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GENETIC VARIATIONS WITHIN TWO SUBTYPES OF SALIS

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ABSTRACT

Background and objectives: The investigation of human blood genetic markers is a convenient tool to study genetic variation within and between human populations. The present investigation reports the variation in the distribution of some genetic markers in Salis, an endogamous sub-population from State of Andhra Pradesh, India.

Methods: 210 venous blood samples collected from health and unrelated individuals living in Vizianagaram and Visakhapatnam cities were used for typing eight genetic markers. The data obtained was tabulated, analyzed, assessed and formulated.

Results: Only 5 enzymes namely 6PGD, G6PD, ESD, ACP1 and GLO1 systems exibit polymorphism in the present study. However, in the 6PGD system, the AC rare heterozygote phenotype was observed 10% of cases. Furthermore, rare variant, TF*CD in the Transferrin system has been observed. The allele frequency of TF*CD was found to be 0.01.

Conclusions: The results of these biochemical genetic markers were found to be in accordance with other populations of Andhra Pradesh, South India.

KEYWORDS : Polymorphism. Caste population. Andhra Pradesh.

INTRODUCTION

Genetic markers such as blood groups, red cell enzymes, plasma proteins and DNA polymorphisms have been, and are, being studied to understand human population variations. Many investigators have studied the genetic structure of sub-divided human populations by the use of specific markers. Vast majority of genetic studies were based on classical genetic markers viz. blood groups, plasma proteins, and red-cell enzyme polymorphisms. These red cell enzyme and plasma protein markers are certainly helpful to identify the different types of genetic diseases in the present scenario. The frequencies of alleles in human populations reflect the genetic structure of populations and are used in establishing the relationship of different populations to each other. The populations of India and other South Asian countries offer great opportunities to study genetic variability. Perhaps, nowhere in the world people in a small geographic area are distributed as such a large number of ethnic, caste, religious and linguistic groups as in India and other South Asian countries. All these groups are not entirely independent, people belong concurrently to two or more of these groups. People of different groups living side by side for hundreds or even thousands of years try to retain their separate entities by practicing endogamy. The phenotype distribution of various enzyme systems in the Indian subcontinent has been the subject of several recent reports [1] [2] [3] [4] [5] which give details relating to different linguistic groups of several regions of India. There is little or no information so far on the caste population of Salis, the object of this study. Therefore, the present population genetic study was done on a caste population, known as Salis, which is categorized into two endogamous sub-castes, the Padmasalis (PS-I) who deal with cotton weaving and Pattusalis (PS-II) who are skilled silk weavers. Both the subgroups are distributed throughout Andhra Pradesh.

This study considers 2 blood group polymorphisms (ABO, RhD), ABH secretor status, 5 plasma protein polymorphisms (HP, GC, CP, TF and ALB), 8 red cell enzyme polymorphisms (6PGD, G6PD, LDH, MDH, ESD, GLO1, ACP_1 and SOD) and Haemoglobin (HB) variants were investigated in Sali sub-populations of Visakhapatnam District, Andhra Pradesh, India. Phenotype and gene frequencies will be discussed considering (1) the extent of the genetic heterogeneity within the Salis and (2) the genetic affinities to other populations of India.

MATERIALS AND METHODS

A total of 210 individuals belonging to two sub-groups of Sali caste (PS-I: 105; PS-II: 105) residing in and around Visakhapatnam and Vizianagaram districts of Andhra Pradesh, India have participated in this study. 5ml of venous blood was collected into sterilized test tubes containing EDTA as anti-coagulant. Samples were processed for separation of plasma and preparation of red cell suspensions and hemolysates, following standard methods. ABO, Rh D and ABH blood groupings of the red cells were done serologically by the tile method using antisera anti-A,-B,-D,-A1 and anti-H. For ABH studies saliva samples collected by means of cotton swabs from the subjects were tested by inhibition method. Haemolysates were used to analyzed for red cell enzymes namely, ACP1, ESD, LDH, MDH, 6PGD, G6PD and SOD by horizontal starch gel electrophoresis using the methods described by Harris and Hopkinson (1976) [6]. While GLO-I were typed on starch-agarose gel electrophoresis following the method of Pflugshaupt et al. (1978) [7]. The plasma protein markers were analyzed for GC, HP, TF, ALB and CP. The samples were typed using standard electrophoresis in acrylamide gels for GC, TF and ALB systems [8]. and for HP and CP systems [9]. The lysates were screened for abnormal HB on cellulose acetate membrane electrophoresis described by Kate et al. (1976) [10]. Allele frequencies were calculated after Mourant et al. (1976) [11] and goodness of fit between the observed and expected phenotype frequencies are tested according to Taylor and Prior (1938) [12]. Chi-square tests were performed to assess significance of deviations from Hardy-Weinberg equilibrium proportions.

RESULTS

Distribution of phenotypes and allele frequencies of blood groups, red cell enzymes, haemoglobins and plasma proteins in both the sub types of Salis are presented in Tables 1 and 2 respectively.

In the ABO system, blood group O predominated in both the sub-groups of Salis with highest frequency (Padmasalis, 49%; Pattusalis,

41%), followed by group B, which showed variation between the two groups (Padmasalis, 24%; Pattusalis, 40%). With regards to sub-types of A group, the frequency of A_1 is higher (Padmasalis: 19%; Pattusalis: 14%) than that of A_2 which recorded just 5% in Padmasalis and 2% in Pattusalis. The frequency of Rh(D) negative blood group is only 3% in Padmasalis, and completely absent in Pattusalis. The incidence of non-secretors registered higher values in Pattusalis 56% followed by Padmasalis who recorded 40%.

Considering Red cell enzymes, the interesting feature in the present study is that the 6PGD enzyme was found to be polymorphic only in Pattusalis which recorded 10% AC phenotypes, while in Padmasalis AC Phenotype was completely absent, the 6 PGD enzyme being monomorphic. The Padmasalis recorded 7.1% G6PD deficiency while Pattusalis registered 1.7% deficiency only. The phenotype ESD*1 is more predominant in both the sub-groups. (Padmasalis :59%; Pattusalis: 62%). In GLO1 enzyme system, the phenotype 2-1 is predominant in both the sub-groups recording 55% in Padmasalis and 51% in Pattusalis. In the present study four phenotypes (A, B, AB and BC) of ACP_1 are observed. It is found that the phenotype B recorded the highest frequency in both Padmasalis (64%) and Pattusalis (83%). The electrophoretic separation for red cell enzymes Superoxide Dismutase, Lactate Dehydrogenase and Malate Dehydrogenase among Padmasalis and Pattusalis reveals the presence of normal SOD 1-1, LDH Normal and MDH 1-1 phenotypes in both the sub groups. The alleles SOD*1, LDH*N and MDH*1-1 were monomorphic. The HB A allele was monomorphic in Padmasalis whereas, polymorphic in Pattusalis (98%). The HB S allele is completely absent in Padmasalis but attained polymorphic frequency in Pattusalis (1.9%).

With regards to the plasma proteins, in GC system, all the three phenotypes (1-1, 2-1, & 2-2) were observed in the present study. The 1-1 phenotypes are found to be the highest, recording 63% in Padmasalis and 66% in Pattusalis. Considering gene frequencies, in the pooled data GC*1 recorded (78%) and GC*2 (22%). The HP system is polymorphic. A higher number of 2-2 phenotype is observed in Padmasalis (62%) and Pattusalis (79%) than 2-1 phenotype. 1-1 phenotype is virtually absent in both the sub groups. Interestingly in this study, apart from TF*C phenotype (98%), CD phenotype is observed in Pattusalis. All samples tested for albumin among both the sub-groups of Salis exhibited the normal phenotype ALB Normal.

Table 1: Phenotype distribution of genetic markers in Salis

System	Genetic Marker	Phenotype	Number Observed (%)		Salis (Pooled)
			Padmasalis	Pattusalis	
Blood Groups	ABO	A_1	19 (19.0)	14 (14.0)	33 (33.0)
		A_2	5 (5.0)	2 (2.0)	7 (7.0)
		B	24 (24.0)	40 (40.0)	64 (64.0)
		A_1B	3 (3.0)	2 (2.0)	5 (5.0)
		A_2B	0 (0.0)	1 (1.0)	1 (1.0)
		O	49 (49.0)	41 (41.0)	90 (90.0)
	Rh (D)	D+	97 (97.0)	100 (100.0)	197 (197.0)
		D-	3 (3.0)	0 (0.0)	3 (3.0)
	ABH	Se	60 (60.0)	44 (44.0)	104 (104.0)
		se	40 (40.0)	56 (56.0)	96 (96.0)
Red Cell Enzymes	6PGD	A	105 (100.0)	95 (90.5)	200 (95.2)
		AC	0 (0.0)	10 (9.5)	10 (4.8)
		C	0 (0.0)	0 (0.0)	0 (0.0)
	G6PD	Normal	65 (92.8)	59 (98.3)	124 (95.4)
		Deficient	5 (7.1)	1 (1.7)	6 (4.6)
	ESD	1-1	62 (59.0)	65 (61.9)	127 (60.5)
		2-1	37 (35.2)	35 (33.3)	72 (34.3)
		2-2	6 (5.7)	5 (4.8)	11 (5.2)
	GLO	1-1	20 (19.0)	26 (24.8)	46 (21.9)
		2-1	58 (55.2)	54 (51.4)	112 (53.3)
		2-2	27 (25.7)	25 (23.8)	52 (24.8)
	ACP_1	A	8 (7.6)	4 (3.8)	12 (5.7)
		AB	25 (23.8)	16 (15.2)	41 (19.5)
		BB	64 (61.0)	83 (79.0)	147 (70.0)
		BC	8 (7.6)	2 (1.9)	10 (4.8)
		CC	0 (0.0)	0 (0.0)	0 (0.0)
	SOD	1	105 (100.0)	105 (100.0)	210 (100.0)
	LDH	N	105 (100.0)	105 (100.0)	210 (100.0)
	MDH	1	105 (100.0)	105 (100.0)	210 (100.0)
HB	HB	A	105 (100.0)	103 (98.1)	208 (99.0)
		AS	0 (0.0)	2 (1.9)	2 (1.0)
		S	0 (0.0)	0 (0.0)	0 (0.0)
Plasma Proteins	GC	1-1	63 (60.0)	66 (62.9)	129 (61.4)
		2-1	35 (33.3)	33 (31.4)	68 (32.4)
		2-2	7 (6.7)	6 (5.7)	13 (6.2)
	HP	1-1	0 (0.0)	0 (0.0)	0 (0.0)
		2-1	43 (41.0)	26 (24.8)	69 (32.9)
		2-2	62 (59.0)	79 (75.2)	141 (67.1)
	CP	B	105 (100.0)	105 (100.0)	210 (100.0)
	TF	C	105 (100.0)	103 (98.1)	208 (99.0)
		CD	0 (0.0)	2 (1.9)	2 (1.0)
	ALB	N	105 (100.0)	105 (100.0)	210 (100.0)

Table 2: Allele frequencies of genetic markers in Salis

Locus	Allele	Allele Frequency		Salis (Pooled)
		Padmasalis	Pattusalis	
ABO	ABO*A1	0.1175	0.0841	0.0932
	ABO*A2	0.0288	0.0166	0.0210
	ABO*B	01462	0.2474	0.3260
	ABO*O	0.7075	0.6519	0.5598
Rh (D)	D	0.8268	1.0000	0.8775
	d	0.1732	0.0000	0.1225
ABH	Se	0.3675	0.2517	0.3519
	se	0.6325	0.7483	0.6481
6PGD	6PGD*A	1.0000	0.9550	0.9750
	6PGD*C	0.0000	0.0450	0.0250
ESD	ESD*1	0.7650	0.7950	0.7800
	ESD*2	0.2350	0.2050	0.2200
GLO	GLO*1	0.4650	0.5050	0.4850
	GLO*2	0.5350	0.4950	0.5150
ACP_1	ACP*A	0.2000	0.1150	0.1550
	ACP*B	0.7600	0.8750	0.7950
	ACP*C	0.0400	0.0100	0.0250
LDH	LDH*N	1.0000	1.0000	1.0000
MDH	MDH*1	1.0000	1.0000	1.0000
SOD	SOD*1	1.0000	1.0000	1.0000
HB	HB*A	1.0000	0.9900	0.9950
	HB*S	0.0000	0.0100	0.0050
GC	GC*1	0.7650	0.7800	0.7800
	GC*2	0.2350	0.2200	0.2200
HP	HP*1	0.2050	0.1200	0.1650
	HP*2	0.7950	0.8800	0.8350
TF	TF*C	1.0000	0.9900	0.9950
	TF*D	0.0000	0.0100	0.0050
CP	CP*B	1.0000	1.0000	1.0000
ALB	ALB*N	1.0000	1.0000	1.0000

Table 3 predicts the statistical significant differences in individual as well as overall allele frequencies of the 12 red cell genetic systems considered in this study. The Chi-square test for heterogeneity in Salis was found to be significant with respect to ABH (5.13; d.f.=1; 0.05>p>0.01), ACP_1 system (9.36; d.f = 3; 0.05>p>0.01), 6PGD (10.50;

d.f.=2; p>0.001) and HP (6.24; d.f.=1; 0.05>p>0.01) systems.

Table 3: Chi-square analysis of allele frequency of Genetic Markers in Salis

Locus	χ^2	d.f.	Significance
ABO	7.95	5	0.20>p>0.10
Rh(D)	3.05	1	0.10>p>0.05
ABH	5.13*	1	0.05>p>0.01
ESD	0.22	2	090>p>0.80
GLO1	1.00	2	0.70>p>0.50
ACP_1	9.36**	3	0.05>p>0.01
6PGD	10.50***	2	p>0.001
G6PD	2.20	1	0.20>p>0.10
HB	2.02	1	0.20>p>0.10
HP	6.24**	1	0.05>p>0.01
GC	0.21	2	0.90>p>0.80
TF	2.02	1	0.20>p>0.10

*p<0.05, **p<0.01, ***p<0.001

DISCUSSION

In order to investigate genetic composition of Sali population, the allele frequencies of 16 genetic traits were calculated and compared with those of other populations of Andhra Pradesh.

ABO blood groups:

The present study comprises of analysis of ABO and Rh(D) blood group systems among the Sali community. In India, the distribution of allele ABO*B frequency is higher (0.233) as compared to allele ABO*A (0.186), whereas the frequency of allele ABO*O is 0.581. This study when compared with different populations in Andhra Pradesh, wide variation is observed with regard to gene frequencies of A, B and O. Gene frequency of A ranges from 0.0098 among Kalinga Vysyas [13] to 0.2373 among Brahmins-I [14]. The present frequency values of 0.1175 in Padmasalis and 0.0841 in Pattusalis fall within this range. The 'B' allele frequency is found to be highest in Mala-I (0.3050) [15] and the least in Kalingas (0.1244) [16]. The lowest frequency of 'O' allele is recorded in Brahmin-I (0.4995) [14] and highest in Golla-I (0.7950) [17]. The frequency of 'O' gene in the two sub-groups of Salis fall within this range.

Rh(D)

Among Indian populations the frequency of allele RH*D averages around 0.803 (varies from 0.532 to 1.000). The present data is compared with that of the castes of Andhra Pradesh. The D allele frequency ranges from 0% in Rellis-I [18] and Brahmin II [19] to 35.23% in Kamma I [19].

ABH Saliva Secretion

The secretor and non-secretor gene frequencies in few Hindu Caste populations of Andhra Pradesh exhibits the non-secretor allele frequency (Se) which ranges from 43.26% in Rellis [18] to 49.73% in Reddis [20]. The Padmasalis and Pattusalis recorded much higher values than all the other population for the non-sector allele (74.83 and 63.25 respectively).

6-Phosphogluconate dehydrogenase (6PGD)

The oxidative decarboxylation of 6-phosphogluconate to ribulose-5-phosphate in the hexosemonophosphate (HMP) shunt is catalysed by the enzyme 6-phosphogluconate dehydrogenase (6PGD). The frequency of allele PGD*A among Indian population varies from 0.754 to 1.000. The 6PGD*C allele in Andhra Pradesh population ranges from 0% in Thrivarnika [21] to 2.94% in both Relli [18] and Brahmin [22]. The interesting feature regarding the 6 PGD*C allele is that, the Pattusalis recorded 5%, the highest ever for any caste in Andhra Pradesh, while the Padmasalis recorded 0%, similar to that of Thrivarnikas.

Glucose-6-Phosphate Dehydrogenase (G6PD)

Glucose-6-phosphate dehydrogenase (G6PD) enzyme is necessary as a catalyst in a biological oxidation-reduction reaction of glucose-6-phosphate--one of the stages in the metabolism of carbohydrates. So far seven different G-6-PD variants namely - G6PD* Andhra Pradesh [23], G6PD*Cutch [24], G6PD* Jammu [25], G6PD* Kalayan [26], G6PD*Kerala [27], G6PD*Porbandar [28] [24] and G6PD*West Bengal [27] have been reported from India. In Andhra Pradesh, the percentage of deficiency ranges from 0% in populations like Arya Vysya, Thrivarnika, Reddy [21], Brahmin II [29], Kamma II, Kurma, Padmasali, Vanjara, Yadava [30] and Vysya I [31] to a highest value of 8.16% in Kalinga Vysya [21]. The present study values fall within this range. Interestingly, we noted that the Padmasalis recorded a higher value of G6PD deficiency than the Pattusalis.

Lactate Dehydrogenase (LDH)

This enzyme exists in three different types: LDH A, LDH B and LDH C. It is present in all tissues and catalyzes the transformation of pyruvate into lactate. So far four kinds of LDH variants, namely LDH Cal-1, Cal-2, LDH Mad-1 and LDH Del -1 have been reported in Indian populations. The Cal-1 is a faster sub-unit variant discovered in Calcutta [32]. The other variants like Cal-2, LDH Mad-1 and LDH Del-1 are not polymorphic in Indian populations. All the castes of Andhra Pradesh are monomorphic for LDH system so far, similar to the present study population Salis.

Malate Dehydrogenase (MDH)

The red cell enzyme MDH exhibits only MDH-1 phenotype among all the samples of the two subgroups of Salis investigated. Earlier, three electrophoretic variants have been reported in Indian populations. Das et al. [33] found MDH 2-1 variant in chamars, a low caste population of India. So far, all the castes of Andhra Pradesh are monomorphic for MDH system.

Esterase D (ESD)

Of the four biochemically and genetically different esterases known in human red cells-A, B, C [34][35] and D [36], only the latter (ESD) has been found to exhibit a genetic polymorphism in man. In populations of India, the frequency of ESD*1 allele is 0.729 (varies from 0.418 to 0.978). The frequency is high in North India (0.775) followed by West, Central, South and East India and is quite low from Islands (0.565). A review of the distribution of ESD system among Andhra Pradesh populations reveals that only two alleles ESD*1 and ESD*2 are present. Rare variants at ESD such as 3-1 (ESD*3) among Konda Kapu [37] have been reported for tribal populations of Andhra Pradesh. The least frequency recorded for ESD*2 allele was in Kamma (0.2190) [30], and the highest was in Arya Vysya (0.5161) [21]. The present study population values fall within the above range.

Glyoxalase I (GLO1)

The GLO *1 allele ranges between 15.5% in Pardhi [38] and 47.8% in Arya Vysya [21]. The values of Padmasalis fall with in this range. But that of Pattusalis, fall out of this range (50%), being the highest reported from caste populations of Andhra Pradesh No rare variants were encountered so far from Andhra Pradesh.

Red cell acid Phosphatase (ACP_1)

Acid phosphatase is a phosphohydrolase and phosphotransferase but the exact functional role of the enzyme is unknown. Five different phenotypes could be seen after starch gel electrophoresis, referred to as ACP1 A, ACP1 BA, ACP1 B, ACP1 CA and ACP1 CB. The frequency of allele ACP1*B is higher (0.756) than ACP1*A (0.242) whereas ACP1*C occurs in very low frequency (0.002) in India. The frequency of ACP_1*B allele in Andhra Pradesh castes ranges from 57% in Trivarnikas, [21] to 87.6% in Kamma II [30]. It is interesting to note that in the ACP_1*B allele reported in Padmasalis of the present study fall within this range. But in Pattusalis it recorded 87.50%, which happens to be the highest reported among castes of Andhra Pradesh. ACP1*C allele is still rare, but an unusual high incidence (6.15%) was reported in one study from Andhra Pradesh [39]. It is worth mentioning here that the ACP1*C allele is either completely absent or records very low frequencies among Indian populations. ACP_1*B allele is found to be the most frequent in both the subgroups

of Salis. ACP_1*C allele is present in both the sub-groups of Salis yet, polymorphic in Padmasalis and idiomorphic in Pattusalis.

Superoxide Dismutase (SOD)

This enzyme is existing in two molecular types: SOD A and SOD B. The biological function of this enzyme can be seen in its ability to protect the organisms from free radicals. In India many populations from nearly all regions of the country have been typed for the SOD system. With the exception of one small group (Vania Soni, Surat, Gujarat, n=82), in which one variant has been observed, all the others showed the phenotype SOD A1-phenotype, so that one can say, that the SOD A*1 allele is also typical for the populations of India, irrespective of their ethnic or regional origin [40]. In almost all the caste populations, the SOD*1 allele is monomorphic. But interestingly an extremely rare superoxide dismutase phenotypes (SOD*2) have been reported from Andhra Pradesh [41].

Hemoglobin (HB)

The general incidence of haemoglobin variants has been observed about 0.5 per cent from the Indian region. The abnormal haemoglobins observed among various population groups are HBS, HB E and HB D. Most of the caste populations are monomorphic for HB*A allele. Among the populations which exhibited polymorphism, Paidi recorded highest value (25%) for HB*S allele [42] and the least was found in Madiga II (0.2%) [43]. The population of Pattusalis falls in this range. Thus, the HB*S allele in general is abscent or present in low frequencies in caste populations of this state.

Group Specific Component (GC)

The frequency of allele GC*1 is observed 0.747 among population groups of India (ranges from 0.591 to 0.911). A wide range of variation is not observed in between the various ethnic groups i.e., 0.733 (caste) to 0.760 (scheduled tribe) and in zones its frequency is high in West India (0.776) and low in North India (0.723). Very few studies were reported on GC system among castes of Andhra Pradesh. The GC*2 allele ranges between 19.46% in Relli [18] and 23.30% in Mala [44]. Both the subgroups of the present study fall within this range.

Haptoglobins (HP)

The frequency of HP*1 is 0.160 in population groups of India (varies from nil to 0.406); the high frequency of this allele is observed in North India (0.208) and low frequency in South India (0.131). HP*2 allele in Andhra caste populations ranges from 74.75% in Kalinga Vysya [21] to 92.4% in Kamma III [30]. It is to say that the HP*2 allele in both Padmsalis and Pattusalis falls within this range. HP*O phenotype was observed sporadically in some caste populations of Andhra Pradesh. No such phenotype has been found in the present study population. Most of the caste populations are monomorphic for HB*A allele. Among the populations which exhibited polymorphism, Paidi recorded highest value (25%) for HB*S allele [42] and the least was found in Madiga II (0.2%) [43] . The population of Pattusalis falls in this range. Thus, the HB*S allele is generally absent or present in low frequencies in caste populations of this state.

Transferrin (TF)

Transferrin is an iron binding protein present in plasma. Among Indians, the transferrin allele found in most individuals is TF*C while TF*D and TF*D alleles are present in quite low frequencies (0.008 and 0.001, respectively). The TF variants are reported in most of the caste populations of Andhra Pradesh. Interestingly Rao et al. [45] reported TF*B Goldsmith variant in Goldsmith populations of Telangana region of Andhra Pradesh. TF*C allele in Andhra Pradesh castes ranges from 89.77% in Mala II [44] to 100%. Both the rare alleles TF*B and TF*D are reported in some populations of Andhra Pradesh. In the present study TF*D allele recorded 1%. The highest frequency recorded in castes of Andhra Pradesh was 10.20% in Mala II [44].

Albumin (ALB)

Albumin functions primarily as a carrier protein for steroids, fatty acids, and thyroid hormones and plays a role in stabilizing extracellular fluid volume. All the castes of Andhra Pradesh are monomorphic for the Albumin system (ALB*N) except for a slow-moving variant reported in Bramin IV by Char et al. [46].

Ceruloplasmin (CP)

This protein belongs to the α2-fraction of the human serum. It is synthesized in the liver and plays obviously an important role concerning the transport and metabolism of the copper. The electrophoretically detectable polymorphism consists of six different phenotypes, which are controlled by three autosomal co-dominant alleles: CP*A, CP*B and CP*C. From the present studies it is evident, that the CP*B allele is the most frequent one in all so far tested populations of India, whereas the CP*C allele is everywhere either completely absent or very infrequent. Caeruloplasmin is found to be monomorphic (CP*B) among all the castes of Andhra Pradesh.

CONCLUSION

To summarize, the genetic variation in the distribution of these polymorphic loci was in accordance with the data available for local populations of Andhra Pradesh. The Sali community falls well in the middle of the other castes. Several studies have been made among tribal and caste populations to understand their affinities and phylogeny. Each of these populations is endogamous from times immemorial and genetic admixture is less possible. Hence, a comprehensive understanding using more polymorphic loci is required to explore the evolution of huge number of endogamous populations from this geographical area especially from India. Gap filling tests on selected populations would make it possible to use the existing observations much more efficient in working out the population structure.

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