

Genetic Serum Protein Markers in Four Tribal Populations from Kerala, India

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ABSTRACT Four tribal populations from Kerala could be typed for serum protein polymorphisms: Paniyans, Kattunaickens, Cholanaickens (HP, GC and PI subtypes), and Kannikars (HP only). Though the population samples are rather small clear genetic differences among them could be observed, which without doubt have been caused by locally acting genetic differentiation processes and could be maintained due to the genetic isolation of these four population groups.

INTRODUCTION

Though in the last decades many population studies concerning the variability of polymorphic serum protein systems have been carried out in India, which were recently summarized and critically evaluated by Bhasin, Walter and Danker-Hopfe (1992) as well as by Walter, Danker-Hopfe and Bhasin (1991), until now only very few data are available for Kerala. Whereas the HP system has been typed already in some tribal and non-tribal groups from Kerala (Papiha, 1979; Saha et al., 1974, 1976) hitherto no data have been reported concerning the polymorphic serum protein systems GC and PI, neither in regard of the so-called conventional phenotypes, nor the subtypes. TF phenotypes and allele frequencies on various Kerala populations have been reported by Papiha and Wastell (1974), Saha et al. (1974, 1976) and Mukherjee et al. (1986), who also considered the TF subtypes.

In order to contribute to our knowledge on the variability of genetic markers in Kerala we present here the results of HP typing in four tribal populations (Paniyans, Kattunaickens, Cholanaickens, Kannikars) and those of GC and PI subtyping in three of them: Paniyans,

Kattunaickens, Cholanaickens. It is worth mentioning that these GC and PI subtype data are the first so far reported for this part of India.

MATERIALS AND METHODS

The serum samples of the four tribal populations under study were collected by two of us (S.T.D. and R.G.) during two field trips (1987 and 1989). They were air-mailed deep-frozen to Bremen, where the typings and statistical analyses were done in the Department of Human Biology of the University of Bremen, following the methods as described by Spielmann and Kühnl (1982) and Prokop and Göhler (1986). The analysis of the heterogeneity in the distribution of allele frequencies was carried out according to Rao (1952).

The *Kattunaickens* are forest dwellers and live in the Mallapuram district of Kerala. The *Cholanaickens* are cave dwellers and live in the same area. They are inaccessible and have been discovered in 1973. The *Paniyans*, living also in the Mallapuram district, are food gatherers. They are, however, spread out in a larger area, covering the Kozhikode and Cannanore districts of Kerala. The *Kannikars*, popularly known as Kannis, are the inhabitants

Table 1: HP phenotype and allele frequencies in four tribal populations from Kerala

Phenotypes	Kattunaickens		Cholanaickens		Paniyans		Kannikars	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
HP 1	2	3.31	—	0.23	—	0.08	—	0.15
2-1	19	16.39	3	2.55	2	1.85	8	7.70
2	19	20.31	7	7.23	11	11.08	97	97.15
Total	40	40.01	10	10.01	13	13.01	105	105.00
$\chi^2_{(1)}$		1.019		0.312		0.090		0.164
p		ns		ns		ns		ns
<i>Alleles</i>								
HP*1		0.2875		0.1500		0.0769		0.0381
HP*2		0.7125		0.8500		0.9231		0.9619
Total		1.0000		1.0000		1.0000		1.0000

of Trivandruan city and Quilan district of Kerala. They are believed to be the original inhabitants of the Tirunelveli district (southern Tamil Nadu), from where they migrated to the eastern slopes of the Western Ghats in Kerala. Fig. 1 shows the geographical location of these four tribal populations.

RESULTS AND DISCUSSION

Table 1 reveals the distribution of HP phenotype and allele frequencies in the four tribal groups under study. Genetic equilibrium can be assumed for all of them. The variation of HP allele frequencies among these groups is



Fig. 1 Location of Kerala (dotted). BH = Bhutan, B.D. = Bangla Desh
1 = Mallapuram district, 2 = Quilon district

Table 2: GC phenotype and allele frequencies in three tribal populations from Kerala

Phenotypes	Kattunaickens		Cholanaickens		Paniyans	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
GC 1F	1	0.63	—	—	1	0.48
1F-1S	6	6.50	—	—	2	2.69
1S	18	16.90	7	7.23	4	3.77
2-1F	2	2.00	—	—	1	1.35
2-1S	9	10.40	3	2.55	4	3.77
2	2	1.60	—	0.23	1	0.94
1F-Var	—	0.25	—	—	—	—
1S-Var	1	1.30	—	—	—	—
2-Var	1	0.40	—	—	—	—
Var	—	0.03	—	—	—	—
Total	40	40.01	10	10.01	13	13.00
χ^2		1.860		0.312		0.863
df		6		1		3
p		ns		ns		ns
<i>Alleles</i>						
GC*1F		0.1250		—		0.1923
GC*1S		0.6500		0.8500		0.5385
GC*2		0.2000		0.1500		0.2692
GC*Var		0.0250		—		—
Total		1.0000		1.0000		1.0000

considerable and statistically highly significant, as the locus specific heterogeneity comes to $\chi^2 = 38.313$, $df = 2$, $p < 0.001$. We still revert to this later on.

The distribution of GC phenotype and allele frequencies is demonstrated in table 2. Genetic equilibrium can be assumed for all the three tribal groups, which could be typed for this polymorphic system.

Though the allele frequencies suggest some heterogeneity among these three groups one has to point out that there is no indication for statistical significance as χ^2 for the locus specific heterogeneity comes to 7.231, $df = 6$, $p = 0.30$. That means that this intergroup variation of GC allele frequencies seem to be due to chance.

Whereas in the Cholanaickens as well as in the Paniyans no GC variants could be observed such are seen in the Kattunaickens, are most likely of GC 1S-1C1 and GC 2-2A1 type.

Table 3 displays the distribution of PI phenotype and allele frequencies in the three tribal groups under study. Genetic equilibrium can

be assumed for all of them. It is worth mentioning that among the Paniyan sample a rare PI variant could be observed, namely PI M1-Z.

As it becomes apparent from table 3 the PI allele frequencies show a considerable intergroup variability. The locus specific heterogeneity comes to $\chi^2 = 14.762$, $df = 6$, $0.05 > p > 0.02$, which, however, is mainly caused by the PI*M1 and PI*M3 frequencies. These allele specific heterogeneities were found to be statistically significant, as $\chi^2 = 10.663$, $df = 2$, $0.01 > p > 0.001$ (PI*M1), and $\chi^2 = 8.570$, $df = 2$, $0.02 > p > 0.01$ (PI*M3), respectively. The others are statistically insignificant.

Though the sample sizes of the tribal groups from Kerala, which could be considered here, are in some cases rather small one can point out that our results indicate considerable genetic differences among the tribal populations of Kerala, which are in line with the observations of other authors (Mukherjee et al., 1986; Papiha, 1979; Papiha and Wastell, 1974; Saha et al., 1974, 1976). One can suppose

Table 3. PI phenotype and allele frequencies in three tribal populations from Kerala

Phenotypes	Kattunaickens		Cholanaickens		Paniyans	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
PI M1	20	19.86	5	5.04	2	2.50
M2-1	6	5.79	1	0.92	2	2.00
M2	—	0.42	—	0.04	—	0.40
M3-1	2	2.48	—	—	3	2.50
M3-2	1	0.36	—	—	2	1.00
M3	—	0.08	—	—	—	0.63
M1-Z	—	—	—	—	1	0.50
M2-Z	—	—	—	—	—	0.20
M3-Z	—	—	—	—	—	0.25
Z	—	—	—	—	—	0.03
Total	29	28.99	6	6.00	10	10.01
χ^2		1.739		0.049		3.200
df		3		1		6
p		ns		ns		ns
<i>Alleles</i>						
PI*M1		0.8276		0.9167		0.5000
PI*M2		0.1207		0.0833		0.2000
PI*M3		0.0517		—		0.2500
PI*Z		—		—		0.0500
Total		1.0000		1.0000		1.0000

that these genetic differences came into existence by locally acting genetic differentiation factors, among which genetic drift can be regarded as one of the most important ones. These differences could be maintained because of the geographical and social isolation of the tribal groups under study from each other by which gene flow did not take place.

The HP allele frequencies observed in this study are in good accordance with those reported in previous studies (Papiha, 1979; Saha et al., 1974, 1976), in which also high *HP*2* and low *HP*1* allele frequencies could be demonstrated. Rather high *HP*2* allele frequencies are characteristic for almost all Indian populations (see Bhasin, Walter and Danker-Hopfe, 1992) and might be at least in part the results of selectively acting factors, which has been discussed in detail by Walter, Danker-Hopfe and Bhasin (1991).

Concerning the polymorphic serum protein systems GC and PI so far comparisons with

other populations from Kerala are not yet possible. However, considering the GC allele distribution pattern for other Indian populations, which has been critically reviewed by Walter and Danker-Hopfe (1992) one can point out that the Kerala data presented here are within the Indian range of variability of *GC*1F*, *GC*1S*, and *GC*2* allele frequencies, and also the frequency of rare GC alleles in Kerala does not differ from that reported on other Indian populations.

Regarding the PI system one can observe that the Kattunaickens and Cholanaickens from Kerala are striking by higher *PI*M1* and lower *PI*M2* allele frequencies that it was found in other Indian populations (Walter and Danker-Hopfe, 1993), which, however, might be due to chance as these two Kerala samples are rather small. This is most likely also the reason for the low *PI*M3* frequency in the Kattunaicken sample and the absence of this allele, respectively, in the Cholanaickens. The fre-

quency of this allele varies in other Indian populations from 0.075 (Punjab) to 0.205 (Karnataka). The PI^*Z allele frequency observed in the Paniyans is in rather good line with that found in other Indian populations. PI^*Z and other rare PI alleles are very infrequent in all so far studied Indian populations.

Summing up one can point out that the HP, GC and PI allele distribution patterns observed in these Kerala populations show some peculiarities, which might be caused by locally acting genetic differentiation factors. However, much more research work has to be done in Kerala - as well as in the adjacent regions of Karnataka and Tamil Nadu - in order to understand the distribution pattern of these genetic serum protein markers in South India in full detail.

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