

HP, TF and GC Phenotype and Allele Frequencies in Four South Indian Population Groups

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ABSTRACT HP, TF and GC serum protein polymorphisms were typed on the Kamma caste group as well as on three Muslim groups (Dawoodi Bohara, Sunni, Shia) from the Visakhapatnam area in Andhra Pradesh (South India). The distribution of HP allele frequencies shows a remarkable intergroup variability, whereas TF and GC allele frequencies do not differ obviously among these four population groups. The results are compared with those obtained on other population groups from Andhra Pradesh.

INTRODUCTION

During the last three decades many investigations on the distribution of genetic serum protein markers have been carried out on the various population groups of Andhra Pradesh, which in their majority were compiled by Bhasin, Walter and Danker-Hopfe (1992). Some new data on the variability of these markers among the populations of this part of South India could be published by Walter et al. (1992, 1993). In this paper the results of HP, TF and GC typings on some so far not yet investigated population groups of Andhra Pradesh – Kamma caste, Dawoodi Bohara Muslims, Sunni Muslims, Shia Muslims – are presented here and compared with those obtained on other Andhra Pradesh populations.

MATERIALS AND METHODS

Serum samples of the Kamma caste group (n = 95), Dawoodi Bohara Muslims (n = 99), Sunni Muslims (n = 94) and Shia Muslims (n = 89) were collected by one of us (P.V.). The investigated individuals – adult males and females – are not related. All those four population groups are located in the area of Visakhapatnam, Andhra Pradesh, South India.

The serum samples were air-mailed to Bremen, where the typings and statistical analyses were done in the Department of Human Biology, University of Bremen (Germany). With slight modifications the typing techniques as described by Spielmann and Kühnl (1982) and Prokop and Göhler (1986) were employed.

RESULTS

Tables 1-3 show the distribution of HP, TF and GC phenotype and allele frequencies in the four population groups under study. Genetic equilibrium can be assumed for all the three polymorphic serum protein systems in these four groups, with the exception, however, of the HP system in the Kamma caste group. As in them the observed numbers of the both homozygous phenotypes are somewhat higher than the observed ones one cannot exclude that this might be due to the generally high frequent consanguineous marriage pattern of the Kamma caste.

In the TF system no rare subtype variants could be observed. Dawoodi Bohara Muslims and Shia Muslims show some GC subtype variants (each one case of GC 1S-V), which, however, could not yet be identified.

Table 1: HP phenotype and allele frequencies

Phenotypes	Kamma		Dawoodi Bohara		Sunni Muslims		Shia Muslims	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
HP 1	5	1.39	7	5.15	1	2.48	1	0.43
2-1	13	20.22	30	33.70	29	26.05	10	11.14
2	77	73.38	57	55.15	67	68.47	73	72.43
Total	95	94.99	94	94.00	97	97.00	84	84.00
χ^2		12.132		1.133		1.249		0.877
df		1		1		1		1
p		<0.001		ns		ns		ns
<i>Alleles</i>								
HP*1		0.1211		0.2340		0.1598		0.0714
HP*2		0.8789		0.7660		0.8402		0.9286
Total		1.0000		1.0000		1.0000		1.0000

Table 2: TF phenotype and allele frequencies

Phenotypes	Kamma		Dawoodi Bohara		Sunni Muslims		Shia Muslims	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
TF C1	48	47.54	38	35.65	31	28.01	36	39.57
2-1	28	30.03	16	21.31	17	23.92	28	22.40
2	6	4.74	6	3.19	9	5.10	1	3.17
3-1	7	6.44	5	4.40	2	1.36	6	4.47
3-2	2	2.03	1	1.32	—	0.58	—	1.27
3	—	0.22	—	0.14	—	0.02	—	0.12
1-D	2	1.44	—	—	1	0.68	—	—
2-D	—	0.45	—	—	—	0.29	—	—
3-D	—	0.10	—	—	—	0.02	—	—
D	—	0.01	—	—	—	<0.01	—	—
Total	93	93.00	66	66.01	60	59.98	71	71.00
χ^2		1.523		4.249		6.664		5.124
df		6		3		6		3
p		ns		ns		ns		ns
<i>Alleles</i>								
TF*C1		0.7150		0.7349		0.6833		0.7465
TF*C2		0.2258		0.2197		0.2917		0.2113
TF*C3		0.0484		0.0454		0.0166		0.0422
TF*D		0.0108		—		0.0084		—
Total		1.0000		1.0000		1.0000		1.0000

Table 3: GC phenotype and allele frequencies

Phenotypes	Kamma		Dawoodi Bohara		Sunni Muslims		Shia Muslims	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
GC 1F	2	2.36	4	3.09	6	4.04	4	3.06
1F-1S	19	16.94	20	21.04	18	21.41	15	17.61
1S	29	30.38	35	35.76	29	28.38	24	25.35
2-1F	6	7.33	7	7.60	10	10.50	10	9.09
2-1S	27	26.29	28	25.85	30	27.84	31	26.15
2	6	5.69	4	4.67	6	6.83	4	6.75
1F-V	—	—	—	0.18	—	—	—	0.19
1S-V	—	—	1	0.59	—	—	1	0.53
2-V	—	—	—	0.22	—	—	—	0.27
V	—	—	—	<0.01	—	—	—	<0.01
Total	89	88.99	99	99.00	99	99.00	89	89.00
χ^2		0.646		1.335		1.800		2.617
df		3		6		3		6
P		ns		ns		ns		ns
Alleles								
GC*1F		0.1629		0.1768		0.2020		0.1854
GC*1S		0.5843		0.6010		0.5354		0.5337
GC*2		0.2528		0.2172		0.2626		0.2753
GC*V		—		0.0050		—		0.0056
Total		1.0000		1.0000		1.0000		1.0000

DISCUSSION

It appears from tables 1-3 that the HP, TF and GC allele frequencies show some inter-group variability, which, however, is statistically significant only concerning the HP system. Using the test of locus specific heterogeneity according to Rao (1952) the following χ^2 -values were obtained:

HP system	$\chi^2 = 20.079$;	df = 3; p < 0.001
TF system	$\chi^2 = 7.463$;	df = 9; 0.70 > p > 0.50
GC system	$\chi^2 = 5.021$;	df = 9; 0.90 > p > 0.80

This heterogeneity concerning the HP allele distribution is mainly caused by the Dawoodi Bohara Muslims and the Shia Muslims, which are striking by extremely differing allele frequencies (Table 1). It is admissible to attribute this to genetic differentiation factors such as genetic drift operating on the gene pool of Dawoodi Bohara Muslims and Shia

Muslims. It would be of considerable interest to analyze these two population groups also for blood group and red cell enzyme polymorphisms in order to understand their genetic structure in more detail.

Comparing the HP, TF and GC allele frequencies of the four Andhra Pradesh population groups under study with those reported previously (Bhasin, Walter and Danker-Hopfe, 1992; Walter et al., in preparation) one can point out the following:

1. HP allele frequencies do not differ from those known for other population groups of Andhra Pradesh. They are further more in good accordance with the observation that in general *HP*1* allele frequencies are obviously lower among South Indian populations as compared with those from other regions of India. *HP*2* allele frequencies are generally much higher. The possible reasons for these distribution gradients have been discussed in detail by Walter, Danker-Hopfe and Bhasin (1991).

2. TF subtype allele frequencies are generally rather similar to those found in Andhra Pradesh caste and community populations, but differ obviously from those obtained on scheduled castes and tribals, in which on the whole especially *TF*CI* and *TF*C3* allele frequencies are comparatively much lower than in castes and communities (Walter et al., in preparation). Concerning the *TF*D* allele frequencies it is interesting to state that the four population groups under study are very similar to other Andhra Pradesh caste and community populations, in which generally this allele is much more infrequent as compared with scheduled castes and tribals (Walter et al., in preparation). Considering the whole Indian sub-continent one can state that the *TF*D* allele frequencies in the four Andhra Pradesh population groups confirm the observation according to which these allele frequencies are generally much higher in South (and East) India as compared to the other regions of this country, which has been discussed in detail by Walter, Danker-Hopfe and Bhasin (1991).

3. Concerning the distribution of GC subtype allele frequencies one can state again that the four populations under study are obviously much more similar to other caste and community populations of Andhra Pradesh as compared to scheduled castes and communities, which are in particular characteristic by higher *GC*IF* and lower *GC*2* allele frequencies than caste and community populations (Walter et al., in preparation). Considering the whole Indian sub-continent one can point out that Andhra Pradesh and the other South Indian regions display a quite different GC allele distribution pattern than the Northern, Western and in particular Eastern parts of India. The possible reasons for these regional and ethnic differences in the variability of GC subtype allele frequencies have been discussed by Walter, Danker-Hopfe and Bhasin (1991) and especially by Walter and Danker-Hopfe (1992) to whom we can refer for details.

Summing up it can be pointed out that the HP, TF and GC allele distributions of the here studied Kamma caste group as well as those of the Dawoodi Bohara Muslims, Sunni Muslims and Shia Muslims are in good accordance with the results of observations on other population groups from Andhra Pradesh. A detailed statistical analysis of all hitherto HP, TF, GC (and also PI) published population data from Andhra Pradesh, which will afford a detailed view of the intra- and interpopulation genetic differentiation processes within this part of India, is in progress and will be published elsewhere (Walter et al., in preparation).

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