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STUDY OF ENZYME POLYMORPHISM AND HAEMOGLOBIN PATTERNS AMONGST SIXTEEN TRIBAL POPULATIONS OF CENTRAL INDIA (ORISSA, MADHYA PRADESH, AND MAHARASHTRA)

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Summary A survey was conducted to study the genetic differentiation among 16 tribal groups of Orissa, Madhya Pradesh, and Maharashtra belonging to different ethnic and linguistic affiliations. Sixteen hundred and fifteen blood samples from both sexes were tested for 5 red cell enzyme systems: ACP, ESD, PGD, GLO, LDH, and Hb pattern. Three hundred and nineteen male individuals were tested for G-6-PD enzyme deficiency. The distribution of the enzyme markers and Hb show a range of variation which are more or less within the Indian range. Cases of homozygous HbSS were detected in all the tribes except 3 tribes in Orissa. Two cases of LDH Cal-1 homozygote were found in two Dravidian language speaking Orissa tribes. The χ^2-values for testing the homogeneity of gene frequencies indicate a non-significant heterogeneity for all alleles in the individual system. Within population diversity seems to be larger than between population diversity. The degree of over all genetic differentiation as measured by G_{ST} value is 0.0154 ± 0.0071.

Key Words genetic polymorphism, tribal groups, Central India, red cell enzymes, haemoglobin, gene diversity

INTRODUCTION

The Indian subcontinent comprises about 40,000 endogamous population groups including 427 tribal groups. The tribal groups numbering about 51,628,638

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individual constitute 7.76% of the total population of India (Census of India, 1971). Their population size ranges from very small (Toda, Toto, Andamanese, Onges) to very large (Santal, Bhil, Gond, *etc.*) groups. In fact, some of the small tribes are likely to become extinct. These tribal groups are quite heterogeneous in respect of their origin, relegion, cultural practices, and linguistic affiliation, and they are found in almost all parts of India having a high concentration in Central India. Among these tribes numerically most dominating are the Gond in Medhya Pradesh, Maharashtra, and Andhra Pradesh; the Bhills of Maharashtra, Madhya Pradesh, Gujrat, and Rajasthan; and the Santal of Bihar, Orissa, and West Bengal. According to morphological and somatoscopic characters the tribes of India can be broadly classified into three ethnic types as Mongoloid, Proto-Australoid, and Europoid. The Mongoloids are mainly found in the northern and north-eastern Himalayas and speak language of the Tibeto-Chinese language family. The Proto-Australoids are mainly concentrated in the hills and plateaus of Central India and the Indo-Gangetic plains, as well as in some parts of Southern and Northern India. Linguistically, they belong to Austro-Asiatic, Dravidian, and Indo-European language families. The south western Indian tribes speak mostly Dravidian languages (Mukherjee, 1984).

The tribes are in various stages of development with primitive means of livelihood like hunting and food gathering to advanced and modern one. Most of the tribes follow rigid endogamy including various types of consanguinity practices. The tribes show so much diversities in their physical make-up, language, social and cultural practices *etc.*, that it would be interesting to study the ongoing genetic differentiation amongst them. Biochemical genetic markers are very useful in the study of the processes of the genetic differentiation within and among them as well as to the understanding of microevolutionary process in Man. Not much informations on the distribution of genetic markers in the Indian tribes are available, particularly in the Central India belt (Walter *et al.*, 1992). A project was therefore undertaken to study various biochemical polymorphisms in 16 tribal groups of three states namely, Orissa, Madhya Pradesh, and Maharashtra of Central India, belonging to different ethnic socio-cultural and linguistic affiliation with the following aims and objects; (1) to find out the allele distribution of five red cell enzyme markers as well as the haemoglobin types, (2) to analyse the genetic diversity within and between the 16 tribes, and (3) to study the extent of genetic relationship between them. The ethnological descriptions and the geographical location of the 16 tribal groups understudy are given elsewhere (Walter *et al.*, 1992).

MATERIALS AND METHODS

Villages in several districts of three states (Orissa, Madhya Pradesh, and Maharashtra) were chosen for the study of 16 tribal population, namely, (1) Desia Khonds, (2) Raj Gonds (Orissa), (3) Savaras, (4) Gadabas (Bade), (5) Konda Doras,

(6) Kuvi Khonds, (7) Parojas (Jhoria), (8) Binjhals, (9) Kisans, (10) Bhatras, (11) Dhurwas, (12) Halbas, (13) Marias (Dandami), (14) Murias, (15) Maria Gonds, and (16) Raj Gonds (Maharashtra). Relevant demographic and linguistic data location *etc.* of each tribe are given in the Table 1 including the number of individuals studied. Six red cell enzyme systems and haemoglobin types were studied: (1) Acid phosphatase (ACP), (2) esterase-D (ESD), (3) 6-phosphogluconate dehydrogenase (PGD), (4) glyoxalase (GLO), (5) lactate dehydrogenase (LDH), (6) G-6-PD deficiency, and (7) haemoglobin types (Hb). Sixteen hundred and fifteen blood samples were collected from the individuals of both sexes of the 16 tribal groups from finger tips in the field during January to March 1989. Separation of blood cells and serum were done in the field and transported by air in ice box to the Anthropometry and Human Genetics Unit of the Indian Statistical Institute, Calcutta, where the screening for enzyme polymorphism were performed. The red cell isozymes were determined following the techniques of Swallow *et al.* (1973) for ACP; Fields and Parr (1963) for PGD; Kompf *et al.* (1975) for GLO-I; Das *et al.* (1972) for LDH; and

Table 1. The names, geographical location, population size, and linguistic affiliation of the 16 tribes studied from Central India together with number of individuals studied from each tribe.

State	District	Population	No. of population in the district (Census, 1971)	No. of individuals studied	Linguistic group	Sub-group
Orissa	Kalahandi	1. Deshia Khonds	114,644	110	Dravidian	Kui
		2. Raj Gonds	123,778	107	Dravidian	Gondi
		3. Savaras	4,148	107	Austro-Asiatic	—
	Koraput	4. Gadabas	46,237	104	Austro-Asiatic	—
		5. Konda Doras	8,129	95	Dravidian	Kui
		6. Kuvi Khonds	325,144	100	Dravidian	Kui
		7. Parojas	193,736	104	Dravidian	Parji
	Sambalpur	8. Binjhals	50,280	104	Indo-Aryan	—
		9. Kisans	87,792	108	Dravidian	—
Madhya Pradesh	Bastar	10. Bhatras	71,095	105	Indo-European	Bhatri
		11. Dhurwas*	—	86	Dravidian	Gondi
		12. Halbas	57,052	97	Indo-European	Halbi
		13. Marias*	—	103	Dravidian	Gondi
		14. Murias*	—	99	Dravidian	Gondi
Maharashtra	Chandrapur	15. Maria Gonds	203,905	116	Dravidian	Gondi
		16. Raj Gonds	—	106	Dravidian	Gondi

* Gond group, total no. of population 858,654.

Hopkinson *et al.* (1973) for ESD. Detailed of these techniques are mentioned in Harris and Hopkinson (1976). The G-6-PD deficiency tests were performed in the field itself within a few hours of collection by using brilliant crystal blue dye (BCB) following Motulsky and Campbell-Kraut (1961). The Hb screening was done by cellogel electrophoresis using TEB buffer at pH 8.6 and compared with control samples. All tribes as well as individuals could not be tested for GLO and G-6-PD deficiency due to lack of resources.

RESULTS AND DISCUSSION

The results of the phenotypic distribution with the Hardy-Weinberg χ^2-values and allele frequencies with s.e. of the different markers studied are given in Tables 2–8.

The distribution

ACP. Genetic polymorphism of red cell enzyme acid phosphatase[1] (ACP) is well known. Table 2 gives the phenotypic and allele frequencies of ACP and it appears that there is genetic equilibrium for all tribal groups except the Raj Gond

Table 2. ACP phenotype frequencies, allele frequencies, and χ^2-test for Hardy-Weinberg equilibrium.

Population (Sample size)	Pheno-type	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Orissa	A	5	5.5		
Deshia Khonds	AB	36	35.0	$p^a=0.2455$	
(n=110)	B	55	55.5	$p^b=0.7545$	0.499
Raj Gonds	A	6	4.4		
(n=101)	AB	30	33.3	$p^a=0.2079$	
	B	65	63.4	$p^b=0.7921$	0.974
Savaras	A	5	5.4		
(n=107)	AB	38	37.2	$p^a=0.2243$	
	B	64	64.4	$p^b=0.7757$	0.045
Gadabas	A	4	3.3		
(n=104)	AB	29	30.4	$p^a=0.1779$	
	B	71	70.3	$p^b=0.8221$	0.226
Konda Doras	A	3	2.2		
(n=98)	AB	22	23.6	$p^a=0.1573$	
	B	64	63.2	$p^b=0.8427$	0.407
Kuvi Khonds	A	6	4.7		
(n=103)	AB	32	34.6	$p^a=0.2136$	
	B	65	63.7	$p^b=0.7864$	0.582
Parojas	A	5	4.6		
(n=91)	AB	31	31.8	$p^a=0.2253$	
	B	55	54.6	$p^b=0.7746$	0.053

Continued

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Binjhals	A	7	6.7		
(n=97)	AB	37	37.6	$p^a=0.2629$	
	B	53	52.7	$p^b=0.7371$	0.024
Kisans	A	4	3.6		
(n=106)	AB	31	31.8	$p^a=0.1840$	
	B	71	70.6	$p^b=0.8160$	0.071
Mahdya Pradesh					
Bhatras	A	6	4.4		
(n=104)	AB	31	34.1	$p^a=0.2067$	
	B	67	65.5	$p^b=0.7933$	0.865
Dhurwas	A	4	3.3		
(n=78)	AB	24	25.4	$p^a=0.2051$	
	B	50	49.3	$p^b=0.7949$	0.249
Halbas	A	5	5.5		
(n=96)	AB	36	35.0	$p^a=0.2396$	
	B	55	55.5	$p^b=0.7604$	0.082
Marias	A	4	4.5		
(n=101)	AB	36	34.4	$p^a=0.2178$	
	B	61	61.8	$p^b=0.7822$	0.214
Murias	A	7	6.0		
(n=105)	AB	36	38.1	$p^a=0.2381$	
	B	62	60.9	$p^b=0.7619$	0.318
Maharashtra					
Maria Gonds	A	4	6.6		
(n=115)	AB	47	41.9	$p^a=0.2391$	
	B	65	66.6	$p^b=0.7609$	1.743
Raj Gonds	A	13	8.9		
(n=105)	AB	35	43.3	$p^a=0.2905$	
	B	57	52.9	$p^b=0.7095$	3.844*

* Significant at 5 per cent level.

of Maharashtra. The tribes here show a wide range of variation, the highest frequency for p^b allele (0.8427) is found in the Konda Dora of Orissa, and lowest in the Raj Gond of Maharashtra (0.7095). There is no consistent trend of increase or decrease of p^b allele frequency across the geographic distances among these tribes but the p^b is found to be elevated among few tribes of Kalahandi, Koraput, and Bastar districts. These allele frequencies are in accordance with the frequencies observed in the earlier studies in the tribes of Orissa (Papiha *et al.*, 1988), Madhya Pradesh (Papiha *et al.*, 1978), and Maharashtra (Mukherjee *et al.*, 1979).

ESD. Out of all the esterases known in Man only the esterase D (ESD) shows

Table 3. ESD phenotype frequencies, allele frequencies, and χ^2-test for Hardy-Weinberg equilibrium.

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Orissa					
Deshia Khonds	1	44	42.4		
(n=109)	2-1	48	51.2	ESD^1=0.6239	
	2	17	15.4	ESD^2=0.3716	0.415
Raj Gonds	1	45	44.9		
(n=103)	2-1	46	46.2	ESD^1=0.6602	
	2	12	11.9	ESD^2=0.3398	0.002
Savaras	1	40	41.9		
(n=107)	2-1	54	50.1	ESD^1=0.6262	
	2	13	14.9	ESD^2=0.3738	0.651
Gadabas	1	45	48.9		
(n=103)	2-1	52	44.1	ESD^1=0.6893	
	2	6	9.9	ESD^2=0.3107	3.289
Konda Doras	1	42	41.6		
(n=91)	2-1	39	39.9	ESD^1=0.6758	
	2	10	9.6	ESD^2=0.3242	0.044
Kuvi Khonds	1	44	44.5		
(n=98)	2-1	44	43.1	ESD^1=0.6735	
	2	10	10.4	ESD^2=0.3265	0.043
Parojas	1	31	32.2		
(n=89)	2-1	45	42.7	ESD^1=0.6011	
	2	13	14.2	ESD^2=0.3989	0.263
Binjhals	1	35	39.1		
(n=100)	2-1	55	46.9	ESD^1=0.6250	
	2	10	14.1	ESD^2=0.3750	3.004
Kisans	1	42	41.8		
(n=109)	2-1	51	51.4	ESD^1=0.6193	
	2	16	15.8	ESD^2=0.3807	0.007
Madhya Pradesh					
Bhatras	1	42	42.5		
(n=104)	2-1	49	48.0	ESD^1=0.6394	
	2	13	13.5	ESD^2=0.3606	0.049
Dhurwas	1	39	37.0		
(n=76)	2-1	28	32.1	ESD^1=0.6974	
	2	9	7.0	ESD^2=0.3026	1.299
Halbas	1	53	51.8		
(n=96)	2-1	35	37.5	ESD^1=0.7344	
	2	8	6.8	ESD^2=0.2656	0.412

Continued

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Marias	1	59	57.4		
(n=102)	2-1	35	38.2	ESD^1=0.7500	
	2	8	6.4	ESD^2=0.2500	0.736
Murias	1	43	44.2		
(n=103)	2-1	49	46.5	ESD^1=0.6553	
	2	11	12.2	ESD^2=0.3447	0.290
Maharashtra					
Maria Gonds	1	46	46.8		
(n=93)	2-1	40	38.3	ESD^1=0.7097	
	2	7	7.8	ESD^2=0.2903	0.178
Raj Gonds	1	56	54.8		
(n=96)	2-1	33	35.5	ESD^1=0.7552	
	2	7	5.8	ESD^2=0.2448	0.474

polymorphism on the basis on two common alleles ESD^1 and ESD^2, besides a few rare alleles. The tribes understudy show a complete agreement with the Hardy-Weinberg equilibrium except among two tribes the Gadaba and the Binjhal where homozygotes exceed in number, and three common phenotypes 1-1, 2-1, 2-2 are present. Table 3 shows a variation in allele frequencies. The ESD^2 allele frequency ranges between 0.2448 in the Raj Gond of Maharashtra and 0.3989 in the Paroja of Orissa. The present allele frequencies of ESD^2 remain within the range of reported allele frequencies among Indian tribes which show a wide range of variation, that is lowest ESD^2 (0.022) among the Gaddi Rajput of Himachal Pradesh (Singh *et al.*, 1982) and a highest (0.475) is in the Kolam of Andhra Pradesh (Ramesh *et al.*, 1979). In general, there has been a gradual decline of ESD^2 allele from east to west direction except for a few transient elevation among the Bhatra of Bastar and among the Paroja of Koraput districts.

PGD. 6-Phosphogluconate dehydrogenase (6-PGD) shows usually three phenotypes controlled by two alleles PGD^A and PGD^C. In regard to *PGD* alleles genetic equilibrium has been observed among almost all the tribes (Table 4). In a few cases when significant χ^2-values have been obtained it seems not to be much meaningful because of small number of *PGDc* allele. Out of the 16 tribes studied the PGD^A appears to be monomorphic in three tribes namely Deshia Khonds, Konda Doras, and Kisans of Orissa and in rest of the populations both PGD^A and PGD^C are present, having maximum PGD^C frequency in the Bhatra (0.160) of Bastar of Madhya Pradesh. Highest frequency of PGD^C was reported among the Kadar (0.167) of Tamilnadu (Saha *et al.*, 1974), and in many of the other tribes this allele is found to be absent. The PGD^A allele frequency remains to be more or less similar

Table 4. PGD phenotype frequencies, allele frequencies, and χ^2-test for Hardy-Weinberg equilibrium.

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Orissa					
Deshia Khonds	A	108	108.0		
(n=108)	AC	—	—	PGD^A=1.0000	
	C	—	—	PGD^C= —	—
Raj Gonds	A	98	98.0		
(n=99)	AC	1	1.0	PGD^A=0.9949	
	C	—	0.1	PGD^C=0.0051	—
Savaras	A	104	104.0		
(n=105)	AC	1	1.0	PGD^A=0.9952	
	C	—	0.1	PGD^C=0.0048	—
Gadabas	A	102	102.0		
(n=104)	AC	2	2.0	PGD^A=0.9904	
	C	—	0.1	PGD^C=0.0096	—
Konda Doras	A	85	85.0		
(n=85)	AC	—	—	PGD^A=1.0000	
	C	—	—	PGD^C= —	—
Kuvi Khonds	A	100	99.0		
(n=102)	AC	1	3.0	PGD^A=0.9853	
	C	1	0.1	PGD^C=0.0147	
Parojas	A	90	90.0		
(n=92)	AC	2	2.0	PGD^A=0.9891	
	C	—	0.1	FGD^C=0.1009	—
Binjhals	A	86	86.2		
(n=94)	AC	8	7.7	PGD^A=0.9574	
	C	—	0.2	PGD^C=0.0426	0.186
Kisans	A	106	106.0		
(n=106)	AC	—	—	PGD^A=1.0000	
	C	—	—	PGD^C= —	—
Madhya Pradesh					
Bhatras	A	66	66.5		
(n=97)	AC	31	26.1	PGD^A=0.8402	
	C	—	2.5	PGD^C=0.1598	3.508
Dhurwas	A	72	72.1		
(n=78)	AC	6	5.8	PGD^A=0.9615	
	C	—	0.1	PGD^C=0.0385	0.125
Halbas	A	74	74.0		
(n=75)	AC	1	1.0	PGD^A=0.9933	
	C	—	0.1	PGD^C=0.0067	—
Marias	A	82	82.2		
(n=91)	AC	9	8.6	PGD^A=0.9505	
	C	—	0.2	PGD^C=0.0495	0.246

Continued

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Murias	A	93	93.0		
(n=96)	AC	3	3.0	PGD^A=0.9844	
	C	—	0.1	PGD^C=0.0156	—
Maharashtra					
Maria Gonds	A	100	98.7		
(n=116)	AC	14	16.6	PGD^A=0.9224	
	C	2	0.7	PGD^C=0.776	2.852
Raj Gonds	A	101	101.1		
(n=106)	AC	5	4.9	PGD^A=0.9764	
	C	—	0.1	PGD^C=0.0236	0.062

among the population of Orissa and then gradually declines towards west.

GLO. Glyoxalase (GLO) marker could be tested only in 9 tribes, and the phenotypic and allele frequencies are given in Table 5. There are two common alleles GLO^1 and GLO^2 and both occur frequently in these populations, of which GLO^2 is more predominant. Hardy-Weinberg equilibrium test shows a statistically significant deviation in case of Gadabas and Parojas of Orissa, and among the Maria Gond of Maharashtra. In this study GLO^1 shows maximum frequency (0.422) in Maria Gonds of Maharashtra (the maximum value present in Marias of Madhya Pradesh but is ignored as the sample size is very small) and minimum (0.263) in Parojas of Orissa. No cline has been observed in regard to *GLO* allele frequency distribution.

G-6-PD deficiency. Glucose-6-phosphate dehydrogenase (G-6-PD) deficiency is a well known X-linked trait. Only 319 male individuals of the five tribes were tested, which are shown in the Table 6. The samples from other tribes could not be tested for the lack of resources. In the present series the incidence of the deficiency have been noticed only in two tribes namely Muria and Bhatra of Madhya Pradesh, the frequencies being 2.74 and 2.94% respectively. In some Indian tribes, tested so far, the deficiency rate is as high as 19.62% in Worli of Nagar Dadar Haviely (Joshi *et al.*, 1975). Amongst the Gond tribe of Nagpur, Maharashtra, and Raipur of Madhya Pradesh the deficiencies are 10.58% (Kher *et al.*, 1967) and 15.08% respectively (Report of Institute of Immunohaematology, ICMR, Bombay, 1986). The deficiency trait is recognised even in many non-tribal populations in India, and it is high amongst the Parsis (17.30%) of Bombay (Kate *et al.*, 1978). The high incidence of G-6-PD deficiency and some abnormal haemoglobins in malarial environment is a well known fact. It has also been suggested that the protection is conferred against malarial parasite by the heterozygous females (Bienzle *et al.*, 1972; Kar *et al.*, 1992) which could be extended to hemizygous also.

Table 5. GLO phenotype frequencies, allele frequencies, and χ^2-text for Hardy-Weinberg equilibrium.

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Orissa					
Gadabas	1	12	7.5		
(n=71)	2-1	22	31.1	GLO^1=0.3239	
	2	37	32.5	GLO^2=0.6761	6.078*
Konda Doras	1	6	4.3		
(n=28)	2-1	10	13.4	GLO^1=0.3928	
	2	12	10.3	GLO^2=0.6071	1.769
Parojas	1	12	6.5		
(n=93)	2-1	25	36.1	GLO^1=0.2634	
	2	56	50.5	GLO^2=0.7366	8.783**
Madhya Pradesh					
Bhatras	1	11	15.0		
(n=104)	2-1	57	49.0	GLO^1=0 3798	
	2	36	40.0	GLO^2=0.6202	2.776
Halbas	1	14	11.6		
(n=97)	2-1	39	43.9	GLO^1=0.3454	
	2	44	41.6	GLO^2=0.6546	1.191
Marias	1	4	3.5		
(n=14)	2-1	6	7.0	GLO^1=0.5000	
	2	4	3.5	GLO^2=0.5000	0.286
Murias	1	9	8.7		
(n=66)	2-1	30	30.6	GLO^1=0.3636	
	2	27	26.7	GLO^2=0.6364	0.021
Maharashtra					
Maria Gonds	1	13	8.0		
(n=45)	2-1	12	22.0	GLO^1=0.4222	
	2	20	15.0	GLO^2=0.5778	9.252**
Raj Gonds	1	5	3.3		
(n=40)	2-1	13	16.4	GLO^1=0.2875	
	2	22	20.3	GLO^2=0.7125	1.709

* Significant at 5 per cent level; ** at 1 per cent level.

Haemoglobin variants. Study of haemoglobin pattern was done in all the tribal groups. The phenotypic and gene distribution are shown in the Table 7. Two major variant haemoglobin types HbE and HbS are common in some Indian populations, of which HbE is mostly restricted among the populations of Eastern and North-Eastern India, whereas HbS is dominant in South, West, and Central India. In the present study HbS is found in all the tribes with varying frequencies,

Table 6. G-6-PD deficiency distribution.

Population (Sample size)	Normal/ deficient	Total observed No.
Madhya Pradesh		
Bhatra	Normal	102
(n=105)	Deficient	3
Dhurwa	Normal	23
(n=23)	Deficient	0
Halba	Normal	69
(n=69)	Deficient	0
Maria	Normal	47
(n=47)	Deficient	0
Muria	Normal	73
(n=75)	Deficient	2

Table 7. Haemoglobin phenotype frequencies, allele frequencies, and χ^2-test for Hardy-Weinberg equilibrium.

Population (Sample size)	Pheno-type	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Orissa					
Deshia Khonds	A	98	98.2		
(n=107)	AS	9	8.6	Hb^A=0.9579	
	S	—	0.2	Hb^S=0.0421	0.206
Raj Gonds	A	98	98.1		
(n=104)	AS	6	5.8	Hb^A=0.9712	
	S	—	0.1	Hb^S=0.0288	0.092
Savaras	A	102	102.0		
(n=102)	AS	—	—	Hb^A=1.0000	
	S	—	—	Hb^S=0.0000	—
Gadabas	A	95	94.2		
(n=104)	AS	8	9.5	Hb^A=0.9519	
	S	1	0.2	Hb^S=0.0481	2.649
Konda Doras	A	72	71.7		
(n=86)	AS	13	13.7	Hb^A=0.9128	
	S	1	0.6	Hb^S=0.0872	0.220
Kuvi Khonds	A	91	90.0		
(n=94)	AS	2	3.9	Hb^A=0.9787	
	S	1	0.1	Hb^S=0.0213	22.489***
Parojas	A	86	84.3		
(n=94)	AS	6	9.5	Hb^A=0.9468	
	S	2	0.3	Hb^S=0.0532	12.612***

Continued

Population (Sample size)	Phenotype	Total number Obs.	Exp.	Allele frequency	χ^2 (1)
Binjhals	A	93	90.4		
(n=103)	AS	7	12.2	Hb^A=0.9369	
	S	3	0.4	Hb^S=0.0631	18.628***
Kisans	A	104	101.1		
(n=108)	AS	1	6.8	Hb^A=0.9676	
	S	3	0.1	Hb^S=0.0324	78.464***
Madhya Pradesh					
Bhatras	A	90	88.5		
(n=102)	AS	10	13.0	Hb^A=0.9314	
	S	2	0.5	Hb^S=0.0686	5.541*
Dhurwas	A	74	72.3		
(n=81)	AS	5	8.5	Hb^A=0.9444	
	S	2	0.3	Hb^S=0.0556	13.730***
Halbas	A	85	83.7		
(n=99)	AS	12	14.7	Hb^A=0.9192	
	S	2	0.7	Hb^S =0.0808	3.354
Marias	A	73	72.4		
(n=94)	AS	19	20.2	Hb^A=0.8777	
	S	2	1.4	Hb^S=0.1223	0.325
Murias	A	85	84.7		
(n=101)	AS	15	15.6	Hb^A=0.9158	
	S	1	0.7	Hb^S=0.0842	0.135
Maharashtra					
Maria Gonds	A	85	84.1		
(n=113)	AS	25	26.8	Hb^A=0.8628	
	S	3	2.1	Hb^S=0.1372	0.482
Raj Gonds	A	92	91.3		
(n=102)	AS	9	10.4	Hb^A=0.9461	
	S	1	0.3	Hb^S=0.0539	1.864

* Significant at 5 per cent level; *** at 0.1 per cent level.

except Savaras of Orissa. HbS in homozygous form is present, surprisingly, in all the tribes except three tribes—Dashia Khonds, Raj Gonds, and Savaras of Orissa. The maximum number of cases (three cases) have been observed in the Kisans of Orissa. The highest HbS allele frequency (0.1372) is found amongst the Maria Gond. It is noteworthy that a few of the HbSS types were detected among the adult and old individuals also. The genetic equilibrium can be assumed for a majority of the groups, though significant deviations are noticed in six of them:

Kuvi Khonds, Paroja, Binjhal, and Kisan of Orissa and Bhatra and Dhurwa of Madhya Pradesh. The genetic equilibrium obtained through χ^2-tests may not be that appropriate because in majority cases HbS homozygous number seems to be inadequate. A geographical cline of *HbS* allele increasing from east to west has been observed. A large number of Indian populations including tribes have been screened for Hb type (Mukherjee and Das, 1990). The presence of several HbSS cases in this region raises the question as to how it is maintained in a high frequencies despite its known lethality in homozygous condition. One of the reasons may be cooccurrence of α-thalassemia along with HbS which reduces the lethality of HbS, and increased level of HbF among the HbS heterozygous or homozygous individuals. High frequencies (about 16%) of *S* allele have been reported amongst the Gamit of Gujrat, Western India (Vyas *et al.*, 1962) and in the Bhilala tribes of Madhya Pradesh (ICMR report, 1986); about 13% in the Konda Paroja or Orissa (Das *et al.*, 1967), and in South India it is also high (about 18%) amongst the Pradhan of Andhra Pradesh (Blake *et al.*, 1981).

LDH. Lactate dehydrogenase is normally monomorphic in world populations. In India, the LDH Cal-1 variant is found to be widely distributed. All the 16 tribes were screened for LDH type and shown in Table 8. LDH Cal-1 variant was detected in many of these tribes, except Savaras, Parojas, Binjhals, Kisans, Halbas, and Raj Gonds (Maharashtra). It is worth mentioning that two cases of Cal-1 homozygous variant is usually rare, were detected in two tribes of Orissa, namely in Deshia Khonds and in Raj Gonds. Maximum number (five cases) of Cal-1 variant were identified amongst the Kuvi Khonds of Orissa. LDH Cal^1 allele is relatively more frequent in the Hindu caste groups rather than tribes in

Table 8. LDH phenotype frequencies and allele frequencies.

Population (Sample size)	Phenotype	Total Obs.	Allele frequency	
Orissa				
Deshia Khonds	N	103	LDH^N	0.9811
(n=106)	CAL 1	2	$LDH^{Cal\ 1}$	0.0189
	CAL 1 (Homo)	1		
Raj Gonds	N	104	LDH^N	0.9859
(n=106)	CAL 1	1	$LDH^{Cal\ 1}$	0.0141
	CAL 1 (Homo)	1		
Savaras	N	105	LDH^N	1.0000
(n=105)	CAL 1	—	$LDH^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		
Gadabas	N	94	LDH^N	0.9947
(n=95)	CAL 1	1	$LDH^{Cal\ 1}$	0.0053
	CAL 1 (Homo)	—		

Continued

Population (Sample size)	Phenotype	Total Obs.	Allele frequency	
Konda Doras	N	87	*LDH*^{A}	0.9943
(n=88)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0057
	CAL 1 (Homo)	—		
Kuvi Khonds	N	93	*LDH*^{A}	0.9745
(n=98)	CAL 1	5	*LDH*$^{Cal\ 1}$	0.0255
	CAL 1 (Homo)	—		
Parojas	N	105	*LDH*^{A}	1.0000
(n=105)	CAL 1	—	*LDH*$^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		
Binjhals	N	102	*LDH*^{A}	1.0000
(n=102)	CAL 1	—	*LDH*$^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		
Kisans	N	103	*LDH*^{A}	1.0000
(n=103)	CAL 1	—	*LDH*$^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		
Maharashtra				
Bhatrass	N	102	*LDH*^{A}	0.9951
(n=103)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0049
	CAL 1 (Homo)	—		
Dhurwas	N	81	*LDH*^{A}	0.9939
(n=82)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0061
	CAL 1 (Homo)	—		
Halbas	N	94	*LDH*^{A}	1.0000
(n=94)	CAL 1	—	*LDH*$^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		
Marias	N	98	*LDH*^{A}	0.9949
(n=99)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0051
	CAL 1 (Homo)	—		
Murias	N	105	*LDH*^{A}	0.9953
(n=106)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0047
	CAL 1 (Homo)	—		
Maharashtra				
Maria Gonds	N	115	*LDH*^{A}	0.9957
(n=116)	CAL 1	1	*LDH*$^{Cal\ 1}$	0.0043
	CAL 1 (Homo)	—		
Raj Gonds	N	107	*LDH*^{A}	1.0000
(n=107)	CAL 1	—	*LDH*$^{Cal\ 1}$	0.0000
	CAL 1 (Homo)	—		

Table 9. Analysis of heterogeneity in 16 tribal groups of Orissa, Madhya Pradesh, and Maharashtra, based on four enzyme and haemoglobin loci.

Locus	Allele	No. of population	No. of individual tested	χ^2	d.f	H_T	G_{ST}	D_{ST}
ACP	p^a	16	1,611	2.5785	15	0.3443	0.0058	0.0020
ESD	ESD^1	16	1,587	0.0227	15	0.4415	0.0100	0.0044
6-PGD	PGD^A	16	1,554	0.0140	15	0.0558	0.0574	0.0032
GLO	GLO^1	9	772	11.0755	15	—	—	—
Hb	Hb^S	16	1,492	1.2408	15	0.1221	0.0164	0.0020

India (Mukherjee and Reddy, 1983). Highest frequency of Cal-1 type has been reported among the Kurumbas of Nilgiri Hill (Saha *et al.*, 1976).

Gene diversity

Table 9 provides χ^2-values for testing the homogeneity of gene frequencies as well as the G_{ST} values. The χ^2-values indicate a non-significant heterogeneity for all alleles in the individual systems. For measuring the extent of gene diversity G_{ST} computation was performed using all 16 populations together and shown in the same Table 9. The total gene diversity (H_T) of the tribes appears to be 0.3678, while the average gene diversity within populations (H_S) is 0.4474 and between populations (D_{ST}) is found to be 0.0044. Within population diversity is larger than between population diversity. The G_{ST} value is smallest (0.0020) for *pa* allele and highest for Hb^S gene (0.0415). The degree of over all genetic differentiation as measured by the total G_{ST} values is 0.0154 ± 0.0071 which seems to be statistically non significant. The sporadic trends of geographical cline observed in the distribution of afore mentioned markers do not, in fact, offer any meaningful explanation for common origin and close relatedness or operation of similar selection mechanism amongst these 16 tribes. Though, the χ^2-values for interpopulations comparisons (Table 9) show non-significant differences in the allele frequency distribution among these tribes but within population heterogeneity (H_S) has been found to be much larger than between populations (D_{ST}). Different factors of population structure such as population size, density, mating pattern, and micro-evolutionary forces like differential selection, migration *etc.*, considerably contribute to the within population diversity.

Common language frequently signifies a common origin of two populations (Ruhlen, 1987), and as such languages provides a rough classification of populations (Cavalli-Sforza, 1991). χ^2-tests among these three linguistic groups of population show largest heterogeneity within the Dravidian speaking group compared to other Austro-Asiatic or Indo-European speaker, Of course, the largest significant heterogeneity may partly be attributed to inclusion of larger number of tribes within the Dravidian group than other two groups.

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