HAPTOGLOBIN SUBTYPES IN TUSCANY (ITALY)

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INTRODUCTION

The genetic polymorphism of haptoglobin (HP) has been first observed, through starch gel electrophoresis, by Smithies *et al* (1955), who demonstrated three common phenotypes: HP1, HP2-1 and HP2. The HP-α chain, which carries the polymorphism, has subsequently been shown to exist in several additional allelic forms ("subtypes") - 1S, 1F, 2FS, 2FF and 2SS - giving rise to three different HP1, six different HP2-1 and six different HP2 phenotypes. Only in the last few years, however, methods suitable for routine HP subtyping have been developed.
For this reason, while allelic frequencies of the "main" HP types in the various human populations are well known, the geographic distribution of the HP subtypes has still not been examined to the same extent (for a recent review see Teige *et al* 1992).
The aim of this study is to present the distribution of HP subtypes in Tuscany (Italy). Up to now, the only available data about the italian population were reported by Santoro *et al* (1983), who determined exclusively the 1F/1S subtypes.

MATERIALS AND METHODS

Sera were collected from a random sample of 200 healthy blood donors born in Pisa.
HP subtypes were determined by the method described by Scherz *et al* (1990), which includes four steps: isolation of HP by immunoprecipitation - reduction and alkilation in the presence of urea - PAGIF - protein staining.
For a cross-validation of the results, the HP "main" phenotypes were also determined, using conventional PAA electrophoresis. Control sera samples were kindly provided by Dr Krüger, from the Legal Medicine Institute of Hannover (BDR).

RESULTS AND DISCUSSION

The HP subtypes distribution and the estimated allele frequencies in our population sample are reported in table 1. The observed numbers are in good agreement with the expected distribution under the Hardy-Weinberg equilibrium (χ^2 = 4.76, df = 10, P> .90). In this sample, nine of the fifteen phenotype combinations have been found. The HP subtypes pattern, obtained by immunofixation/PAGIF technique, is shown in fig.1 (the 1F-2FF and 1F-2SS types, in the last two lanes, are control sera).
Allelic frequencies in Tuscany are consistent with those reported in other European populations (see table 2). In particular, the frequency of HP*1F allele, which is the most discriminating parameter between different ethnical groups (Teige *et al*, 1992), is included in the Caucasian population range.
The heterogeneity test between our gene frequencies and those reported by Santoro *et al* for Continental Italy was not significant (G^2 = 0.595, df = 2, P = 0.70-0.90); the same test, applied to Sardinian data was at the boundary (G^2 = 6.947, df = 2, P = 0.05-0.02).
The theoretical exclusion rate in cases of disputed paternity (32.8 %) is comparable with that of more informative classical systems (MNSs, GC and PGM1). This is a good reason to include HP system within the conventional markers to be used in combination with DNA polymorphisms for paternity testing.

Subtypes	Observed	Expected	χ^2	Allelic Frequencies
1F	5	4.35	0.097	HP*1F = 0.1475
1F-1S	13	13.57	0.024	
1S	10	10.58	0.032	HP*1S = 0.2300
1F-2FF	0	0.30	0.295	
1F-2FS	36	34.81	0.041	HP*2FF = 0.0050
1F-2SS	0	1.62	1.623	
1S-2FF	0	0.46	0.460	HP*2FS = 0.5900
1S-2FS	57	54.28	0.136	
1S-2SS	2	2.53	0.111	HP*2SS = 0.0275
2FF	0	0.01	0.005	
2FF-2FS	2	1.18	0.570	
2FF-2SS	0	0.06	0.055	
2FS	66	69.62	0.188	
2FS-2SS	9	6.49	0.971	
2SS	0	0.15	0.151	
Total	200	200.00	4.758	

Table 1: subtypes distribution and allele frequencies in the population sample from Tuscany

Country	N	*1F	*1S	*2FF	*2FS	*2SS	References
Norway	6668	.158	.220	.004	.578	.040	Teige '92
Sweden	564	.156	.231	.001	.571	.041	Hjalmarson '88
Denmark	2184	.151	.241	.002	.565	.040	Thymann '90
Germany							
Berlin	1275	.147	.250	.002	.575	.025	Patzelt '85
L.Saxony	1500	.153	.252	.003	.562	.029	Rothämel '89
L.Saxony	431	.153	.240	.002	.568	.036	Basler '92
Rhine-Ruhr	1035	.139	.257	.001	.583	.019	Bertrams '87
Southwest	182	.144	.254	.000	.574	.024	Zischler '87
Stuttgart	1485	.158	.217	.004	.600	.020	Härle '92
Hungary	615	.119	.221	.004	.665	.001	Hever '78
Switzerland							
Berne	1266	.126	.239	.010	.583	.042	Scherz '90
Lausanne	500	.147	.249	.003	.567	.034	Dimo-Simonin '90
France	202	.139	.245	.012	.547	.045	Shibata '82
Spain							
Madrid	250	.168	.232	.020	.552	.028	Alonso '90
Barcelona	317	.142	.238	.006	.621	.002	Moral '83
Italy							
Continental	441	.133	.241	---	.626	---	Santoro '83
Sardinia	165	.215	.245	---	.540	---	Santoro '83
Tuscany	200	.148	.230	.005	.590	.027	this paper
Greece	212	.042	.311	.005	.463	.179	Stromatias '87

Table 2: HP allele frequencies in Europe

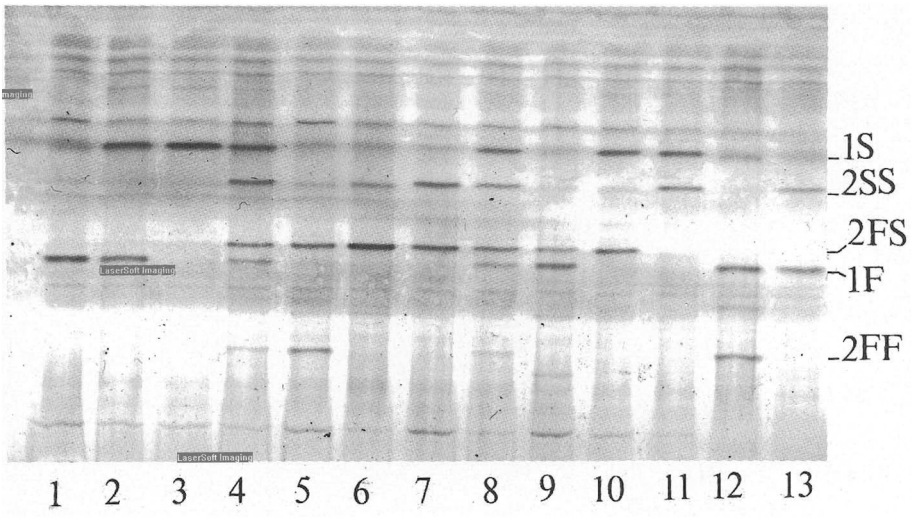

Figure 1: HP subtypes. (1) 1F, (2) 1F-1S, (3) 1S, (4) mix, (5) 2FF-2FS, (6) 2FS, (7) 2FS-2SS, (8) mix, (9) 1F-2FS, (10) 1S-2FS, (11) 1S-2SS, (12) 1F-2FF, (13) 1F-2SS

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