

A Genetic Study of Four Population Groups of Uttara Kannada District of Karnataka

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ABSTRACT Four population groups, namely, Halakkis, Siddis, Gonds and Havyak Brahmins of Uttara Kannada district of Karnataka state of South India, have been studied for six serological, and red cell enzyme markers to find out genetic affinities of these population groups. In the ADA system, only Siddis showed the fast variant allele ADA*V with a frequency of 1.4 percent. To the best of the authors' knowledge, this variant has not been reported from the populations of southern India. In another red cell enzyme system PGM2, we found Atkinson variant among Siddis with a frequency of 4.8 percent. It is African specific variant and thus, its presence in Siddis lends support to their African ancestry. The level of average heterozygosities was found to be high for all groups. The genetic distance analysis does not reveal any significant differentiation. The average gene diversity (H_e) is 33.13 % and the coefficient of gene differentiation 0.032, indicating that a small contribution to the total variability comes from the inter population variation. Intensive studies with high resolution DNA markers among these populations are likely to provide meaningful insight into the population structure and migration history, and are more suitable to understand the role of evolutionary forces in genetic divergence.

INTRODUCTION

The sub-division of the Indian population into a large number of tribes, castes and communities provide an excellent opportunity to study genetic variation among these groups. The tribes of the state of Karnataka in South India have drawn the attention of numerous anthropologists. A number of genetic studies have been undertaken in the state of Karnataka to find out the pattern of variation and population structure among the different population groups. Owing to considerable ethnic and cultural heterogeneity in the Indian population, it is imperative to study different ethnic groups to gather base line data on their genetic profile. It may be worth mentioning here that the populations groups under study, namely, Siddis, Gonds, Halakkis and Brahmins, are isolated small populations residing in the interior regions of the Uttara Kannada district of Karnataka. Further, to the best of the authors' knowledge, only a handful of studies (Vijaykumar et al. 1987) have been undertaken to assess the genetic structure of the populations

in the area under study. Keeping these views into consideration, the present study was aimed to study four population groups of Uttara Kannada district of Karnataka.

The state of Karnataka has around 50 tribal groups and the numerical strength of tribal population of Karnataka has increased from 1.92 million in 1991 to 3.46 million in 2001. Uttara Kannada is one of the districts in the southern Indian state of Karnataka. It is also called as North Canara, or North Kanara. It is bounded on the northwest by the state of Goa, on the north by Belgaum District, on the northeast by Dharwad District, on the east by Haveri District, on the southeast by Shimoga District, on the south by Udupi District, and on the west by the Arabian Sea. The languages spoken in the district are Kannada, Konkani, Marathi, Tulu and Urdu. The population is predominantly Hindu comprising of many communities.

The present study was undertaken among the Hallakis, Gonds, Siddis and Havyak Brahmins of Uttara Kannada district of Karnataka state in South India. These groups have unique historical past as most of them are migrants. This study aims to find out genetic heterogeneity and genetic affinities of these four population groups of Karnataka.

A brief description of each of these four groups is given below.

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Halakki

Halakki Vakkals, also spelt as Halwakki Vakkal, are a major cultivating community and are confined to the coastal taluks of Uttara Kannada district of Karnataka. They are agriculturists living on farm lands located at the outskirts of towns that are sandwiched between the mighty Western Ghats in the East and the expanse of the Arabian sea on the West, 75,000 Halakkis live in Koppas under direct control of their community heads. They were one of the earlier settlers in the Uttara Kannada district and are said to have come from Tirupati. The term Halavakki is said to be derived from the Kannada term *halu* which means milk and *akki* means rice. They have exogamous divisions called Bali, but remember only the names of *Baiyan Bali* and *Kadiyan Bali*. Endogamy at the community level is the rule of the marriage among them and "Halakki Kannada" refers to the dialect of the state language in which these people converse. They have a rich folklore.

Siddis

Siddis of the state of Karnataka are a scheduled tribe of African origin. The Siddis of Karnataka were mainly brought by Portuguese as slaves on coastal regions of western India and the vast majority of them are now settled in the Uttara Kannada district of Karnataka. Although they have three religious groups, namely Hindus, Christians and Muslims, but inter religion marital alliances are not infrequent. They have a clan system known as *Bedaga*, and in few of the villages, the reminiscent of the African clan system is still persisting (Gauniyal et al. 2008).

Gonds

They are the largest tribe in India numbering about 4 million according to 2001 census. They contribute to 13.75% of the total scheduled tribes in India and they are largely concentrated in Madhya Pradesh, Maharashtra, Chattisgarh, Orissa, Andhra Pradesh and Karnataka. The term Gond is derived from the word 'Khond' which means hill and these people are generally found in hilly and forest areas. The Gonds of Karnataka are said to have migrated from Andhra Pradesh about 200 years back (District Gazetteer of Uttara Kannada, 1981). They were brought in as guardsmen of queen Channabhaira devi known

as the pepper queen by the Britishers. Once they came here, they settled down at Bhatkal in Uttara Kannada. Now they number about 8000. They have a clan system known as *Bali*, and follow clan exogamy.

Havyak Brahmins

This Brahmin community is settled in Karnataka and Kerala, and is believed to have been brought to this part by the Kadamba king, Mayur Varma, for performing yagna or sacrificial rituals. In Karnataka, the Havyak Brahmins live in the Uttara Kannada and speak Kannada language. Hegde, Habbar and Bhat are the surnames used by them. The Havyak Brahmins have seven gotras associated with the seven sages (rishi), Vishwamitra, Vashishtha, Kashyap, Bhardwaj, Jamadagni, Atri and Bhargav. The Havyak Brahmins are primarily areca nut growers but there are also priests and businessmen.

The four population groups studied in the present investigation belong to the Uttara Kannada district of Karnataka. Except for the Siddis, all the other population groups belong to the Dravidian family of languages. Siddis are the tribe of the African origin.

MATERIALS AND METHODS

Blood specimens were collected from Halakkis (51), Siddis (218), Gonds (203) and the Brahmins (121). The number of blood samples on which the results were obtained varied in all the markers, due to unavoidable laboratory constraints. Informed consent was obtained from the subjects before the blood collection and unrelated individuals were chosen for the blood sample collection taking all the necessary precautions. 1 ml of blood was collected in an Eppendorf tube containing EDTA as an anti coagulant. The blood samples were analyzed for the following six serological and red cell enzyme markers, namely A1A2BO, Rh (D), ADA, ESD, PGM1 and PGM2.

Blood Group system A1A2BO and Rh (D) were typed according to the methods described by Race and Sanger (1975). Red cell enzymes were analyzed following the protocol for each marker. Firstly, hemolysates were prepared and then they were typed biochemically for 4 different polymorphic red cell enzymes, following standard horizontal electrophoretic techniques. Isozymes of erythrocyte enzymes Esterase D (ESD) and Phospho-

glucosylase locus 1 (PGM1) were electrophoresed together on one agarose gel and stained in the same order (Wraxall and Stolorow 1986). Similarly, Adenosine Deaminase (ADA) was separated on the agarose gel and simultaneously stained as described by Murch et al. (1986). The allele frequency estimates for the 20 markers in the Siddis were computed by the maximum-likelihood method (Reed and Schull 1968). Genetic distances among the populations were computed following Nei (1972) and their standard errors (SE) following Nei and Roychoudhury (1974).

RESULTS AND DISCUSSION

Allele frequencies of the all the six markers (A1A2BO, Rh (D), ADA, ESD, PGM1, PGM2) among the four populations under study have been presented in table 1. The allele frequency estimates were used for the goodness-of-fit chi-square test to determine whether the phenotype and genotype frequencies among all the four study population groups depart from Hardy-Weinberg proportions, and it was found that all the four population groups were in the Hardy-Weinberg equilibrium.

In the A1A2BO marker system, the average frequency of *A1 is found to be 16.57 percent, and varies from 26 percent among the Gonds to 11.3 percent among the Brahmins. The average frequency for allele *A2 has been observed to be 4.15 percent, and varies from 5.8 percent among the Gonds to 1.7 percent among the Halakki Vokkals. The frequency of allele *B has been found to vary from 20.8 percent among the Halakki

Vokkals to 10.9 percent among the Brahmins with a mean frequency of 17.72 percent. Similarly, the frequency of gene *O varies from 72.9 percent among the Brahmins to 48.4 percent among the Gonds, with an average of 61.56 percent. The distribution pattern of ABO blood group system is quite wide-ranging among the south Indian populations. The frequency of allele ABO*A1 averages around 13.9 percent and the frequency ranges from 0 among Kotas (Chaudhuri et al. 1962; Lehmann and Catbush 1952) to 40.63 percent among the Paniyans of Tamil Nadu (Lehmann and Catbush 1952). The frequency of allele ABO*A2 in South India averages around 2.85 percent and ranges from 0 among Chenchus and Pokkanatis of Andhra Pradesh (Chaudhuri et al. 1962; Reddy and Mukherjee 1982); Canarese, Kotas, Kurumbas, Todas, Badagas of Tamil Nadu (Lehmann and Catbush 1952; Chaudhuri et al. 1962; Ghosh et al. 1977) and Kurawas of Kerala (Chaudhuri et al. 1962) to 13.39 percent among Namboodri Brahmins (Banerjee et al. 1988). Alleles ABO*B and ABO*O have the frequency averaging 21.25 percent and 62.71 percent respectively. Allele ABO*B ranges from 5.5 percent among the Havig Brahmins of Karnataka (Vijaykumar et al. 1987) to 50.06 percent among the Todas of Nilgiri Hills (Chaudhuri et al. 1962). The frequency of the allele ABO*O ranges from 49.67 percent among the Savaras of Andhra Pradesh (Rao et al. 1987) to 78.9 percent among the Havig Brahmins of Karnataka (Vijaykumar et al. 1987). Thus, the distribution of ABO blood groups genes in the present study conforms to its distribution in southern population groups.

Table 1: The allele frequency distribution for all the six loci among population groups of Karnataka

Locus	Allele	Halakkis	Siddis	Gonds	Brahmins
A1A2BO	ABO*A1	0.173	0.117	0.260	0.113
	ABO*A2	0.017	0.042	0.058	0.049
	ABO*B	0.208	0.194	0.198	0.109
	ABO*O	0.602	0.647	0.484	0.729
Rh	Rh*D	0.860	0.677	0.788	0.759
	Rh*d	0.140	0.323	0.212	0.241
ADA	ADA*1	0.920	0.940	0.737	0.844
	ADA*2	0.080	0.046	0.263	0.156
	ADA*V	0.0	0.014	0.0	0.0
ESD	ESD*1	0.640	0.890	0.739	0.808
	ESD*2	0.360	0.110	0.261	0.192
PGM1	PGM1*1	0.710	0.761	0.695	0.657
	PGM1*2	0.290	0.237	0.305	0.335
	PGM1*3	0.0	0.002	0.0	0.004
	PGM1*7	0.0	0.0	0.0	0.004
PGM2	PGM2*1	1.000	0.952	1.000	1.000
	PGM2*A	0.0	0.048	0.0	0.0

In the Rh(D) system, the average frequency of *D allele is observed to be 77.1 percent, and varies from 86 percent among the Halakki Vokkals to 67.7 percent among the Siddis. Considering the distribution of Rh*D allele in India, the frequency is highest in the eastern India and starts declining towards north and west India, and then gradually starts increasing towards southern India. The distribution of the frequency of gene D among the present study is similar to that observed for southern populations (Bhasin et al. 1992).

In the ADA system, *1 allele varies from 94 percent among the Siddis to 73.7 percent among the Gonds and averages around 86.02 percent. Only the Siddis show the fast variant allele ADA*V with a frequency of 1.4 percent. Moreover, this variant has not been observed in any of the population of Southern India, and we are reporting it for the first time from this region. Among the populations of South India, the frequency of the ADA*1 allele averages about 88.94 percent and ranges from 83.3 percent among the Hindu Siddis of Karnataka (Vijaykumar et al. 1987) to 98.5 percent among the Jalaris of Andhra Pradesh (Naidu et al. 1985). Again ADA*1 allele is invariably higher than 70 percent in all the southern populations irrespective of any specific community.

In the EsD system, the average frequency of *1 allele is found to be 76.92 percent and varies from 89 percent among the Siddis to 64 percent among the Halakki Vokkals. In the populations of South India, the frequency of EsD*1 allele averages 70.1 percent and varies from 49 percent among the Vysyas of Andhra Pradesh (Rao et al. 1985) to 90 percent among the Hindu Siddis (Vijaykumar et al. 1987). Thus, the distribution of EsD*1 allele in present study is similar to its distribution observed for southern populations.

In the PGM1 system, the average frequency of alleles *1, *2 and *3 is observed to be 70.57 percent, 29.18 percent and 0.15 percent

respectively. We are reporting few variants in the present study. PGM¹ 1-3 and PGM¹ 1-7 variants are found among Brahmins, and PGM¹ 1-3 variant among Siddis. Few variants at this system have also been reported in some studies from southern India (Bhasin et al. 1992). The distribution pattern of alleles *1, *2 in the four populations under study is similar to the South Indian populations (Bhasin et al. 1992).

In the PGM2 marker system, all the populations are found to be monomorphic except Siddis, who show a rare variant, Atkinson, with a frequency of 4.8 percent. Incidentally, Atkinson Phenotype (PGM2*A) is African specific, which lends support to Siddi's African origin. PGM2 has been found to be monomorphic among all the population groups of southern India.

The heterogeneity Chi-square statistic for specific alleles across the four populations for six genetic markers is presented in table 2. The results of the analysis indicate that there is no significant heterogeneity among the population for each of these six markers in the present study.

The genetic differences were estimated using Nei's standard genetic distance among all pairs of populations with their respective standard

Table 2: Heterogeneity Chi-square analysis among the four populations in the present study

Locus	Allele	χ^2
A1A2BO	ABO*A1	0.1207
	ABO*A2	0.0070
	ABO*B	0.1283
	ABO*O	1.5302
Rh	Rh*D	0.1697
	Rh*d	0.0029
ADA	ADA*1	0.3276
	ADA*2	0.0335
ESD	ESD*1	0.1621
	ESD*2	0.1340
PGM1	PGM1*1	1.0230
	PGM1*2	.0012
PGM2	PGM2*1	.2432
	PGM2*1	.1023

χ^2 at d.f. = 3, p>0.05

Table 3: Standard genetic distance and its standard error for population groups of Karnataka

	Siddis	Brahmins	Halakkis	Gonds
Siddis	29.01 ± 07.42	0.4616	0.8072	0.8917
Brahmins	0.0074 ± 0.0015	30.86 ± 6.88	0.4346	0.3825
Halakkis	0.0196 ± 0.0148	0.0086 ± 0.0057	31.02 ± 8.83	0.3679
Gonds	0.0347 ± 0.0092	0.0149 ± 0.0099	0.0081 ± 0.0064	38.62 ± 8.93

Figures on the diagonal are the average heterozygosities expressed in percentage; below the diagonal are standard genetic distances and above the diagonal are F_{ST} values (polymorphic loci) with d.f.=11, p>0.05

Table 4: Genetic diversity among population groups of Karnataka

Number of populations	Number of loci	Ht	Hs	G _{sr}
4	6	0.3313	0.3206	0.0321

errors (Table 3). The genetic distance between the populations under study varied from 0.0074 among the Siddis and the Brahmins to 0.0347 among the Gonds and the Siddis. The average heterozygosity was found to be varying from a minimum of 0.290 among the Siddis to a maximum of 0.386 among the Gonds. It can be observed that the average heterozygosity is relatively low among the Siddis as compared to the other population groups indicating that the Siddis might have experienced lesser gene flow due to their isolated habitat. Further, the genetic distance analysis (table 3) does not reveal any significant differentiation, as examined by the pair-wise chi-square statistics (Nei and Roychoudhury 1974).

Table 4 presents gene diversity analysis among the four population groups under study. The average gene diversity (H_T) is 33.13 % and the coefficient of gene differentiation 0.032, indicating that a small contribution to the total variability comes from the inter population variation.

Six serological and red cell enzyme systems investigated in the present study are found to be polymorphic, but, no significant heterogeneity exists for different alleles across six loci in the four populations. It is worthwhile to state that few variants have been found in the Siddis with respect to ADA, PGM1 and PGM2 red cell enzyme systems, which are of immense importance for undertaking population genetic studies in the near future within the framework of population divergence. Thus, intensive studies with high resolution DNA markers among these populations will not only provide meaningful insight into the population structure, but, will also be of great utility in the various genetic epidemiological studies.

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