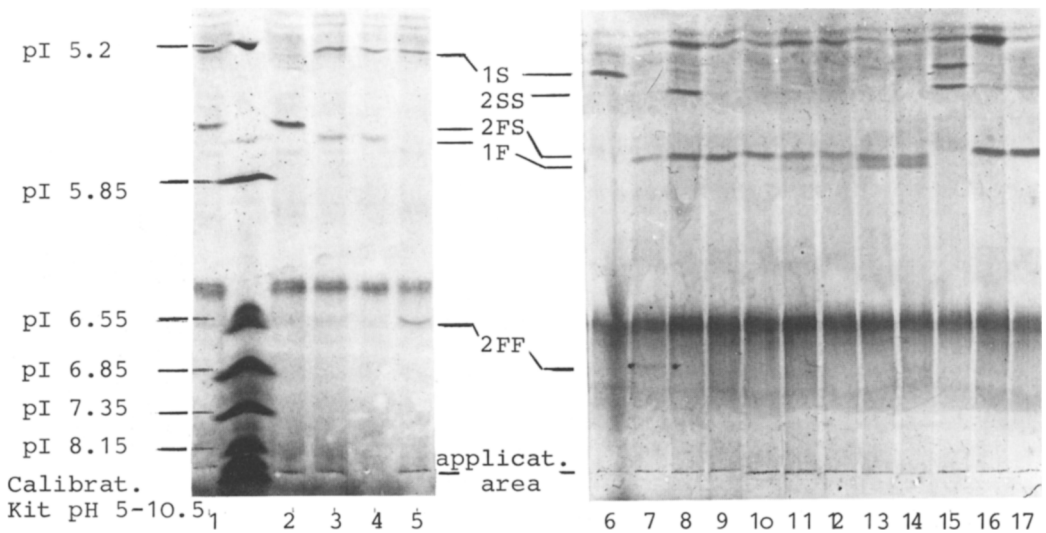


Fig. 1. Hp subtypes from left to right: 1) 1S-2FS 2) 2FS 3) 1S-1F 4) 1S-1F 5) 1S-2FF 6) 1S 7)2FS-2FF 8)2SS-2FS 9) 2FS 10) 2FS 11) 2FS 12) 2FS 13) 2FS-1F 14) 2FS-1F 15) 1S-2SS 16) 2FS 17) 2FS

Observed and expected phenotype frequencies and the corresponding gene frequencies of Hp subtypes are presented in Table 1. There is no deviation of the observed from the expected values.

Comparison with allele frequencies obtained by other investigators including different techniques also yielded very good agreement (Table 2).

Table 1. Hp phenotype distribution among 1035 unrelated individuals and corresponding gene frequencies

Phenotype	Observed		Expected	χ^2	allele frequencies
	n	%	n		
1F -1F	19	1.84%	20.03	0.05	
1F -1S	74	7.15%	74.16	0.00	
1S -1S	69	6.67%	68.62	0.00	Hp*1F = 0.1391
1F -2FF	0	0.00%	0.42	0.42	*1S = 0.2575
1F -2FS	172	16.62%	167.93	0.10	*2FS = 0.5831
1F -2SS	4	0.39%	5.43	0.37	*2SS = 0.0188
1S -2FF	0	0.00%	0.77	0.77	*2FF = 0.0014
1S -2FS	309	29.86%	310.79	0.01	
1S -2SS	12	1.16%	10.04	0.38	
2FF-2FF	0	0.00%	0.00	0.00	
2FF-2FS	3	0.29%	1.75	0.89	
2FF-2SS	0	0.00%	0.06	0.06	
2FS-2FS	350	33.82%	351.90	0.01	
2FS-2SS	23	2.22%	22.74	0.00	
2SS-2SS	0	0.00%	0.37	0.37	
Sum of Chi-square for (df 10)=3.44 (0.975>p>0.95)					
(df 5)=0.97 (0.975>p>0.95)					

Table 2. Hp allele frequencies of different studies

Study	n	Hp alleles				
		*1F	*1S	*2FS	*2SS	*2FFS
Bertrams et al.1987	1035	0.1387	0.2538	0.5864	0.0196	0.0015
Thymann et al.1977	208	0.16	0.27	0.54	0.03	0.00
Oleisen et al.1981	52	0.13	0.21	0.63	0.03	0.00
Shibata et al.1982	202	0.1421	0.2462	0.5533	0.0457	0.0127
Patzelt and Schröder 1986	1275	0.1471	0.2502	0.5753	0.0251	0.0020
Teige et al. 1986	606	0.162	0.209	0.588	0.038	0.003
Zischler et al.1987	182	0.144	0.254	0.574	0.024	0.0004

DISCUSSION

The excellent agreement of Hp allele frequencies obtained by different groups especially among the same population demonstrates the usefulness of Hp subtyping for paternity testing. No single deviation for expected Hp subtypes according to results obtained by SGE was observed among more than 200 matings. The exclusion chance of the Hp system increases from 18% by SGE to 33% by IEF. This is the highest exclusion chance of all IEF systems as shown in Table 3.

Table 3. Exclusion chance of IEF systems (Mendner and Kühnl 1986)

System	Exclusion chance	System	Exclusion chance
Hp	33%	C8	19.27%
PGM1	31.91%	C6	18.77%
GC	29.74%	A2HS	17.81%
PI	29.29%	FUCA	15.10%
GDH	26.90%	ESD	9.77%
PLG	22.58%	AMY2	4.52%
F13B	22.29%	C2	2.83%
TF	19.43%		

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