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Genetic Profile of Jenu Kuruba, Betta Kuruba and Soliga Tribes of Southern Karnataka and Their Phylogenetic Relationships

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ABSTRACT The genetic affinity of the three tribes, two belonging to Kuruba/Kurumba cluster (*viz.* Jenu Kuruba and Betta Kuruba) and the third (*viz.* Soliga tribe)- immediate neighbor of the first two but not the part of Kuruba/Kurumba cluster has been studied using ten polymorphic genetic markers. To investigate, whether all the Kuruba/Kurumba groups are related to the Pallava dynasty and are the off shoots of the same stock as suggested in many ethnographic studies. The distribution of the allele frequencies of ten polymorphic loci, and population genetic models calculated there upon; do not support the relationships of the Kuruba cluster for the Jenu Kuruba and Betta Kuruba. However the studied three tribes show a low genetic distance suggesting a recent divergence or low degree of genetic isolation.

INTRODUCTION

There exist biological variation among human individuals as well as among groups of individuals at various levels like tribe, caste and race living in different geographical areas. Study of human biological variations between populations helps in understanding historical relationships between them as well as impact of particular environment and ways of life upon ongoing evolution.

The study of human inheritance involves etiology of heredity, similarity and diversity of various genetic and morphogenetic characters among different population groups. For investigating variation between and within the populations, easily accessible genetic characters are the obvious choice as morphological characters are subjected to the influence of environment, nutrition and cumulative effect of various polygenes, though they are important in evolution, which is after all, largely about changes in shape and appearance. However we know far less about it than we do about biochemical diversity. Serological and biochemical characters with their distinct hereditary mechanisms constitute major genetic markers. Thus study of population based genetic polymorphisms for some time now has been employed to infer exact genetic description and phylogenetic relationships of such populations. Comprehensive reviews of such polymorphic markers and their distribution among human populations have been given by Mourant et al. (1976), Steinberg and Cook (1981), Tills et al. (1983), Roychoudhury and Nei (1988), Bhasin et al. (1994, 2001), Walter (1998).

There are many population groups namely, the Kuruba, the Jenu Kuruba, the Betta Kuruba, the Kadu Kuruba, the Mullu Kurumba, the Urali Kurumba and the Kurumba living in the peninsular India and there exist confusion in the literature over the identity and origin of these groups. Thurston (1909) quoting the Madras Census Report 1891 writes that "*the Kurubas or Kurumbas are modern representative of the ancient Kurumbas or Pallavas who were once very powerful in South India. Their powers gradually decline owing to the rise of Kongu, Chola and Chalukya chiefs. Chola King Adondi about the 7th and 8th century A.D affected the final overthrow of Kurumba sovereignty. This led to the dispersion of the Kurumbas far and wide. Many fled to the hills of Malabar, Nilgiris, Coorg, Wynad and Mysore. Thus during the long laps of time, they have become wild and uncivilized and have owing to their comparative isolation, lost their ancient culture. Indeed Kurumbas must be regarded as very old inhabitant of this land, which can contest with their Dravidian kinsmen the priority of occupation of the soil.*" whereas he has also stated that at least physically all the groups do not resemble, and some of them shows similarity with some other tribes. Aiyappan (1948) writes, "*The Kuruba is the name of the large shepherd community of the Karnataka plateau. They*

speak Kannada. In Mysore these Kuruba are divided into Uru Kuruba and Kadu Kuruba. Kadu Kuruba is further divided into Jenu Kuruba and Betta Kuruba". Likewise many authors attempted to identify one group with other and a common origin of Kuruba groups. Misra (1969) in his report on Jenu Kuruba, discussed this problem in detail and writes that there exist marked cultural and physical variation of varying degree among different Kuruba groups and in the event of lacking authentic evidences it is difficult to say whether all the Kuruba/ Kurumba groups are related to the Pallava dynasty and are the off shoots of the same stock.

In the backdrop of the above ethnic account, the present study aims to investigate the genetic affinity of the two Kuruba tribes (namely Jenu Kuruba and Betta Kuruba) and one of their immediate neighbor (namely Soliga tribe) using ten polymorphic genetic markers.

MATERIAL AND METHODS

The population groups of present study are scheduled tribe and inhabit the same geographical locale spreading over the tri-junction of Karnataka, Kerala and Tamil Nadu states.

Population Groups Studied

Jenu Kuruba: The Jenu Kuruba a primitive tribe in Karnataka, who's population as per the Census of India 1991, was 29,371, out of which 15,156 were male and 14,215 were females. Approximately 70 per cent of their population is found in H. D. Kote, Hunsur, and Piriyapatana taluks of Mysore district, Gundlupet taluk of Chamrajanagar district and Virajpet, Somavarpet and Medikeri taluks of Kodagu district.

Physically Jenu Kuruba are short statured with mesocephalic head shape and broad facial and nasal profile (Karve, 1954) and show affinity to Kurumba of Nilgiri and Betta Kuruba to some extant, but there exits marked differences in material culture of Jenu Kuruba and Betta Kuruba. Jenu Kuruba speak Jenu nudi a dialect of Kannada, but while communicating with others they speak standard Kannada language.

Betta Kuruba: The Betta Kuruba an endogamous population in Karnataka, who on the other side of the border in Kerala and Tamil Nadu, are called as Urali Kurman. Their number is roughly not more than 10 to 12 thousand, but enumerated 63,218 persons in Karnataka alone, under the name Kadu Kuruba in the Census of India 1991, whereas no separate census is available for this endogamous population in any of the state.

Physically Betta Kurubas are mostly short to very short stature people with a mean stature of 1548.1 mm (Sirajuddin et al, 1992). They possess dolichocephalic heads (cephalic index: 75.84) and mesorhine noses (nasal index: 76.42). Betta Kuruba speaks a dialect of their own, which is having similarity with Kannada language.

Soliga: The Soligas are an aboriginal forest tribe inhabiting the state of Karnataka and Tamil Nadu. In Karnataka they are mainly distributed in the interior of the forests skirting the slopes of the Biligirirangan (BR) hills and other hilly part of the Mysore and Chamrajanagar districts. According to Buchanan, they speak a bad or old dialect of Canarese language. In the hill tract of Ramagiri, other natives call these people as Cad Eraligaru; but they call themselves *Cad Chansu*. The language of Chansu is a dialect of Tamil with occasionally a few of Canarese or Telugu words intermixed, but their accent is different from that of Madras. Their original country is said to be the Anamalay forests below the Ghauts, which is confirmed by their dialect.

In the Census of India 1991 they are numerated into two groups the Soligaru and Solaga, who numbered 23,955 and 6,754 respectively. Soligarus are restricted in Karnataka only and approximately their 80 per cent of the population lives in Mysore and Chamraja nagar districts. Sholaga are found in both Karnataka and Tamil Nadu states, but predominantly concerted in Tamil Nadu with 90 percent of their population in Periyar district.

Physically Soligas are below medium statured people, with long and narrow head shape, oval face and broad nose (Karve, 1954).

Population Samples

The data and whole blood sample in EDTA vials for the present study were collected at random from a total of 358 apparently healthy and unrelated individuals of either sex, comprising 177 from Jenu Kuruba, 101 from Betta Kuruba and 80 from Soliga tribe inhabiting Mysore district of Karnataka. The blood samples were transported to the laboratory with in the shortest time possible, by keeping them on ice.

Laboratory Analysis

Red cells were tested for A1A2 BO, and Rhesus (RH-D) blood group systems, using Pan Diagnostics Ltd/ Tulip India make antisera, following manufacturers instructions and standard serological techniques.

The isozyme polymorphic systems, Esterase-D (ESD), Phosphoglucomutase- I (PGM-I) and Glucose Phosphate Isomerase (GPI) were typed as per the methods listed in Haris and Hopkinson (1976). Whereas Glyoxalase-I (GLO –I) was typed using technique described by Scott and Fowler (1982) and Glucose 6 phosphate dehydrogenase (G6PD) deficiency screening was done by fluorescence spot test after Beutler (1966); Beutler and Mitchell, (1968), which has also been recommended by international committee for standardization in Haematology (ICSH) (Beutler et al., 1979).

Typing of Haptoglobin (HP) and Transferrin (TF) serum proteins was done by starch slab gel electrophoresis using technique described by Smithies (1955-59), cited from Bhasin et al. (1995).

The haemoglobin variant screening was done on agar electrophoresis technique described by Robinson et al. (1957), cited from Bhasin et al. (1995).

Gene nomenclature and gene symbols have been used as describe in (ISGN, 1987).

Statistical Analysis

The gene frequency calculations have been done after Mourant et al. (1976) and the test of significance (chi-square test) has been used. The chi-squared statistic for marker wise biological distance has also been calculated using formula of Constandse-Westermann (1972).

Wahlund's variance (Wahlund, 1928) and a set of gene diversity measures developed by Nei (1973) have been used to analyze the genetic differentiation. Nei's Standard Genetic Distance (Ds) (after Nei, 1972) has also been calculated for the population of present study to understand the genetic relationship and Phylogeny.

RESULT AND DISCUSSION

The observed and expected phenotype numbers and allele frequencies calculated from the observed numbers for the studied ten polymorphic genetic markers among the Jenu Kuruba, Betta Kuruba and Soliga tribes are given in table 1. In no systems except G6PD deficiency and haemoglobin variants where pronounced natural selection operates, did the expected phenotype numbers calculated assuming Hardy-Weinberg equilibrium shows any statistically significant variation from the observed phenotype numbers.

The frequency of *ABO*A* allele is observed comparatively higher than the *ABO*B* among Jenu Kuruba (*ABO*A*=27.02 per cent; *ABO*B*=13.39 per cent) and Soliga (*ABO*A*=31.89 per cent; *ABO*B*=15.12 per cent), whereas among Betta Kuruba allele *ABO*B* is found in higher frequency 27.30 per cent than allele *ABO*A* 21.8 per cent. The allele *ABO*O* frequency varies from 59.58 per cent among Jenu Kuruba to 50.90 per cent among Betta Kuruba. The allele *ABO*A*2 frequency comparatively show wide variation i.e. 1.42 per cent among Jenu Kuruba to 5.48 per cent among Soliga.

There is lot of heterogeneity in the distribution of ABO allele frequencies among the population groups of Indian region, but on an average allele *ABO*B* is higher (average 23.3 per cent; ranges 0.9 to 52.8 per cent) as compared to the allele *ABO*A* (average 18.6 per cent; ranges 1.0 to 54.4 per cent), whereas frequency of allele *ABO*O* averages to 58.1 per cent (ranges 24.3 per cent to 96.0 per cent). The *ABO*A*2 allele, shows an average frequency of 2.5 per cent (varies from 0.0 to 14.0 per cent). If we look into the South India zone and scheduled tribe in particular on an average allele *ABO*A* shows preponderance (average 21.2 per cent; ranges 1.1 to 49.0 per cent) over allele *ABO*B* (average 20.1 per cent; ranges 0.9 to 52.8 per cent), whereas allele *ABO*O* shows higher average frequency i.e. 58.7 per cent (ranges 24.3 to 81.4 per cent) as compared to the other geographical zones of India except Islands (Bhasin et al., 1994; Bhasin and Walter, 2001). The allele frequencies for ABO system among the present study tribes fit well with in the Indian range as well as South India, scheduled tribe range.

The frequency allele *RH*D* has been observed 100.00 per cent in Soliga tribe, 80.11 per cent in Jenu Kuruba and 77.75 per cent in Betta Kuruba tribe.

Among Indian populations the frequency of allele *RH*D* averages around 80.3 per cent (ranges 53.2 to 100 per cent). It is highest among the scheduled tribes (average 87.6 per cent; ranges 60.8 to 100 per cent). In the South India zone it

Table 1: Phenotype and allele frequencies of 10 polymorphic marker systems investigated among Jenu Kuruba, Betta Kuruba and Soliga tribes.

System and phenotype	*Observed and expected phenotype numbers*							*Allele frequencies*		
	Jenu Kuruba		*Betta Kuruba*		*Soliga*		*Alleles*	*Jenu Kuruba*	*Betta Kuruba*	*Soliga*
	Obs.	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*				
A1A2BO										
O	62	62.84	25	26.17	23	22.47				
A1	66	66.89	24	25.12	31	30.28	*ABO*A1*	0.2560	0.198	0.2641
A2	3	3.04	2	2.09	5	4.88	*ABO*A2*	0.0142	0.020	0.0548
B	31	31.42	34	35.59	15	14.65	*ABO*B*	0.1339	0.273	0.1512
A1B	13	12.14	14	10.92	5	6.39	*ABO*O*	0.5958	0.509	0.5299
A2B	2	0.68	2	1.1	1	1.33				
Total	177	177.00	101	101.00	80	80.00		1.0000	1.0000	1.0000
							χ^2 Value	*2.6895*	*1.7809*	*0.4226*
Rhesus (RH)										
RH D+	170	-	96	-	80	-	*RH*D+*	0.8011	0.7775	1.0000
RH D-	7	-	5	-	0	-	*RH*D-*	0.1989	0.2225	0.0000
Total	177	-	101	-	80	-		1.0000	1.0000	1.0000
Haptoglobin (HP)										
HP 1-1	25	27.76	4	4.08	9	11.69	*HP*1*	0.3994	0.2806	0.3896
HP 2-1	89	83.48	47	47.96	42	36.62	*HP*2*	0.6006	0.7194	0.6104
HP 2-2	60	62.76	47	47.96	26	28.69				
Total	174	174.00	98	98.00	77	77.00		1.0000	1.0000	1.0000
							χ^2 Value	*0.7608*	*3.4592*	*1.6595*
Transferrins (TF)										
TF C-C	168	168.05	93	93.04	75	75.01	*TF*C*	0.9828	0.9794	0.9870
TF B-B	0	0	0	0	0	0	*TF*D*	0.0172	0.0206	0.0130
TF D-D	0	0.05	0	0.04	0	0.01				
TF C-B	0	0	0	0	0	0				
TF C-D	6	5.9	4	3.92	2	1.97				
Total	174	174.00	97	97.00	77	77.00		1.0000	1.0000	1.0000
							χ^2 Value	*0.0536*	*0.0429*	*0.00002*
Glyoxalase-I (GLO-I)										
GLO-I 1-1	29	26.27	12	11.23	6	8.01	*GLO-I*1*	0.3864	0.3402	0.3205
GLO-I 2-1	78	83.45	42	43.55	38	33.97	*GLO-I*2*	0.6136	0.6598	0.6795
GLO-I 2-2	69	66.27	43	42.23	34	36.01				
Total	176	176.00	97	97.00	78	78.00		1.0000	1.0000	1.0000
							χ^2 Value	*0.7518*	*0.1223*	*1.0951*

Table 1: Contd.....

System and phenotype	*Observed and expected phenotype numbers*						*Alleles*	*Allele frequencies*		
	Jenu Kuruba		*Betta Kuruba*		*Soliga*			*Jenu Kuruba*	*Betta Kuruba*	*Soliga*
	Obs.	*Exp.*	*Obs.*	*Exp.*	*Obs.*	*Exp.*				
Esterase-D (ESD)										
ESD 1-1	83	80.70	54	53.63	39	38.08	*ESD*1*	0.681	0.7553	0.6987
ESD 2-1	71	75.59	34	34.74	31	32.84	*ESD*1*	0.319	0.2447	0.3013
ESD 2-2	20	17.70	6	5.38	8	7.08				
Total	174	174.00	94	94.00	78	78.00		1.0000	1.0000	1.0000
							χ^2 Value	*0.6428*	*0.0432*	*0.2448*
Phosphoglucomutase-I (PGM-I)										
PGM-I 1-1	29	34.43	16	19.22	11	14.52	*PGM I*1*	0.4500	0.4521	0.4400
PGM-I 2-1	95	84.15	53	46.57	44	36.96	*PGM I*2*	0.5500	0.5479	0.5600
PGM-I 2-2	46	51.43	25	28.22	20	23.52				
Total	170	170.00	94	94.00	75	75.00		1.0000	1.0000	1.0000
							χ^2 Value	*2.8262*	*1.7925*	*2.7211*
Glucose Phosphate Isomerase (GPI)										
GPI 1-1	168	168.02	92	92.02	76	76.01	*GPI*1*	0.9884	0.9842	0.9872
GPI 3-1	4	3.95	3	2.95	2	1.97	*GPI*3*	0.0116	0.0158	0.0128
GPI 3-3	0	0.02	0	0.02	0	0.01				
Total	172	172.00	95	95.00	78	78.00		1.0000	1.0000	1.0000
							χ^2 Value	*0.0238*	*0.0245*	*0.0132*
Glucose 6 Phosphate Dehydrogenase (G6PD) Deficiency (Only male samples)										
G6PD-										
Normal	86	-	39	-	38	-	*G6PD*N*	1.000	0.8298	0.9744
Def.	0	-	8	-	1	-	*G6PD*D*	0	0.1702	0.0256
Total	86	-	47	-	39	-		1.0000	1.0000	1.0000
Haemoglobin (HB) variants										
HB A-A	156	-	89	-	73	-	*HB*A*	0.9457	0.9495	0.9679
HB A-S	17	-	10	-	5	-	*HB*S*	0.0486	0.0505	0.0321
HB A-C	2	-	0	-	0	-	*HB*C*	0.0057	0.0000	0.0000
Total	175	-	99	-	78	-		1.0000	1.0000	1.0000

averages to 81.1 per cent among caste groups 80.9 per cent among scheduled caste and highest among scheduled tribe 83.1 per cent; range 61.8 to 100 per cent (Bhasin et al., 1994). The tribes of present study fit well within the all India and South India range reported for the scheduled tribe populations.

The frequency of alleles *HP*1* (varies from 28.06 per cent among Betta Kuruba to 39.94 per cent among Jenu Kuruba) is lower than the *HP*2* allele (ranges from 60.06 per cent among Jenu Kuruba to 71.94 per cent among Betta Kuruba). In India, the frequency of *HP*1* is 16.0 per cent (varies from complete absence among scheduled tribe of West Bengal to 40.6 per cent among Dawoodi Bhoras of Rajasthan). In South India zone allele *HP*1* frequency shows highest frequency among caste groups (average 15.1per cent; ranges 10.9 to 21.3 per cent) followed by scheduled tribes (average 12.8 pr cent; ranges 2.5 to 37.0 per cent) and scheduled caste (average 12.1per cent; ranges 2.9 to 24.4per cent) (Bhasin and Walter, 2001). All the population groups of present study fits well within the Indian range, but Jenu Kuruba and Soliga tribes of present study shows comparatively higher frequency of allele *HP*1* to that of the South India scheduled tribe range.

The allele *TF*C* is present among all the studied population in higher frequency of nearly 98 per cent. The rare allele *TF*D* has also been observed among all the three population in the frequency of 1.72 per cent among Jenu Kuruba, 2.06 per cent among Betta Kuruba and 1.3 per cent among Soliga tribes.

Among Indians, common transferrin allele found in most individuals is of the type *TF*C* (average 99.1 per cent; varies from 89.8 per cent to 100 per cent), whereas frequencies of allele *TF*D* (average 0.8 per cent; ranges 0 to 10.2 per cent) and allele *TF*B* (average 0.1 per cent; ranges 0 to 1.9 per cent) are quite low. In South India zone, apart from the common allele *TF*C*, allele *TF*D* is found in higher frequency among scheduled tribes (average 1.9 per cent; ranges 0.0 to 10.2 per cent) followed by scheduled caste (average 1.5 per cent; ranges 0.0 to 10.2 per cent) and then caste groups (average 0.4 per cent; ranges 0.0 to 3.3 per cent). The allele *TF*B* is almost negligible among all the ethnic groups (Bhasin et al., 1994). All the three tribal groups of present study fits well within the Indian range as well as scheduled tribe range for South India.

The frequency of allele *GLOI*1* has been observed comparatively high among all three tribes of present study, i.e. highest among Jenu Kuruba (38.64 per cent) followed by Betta Kuruba (34.02 per cent) and Soliga (32.05 per cent). Allele *GLOI*2* varies from 67.95 per cent among Soliga to 61.36 per cent among Jenu Kuruba.

The frequency of *GLOI*1* allele is quite high among Europeans (44 per cent) and low among Japanese (5.3 per cent). From India only few studies are available in the literature among whom a high frequency of *GLOI*1* has been observed among Gujaraties (38 per cent) and low among Bhotias (7.5 per cent) (Bhasin et al., 1995). Whereas no study is available on the neighboring area tribes for this system.

The frequency of allele *ESD*1* is high as compared to the *ESD*2*. Amongst the present study populations *ESD*1* allele is observed highest in Betta Kuruba (i.e. 75.53 per cent) followed by Soliga (i.e. 69.87 per cent) and Jenu Kuruba (i.e. 68.10 per cent).

Among Indian populations the frequency of allele *ESD*1* is 72.9 per cent (varies from 41.8 per cent to 97.8 per cent). The frequency is low among scheduled tribes (i.e. 69.0per cent) as compared to the other ethnic groups. In Southern India *ESD*1* is found in higher frequency among caste groups (average 71.7 per cent; ranges 65.3 to 85.6 per cent) followed by scheduled tribes (average 68.3 per cent; ranges 52.5 to 86.5 per cent) and scheduled caste (average 67.8 per cent; varies from 59.5 to 81.7 per cent) (Bhasin et al., 1994). All the populations of present study fit well in the total Indian as well as South India frequency ranges for ESD system.

Among all the three tribe frequency allele *PGMI*2* is comparatively higher than the allele *PGMI*1*. Though there is not much of a difference between the three tribes for the *PGMI*1* allele frequency, Betta Kuruba shows highest frequency of PGMI*1 (i.e. 45.21per cent) followed by Jenu Kuruba (45 per cent) and Soliga (44 per cent).

The frequency of allele *PGMI*1* is average to 70 per cent among Indian populations (i.e. varies from 44.2 per cent among Kuruba to 95.0 per cent among Chaudhuri tribes). Among scheduled tribes average frequency of allele *PGMI*1* is low (i.e. 69 per cent) as compared to the other ethnic groups (caste 69.4 per cent and scheduled caste 73.1 per cent). In southern Indian region frequencies of allele *PGMI*1* is low among all the ethnic groups as compared to the

other regions of India, i.e. caste 69.2 per cent (ranges 62.9 to 79.2 per cent), scheduled caste 63.1 per cent (ranges 60 to 66.3 per cent) and scheduled tribe 69.6 per cent (ranges 44.2 to 82.4 per cent) (Bhasin et al., 1994). The frequencies of *PGMI*1* among Jenu Kuruba, Betta Kuruba and Soliga tribes of present study is comparatively low, but well within the all India and Southern Indian ranges.

The rare allele *GPI*3* has been observed in an appreciable frequency among all the three tribes (i.e. Betta Kuruba 1.58 per cent; Soliga 1.28 per cent; Jenu Kuruba 1.16 per cent).

Besides the most common allele *GPI*1*, the other allele are rare and sporadic in occurrence. Out of the 9 known alleles, the allele of anthropological interest are *GPI*3*, *GPI*4*, *GPI*5* and *GPI*7.* The rare allele *GPI*3* mainly found among Asians and Europeans. Though, the electrophoretic investigation of GPI has shown the presence of six out of nine known heterozygous phenotypes and one rare homozygous phenotypes within the geographical region of India (Bhasin et al., 1992), but alleles *GPI*2, GPI*4, GPI*5, GPI*7, GPI*8* and *GPI*9* are rare and of sporadic occurrence in some endogamous groups of India. In general, the rare allele *GPI*3* is frequently observed in India, mostly in heterozygous phenotype GPI 31. The allele frequency varies from 0.2 per cent among Kanet (Kalpa) of Himachal Pradesh and Hindus of Andhra Pradesh reported by Papiha et al. (1984) and Roberts et al. (1980) respectively, to 5.3 per cent among the Kamboh of Punjab reported by Chahal et al. (1989b). This allele shows polymorphic frequencies among several populations of India. In Southern India zone frequency of allele *GPI*3* ranges from 0.2 to 2.5 per cent (Roberts et al. 1974). The three tribes of present study show presence of rare allele *GPI*3* with frequencies with the South India range.

It has been observed that tribe Betta Kuruba show a high frequency of G6PD deficiency i.e. 17.02 per cent, which may be due to the small male sample size, whereas among 86 Jenu Kuruba males G6PD deficiency could not be detected i.e. complete absence of G6PD deficiency. The Soliga tribe shows a frequency of 2.56 per cent for G6PD deficiency.

According to WHO Report (1966), the frequency of G6PD deficiency in India ranges between 4 to 19 per cent. Since most of the studies published prior to the said report were based on the investigations carried out on patients in hospitals, studies on well-defined population are too few to allow a fair estimate of regional variations in the enzyme deficiency. From a total of 224 studies reported among Indian populations the frequency of G6PD deficiency is 4.5 per cent (varies from 0.0 to 27.1 per cent among Angami Nagas studied by Seth et al., (1971) in South India zone the average frequency is below 3 per cent among different ethnic group, but scheduled tribe shows a higher range (i.e. 0.0 to 12.5 per cent) (Bhasin et al., 1994). The Betta Kuruba of present study shows a high frequency of G6PD deficiency (i.e. 17.02 per cent) as compared to the South India range for scheduled tribe.

Apart from the normal allele *HB*A*, the allele *HB*S* has also been observed in all the studied tribes, among whom Betta Kuruba shows the highest frequency (i.e. *HB*S* = 5.05 per cent) followed by Jenu Kuruba (i.e. *HB*S* = 4.86 per cent) and Soliga tribes (i.e. *HB*S* = 3.21 per cent). The rare allele *HB*C* was found only among Jenu Kuruba in the frequency of 0.57 per cent.

Out of more than 300 abnormal haemoglobin variants described in the literature, sickle cell trait is one of the most interesting and widely studied variant. It is found in highest frequency in tropical Africa (10 to 40 per cent). The trait has also been reported in high frequency in India, Greece and Southern Turkey (5 to 10 per cent) and less than 10 per cent frequency among population groups living around the Mediterranean Sea. In India sickle cell trait was first detected in Nilgiri Hills by Lehmann and Cutbush (1952 a,b,c). The average frequency of this trait among Indian populations is 3.1 per cent (varies form complete absence to 41.0 per cent). Among ethnic groups the sickle cell trait frequency is comparatively high in scheduled tribes (average 5.4 per cent) than scheduled castes (2.4 per cent) and caste groups (almost negligible) (Bhasin et al., 1994; Bhasin and Walter, 2001). In South India zone particularly among scheduled tribes frequency of *HB*S* is 7.0 per cent (ranges 0.0 to 41.0 per cent).

The distribution of the alleles frequencies of ten polymorphic loci, suggest that non of the studied population shows clear genetic affinity to one and distance to other, however in contrast the three studied tribe shows a very low degree of genetic difference with each other as expected from the populations of the same geographic region.

For A1A2BO and G6PD markers the studied tribes show statistically significant difference with each other. Whereas Soliga tribe shows significant difference with the other two for Rhesus markers, Betta Kuruba shows for Haptoglobin markers. The statistically significant difference between the studied tribes could not be detected for other markers.

To understand the genetic structure, the content of genetic variation, mechanisms of maintenance of population differences in the gene frequencies and finally the relationship among the Jenu Kuruba, Betta Kuruba and Soliga tribes of the present study, further analysis has been attempted using various population genetic structure models.

Heterozygosity

The average heterozygosity calculated for each of the tribes of present study over ten loci are presented in table 2. These values show a comparatively low level of heterozygosity (average 0.2892) in all the three populations studied, which may indicative to the fact of large-scale inbreeding practiced in these populations. Out of the three, Betta Kuruba found to be the most heterozygous with an average heterozygosity value of 0.314 followed by Jenu Kuruba (Heterozygosity = 0.2923). Soligas were observed to be lowest in heterozygosity (i.e. 0.2612). The present value fit well in the heterozygosity range 0 .21 to 0.37 calculated on world population by Cavalli-Sforza et al. (1994) using various polymorphic loci.

Table 2: Heterozygosity in Jenu Kuruba, Betta Kuruba and Soliga Tribes. - estimates by populations based on 10 polymorphic loci.

S.No.	*Populations*	*Heterozygosity (H)*
1	Jenu Kuruba	0.2923
2	Betta Kuruba	0.3140
3	Soliga	0.2612
4	Mean	0.2892

Wahlund's Variance (f)

The value of Wahlund's Variance (*f*) calculated for 10 diallelic genes are listed in table 3. A very high value of (*f*) for *RH*D* and *G6PD* Def* (i.e. 0.1237 and 0.138 respectively) may suggest some natural selection, operating for these systems among the studied populations. A comparatively high *f* mean value and wide variation in the individual *f* values over 10 di-allelic loci, suggests a comparatively high degree of inbreeding practiced among the studied populations. The mean *f* values over the 10 genes (i.e. 0.0303) give an estimate of overall magnitude of gene differentiation among the three tribes of present study.

Table 3: Mean allele frequency, variance and Wahlund's variance among Jenu Kuruba, Betta Kuruba and Soliga tribes based on 10 polymorphic loci.

S. No.	*Gene*	*Mean* ($\bar{p}$)	*Variance* (σp^2)	*Wahlund's Variance* $(f)=\frac{\sigma p^2}{\bar{p}(1-\bar{p})}$
1	RH*D	0.8595	0.0149	0.1237
2	GLO I* 1	0.3490	0.0011	0.0050
3	ESD* 2	0.2883	0.0015	0.0073
4	PGM I* 1	0.4474	0.0000	0.0002
5	GPI* 3	0.0134	0.0000	0.0003
6	HP* 1	0.3565	0.0043	0.0190
7	TF* D	0.0169	0.0000	0.0009
8	HB*S	0.0437	0.0001	0.0025
9	HB*C	0.0019	0.0000	0.0057
10	G6PD* def	0.0653	0.0084	0.1380
	Mean			0.0303

Nei's Gene Diversity Analysis

The gene diversity (H_T) among the three tribes (0.2939) has been analyzed into its two component, i.e. intra population gene diversity (H_S = 0.2892) and inter population gene diversity (D_{ST} = 0.0047), which shows a very low inter population gene diversity as compared to the intra population gene diversity. This suggests that only a small fraction of the total population gene diversity is due to the differences between the population groups, while at large this diversity is attributable to individual variations, within the population groups. Further conclusion may be drawn that the populations under investigation are at an early stage of gene differentiation.

The coefficient of gene diversity (G_{ST}) value among three tribal groups of present study is comparatively high at A1A2BO, Rhesus, Haptoglobin and G6PD loci (i.e. 0.0105; 0.0825; 0.0126 and 0.0920 respectively). On the other hand, little differentiation has been recorded for PGMI, GPI and TF loci, while values are moderate at GLOI, ESD and HB loci (Table 4). It has been observed that among the present population groups the average G_{ST} is 0.0303.

Table 4: Estimates of Nei's measures of gene diversity among Jenu Kuruba, Betta Kuruba and Soliga tribes based on 10 polymorphic.

Locus	H_T	H_S	D_{ST}	G_{ST}
A1A2BO	0.6103	0.6039	0.0064	0.0105
RHESUS	0.2415	0.2215	0.0199	0.0825
GLO-I	0.4544	0.4529	0.0015	0.0034
ESD	0.4104	0.4084	0.0020	0.0049
PGM-I	0.4945	0.4944	0.0001	0.0001
GPI	0.0265	0.0265	0.0000	0.0002
HP	0.4588	0.4530	0.0058	0.0126
TF	0.0333	0.0333	0.0000	0.0006
HB	0.0872	0.0871	0.0002	0.0020
G6PD	0.1220	0.1108	0.0112	0.0920
Mean	0.2939	0.2892	0.0047	0.0209

H_T = Gene diversity in the total population.
D_{ST} = Inter-population gene diversity.
H_S = Intra-population gene diversity.
G_{ST} = Coefficient of gene differentiation.

Genetic Distance

Nei's standard distance matrix for the present study is presented in table 5. It has been observed that the genetic distance measure (D) is comparatively low between Jenu Kuruba and Soliga tribes (i.e. 0.0065) to that of Jenu Kuruba – Betta Kuruba (i.e. 0.0095) and Betta Kuruba – Soliga (i.e. 0.013) inter groups.

Table 5: Nei's Standard Genetic Distance matrix among Jenu Kuruba, Betta Kuruba and Soliga Tribes based on 10 polymorphic loci.

Populations	*Jenu Kuruba*	*Betta Kuruba*	*Soliga*
Jenu Kuruba	0		
Betta Kuruba	0.009466	0	
Soliga	0.006516	0.012998	0

The over all genetic relationship between the tribes of present study is summed up in the UPGMA trees constructed from the Nei's standard genetic distance matrix (Fig. 1). It is clears from the figure that Jenu Kuruba and Soliga tribe who exhibit less intergroup genetic distance form a cluster, whereas Betta Kuruba who posses comparatively higher genetic distance with the former populations fall out of the cluster.

CONCLUSION

From the above results it can be fairly concluded that the genetic structure and genetic affinity of the studied populations do not support the relationships of the Kuruba cluster for the Jenu Kuruba and Betta Kuruba, as suggested in the various ethnographic studies. However the studied three tribes show a low genetic distance suggesting a recent divergence or low degree of genetic isolation. A common situation observed in India by many studies that genetic makeups of the populations shows more affinity if they are geographically close rather due to the ethnic or socio-cultural affinity.

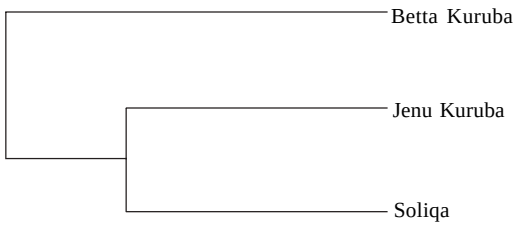

Fig. 1. UPGMA – Tree of Nei's Standard Genetic Distances among Jenu Kuruba, Betta Kuruba and Soliga Tribes.

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