

Sero-genetic Profile and Phylogenetic Relationships of Tribes of Rajasthan

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KEYWORDS Genetic Polymorphisms. Population Variations. Phylogenetic Relationships. Rajasthan Tribes

ABSTRACT Genetic structure and polygenetic relationship of six numerically larger endogamous tribes, Mina, Bhil, Garasia, Damor and Kathodi of Rajasthan, who exhibit varied ethnographic history, have been investigated using 12 sero-genetic polymorphic marker systems viz. A1A2BO, MNSs, Rhesus, Duffy, Lewis, Kell, Kidd, HP, TF, GPI, G6PD deficiency and HB variants. Genetic differentiation with respect to studied genes has been observed small (except for HB* variants and G6PD*Def, which may be under the influence of natural selection) among the studied tribes and it appears that there has been little effect of population subdivision on these genes or late divergence of these populations from one another. The studied tribes make two main clusters, one of Mina and Saharia, other of Bhil, Damor, Garasia and Kathodi. Within the later cluster Bhil and Damor are closest joined by Garasia and then Kathodi. The present study partially supports the ethnographer's views of their origin and divergence.

INTRODUCTION

Human populations are not merely groups of individuals but a coherent system. They are structured in a way that the structure in time and space may change but a certain amount of continuity always exists.

Analysis of phenotypic and allele frequency data from polymorphic loci is an important method for describing the pattern of genetic variation within species and inferring the phylogenetic relationships between the populations. In the early days of genetic studies, the genetic relationships among different populations were studied by examining the geographical distributions of gene frequencies at a few loci such as the ABO and RH blood group systems mainly from Indian region (Bhasin et al. 1992). It was later realized that comparison of gene frequencies for one or two loci is not reliable since each locus has a different distribution. Only when a large number of loci are examined, the genetic relationship becomes clear (Cavalli-Sforza and Edwar 1964; Bhasin 2009). This is partly because the inter-population genetic variation is very small compared with the intra-population variation at the gene level (Lewontin 1972; Nei and Roychowdhury 1972, 1974, 1982; Bhasin 2009). However, if a large number of loci are examined even small differences can be detected with sufficient accuracy (Bhasin 2009).

The tribes are possibly the original inhabitants of India (Thapar 1966; Ray 1973) who contribute 8.08 per cent to the total Indian po-

pulation (Census of India 2001) and constituted of 450 different communities (Singh 1992), although their evolutionary histories and biological contributions to the non-tribal populations have been debated (Risley 1915; Guha 1935; Sarkar 1958; Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2009).

MATERIAL AND METHOD

Area of Present Study

Situated in the north-western part of India, between 23°3' to 30°12' North latitudes and 69°39' to 30°17' East longitudes, Rajasthan - the abode of Rajputs, is also the home of some of the original inhabitants of the Indian land. The origin of this frontier state of India goes back to prehistoric time, so as of its populations. While looking into the ethnic accounts of the scheduled tribes of Rajasthan- the tribes Bhil, Mina and Saharia have dwelled on this land from ancient time along with some other communities like Gujjars (Tod 1881). The tribes Bhil and Mina, who as per the Census 1991, account for nearly 93.2 per cent of the total scheduled tribe population of the state, had at one time ruled different parts of Rajasthan before the advent of Rajputs. The other groups like Garasia and Damor trace their origin from Rajputs or Bhil-Rajput interaction in the recent past, while Kathodi tribe is clearly an immigrant population from Maharashtra state (For details see Bhasin and Bhasin 1999; Bhasin 2005).

To understand the population structure and evolutionary interrelationship of the tribal groups of Rajasthan, who exhibit very varied ethnographic history, we have studied the distributions of 12 sero-genetic polymorphic marker systems viz. A1A2BO, MNSs, Rhesus, Duffy, Lewis, Kell, Kidd, HP, TF, GPI, G-6-PD deficiency and HB variants among six numerically larger endogamous tribes namely, Mina, Bhil, Garasia, Damor and Kathodi.

About the Populations

Mina: They trace their descent to Minavatar, believed to be the incarnation of Vishnu in the form of a fish. History says that the Mina had one time, their own petty kingdoms in Naen, Karoli, Dhoondar, Kota, Jhalawar, Bhanwargarh, Chopoli and held power over a large part of Rajasthan before the advent of the Rajputs (Pal 1968; Kaviraj 1886; Singh 1994). Those loyal to the new rulers were granted land and other sources of production. Those who could not reconcile to their defeat formed organized bands and adopted the path of resistance, crime and violence. Attempts were made to rehabilitate them by offering them the job of the village watchman. That is why there are two divisions—the Zamindars and the Chowkidars—which continue till date. There are around 2,969,456 Mina (Census of India 1981) in Rajasthan who constitute the largest part (49.47%) of the total Scheduled Tribe population of the State. They are not Scheduled Tribe in Ajmer. They are spread over the whole state, but are mainly concentrated in Jaipur, Alwar, Bharatpur, Sawai Madhopur, Tonk, Bundi and Udaipur districts of the state, where over 51 per cent of their population reside. Unlike the other scheduled tribes of Rajasthan, the Mina has not been relegated to a socially inferior position by the caste Hindus. They place themselves at a high level of social hierarchy, equal to that of Rajputs, Jat, Thakur, Mahajan and Gujjar of the area. They cultivate land, and both men and women participate in agricultural activities. The Mina economy is predominantly agriculture based. They also depend upon animal husbandry, labor and service for their livelihood. Some of them hold good positions all-over India and in state services. They are Hindus but have certain animistic traits as well.

Bhil: They derive their name from the Dravidian word: *vil*, meaning a bow or arrow

man. They are the ancient inhabitants of the Aravallis, where they are largely distributed even today (Tod 1881). This view is supported by Sherring (1881) and Russell and Hiralal (1916). The Bhils had been rulers in certain parts of Rajasthan, Gujarat, and Madhya Pradesh and were dislodged by the incoming Rajputs. History speaks of compromise as well as conflict in the Bhil and non-Bhil relationship. Tod (1881) mentions that the Rajputs would accept food from the Ujale Bhils or those of pure aboriginal descent. All other castes would also accept water from them. However, later as the orthodox form of Hinduism spread in Rajputana, the tribes position along with their associated groups vis-à-vis caste Hindus of higher segments sharply deteriorated.

At present they live in scattered hutments separated widely or perched on hill tops, depending upon the topography. There are 1,861,502 Bhils (Census of India 1981) in Rajasthan. They constitute 44.50 per cent of the total population of Scheduled Tribes. The Bhils' social organization is characterized by the presence of diverse social groups recognized on the basis of kinship, culture contact, religious tenets, etc. They maintain nuclear pattern of families. Compound families of a polygynous nature, though very small in number, are accorded a higher social status. They inhabit the villages of the state where they practice agriculture, wherein both men and women participate. They are spread all over the state but are mainly concentrated in the districts of Udaipur, Banswara, and Dungarpur. About 40 per cent of them speak Bhilli and its allied dialect called Wagdi, which is spoken in Banswara and Dungarpur. Bhils living in other parts have adopted local dialects.

Garasia: In one opinion, Girasia means people dwelling in the hills. As per Meharda (1985), the word Garasia originated around the tenth century from the term Garasia, which means forest dwelling people. Another version states that they have been so named because of being girahua or degraded from Rajputs. The existing ethnographic account (Census 1891) states that when the Turks defeated the Chauhan king of Jaipur, the Rajputs were forced to take shelter in the hills where they overpowered Bhils and settled down on grant of subsistence or *gras*. To pacify Bhils they also parted with some subsistence in their favour. These Bhil grant-holders

came to be known as Garasias. According to Rajputana Gazetteer, the Garasias are the 'half-breed', being the descendants of Rajputs who married the Bhils. The settlement pattern, use of bow and arrow and the general way of life of Garasia are all similar to those of Bhils.

Rajasthan has 121,939 Garasia who constitute 2.91 per cent of the total Scheduled Tribe population of the state. Most marriages are contracted by way of elopement which is an accepted practice among the Garasia tribe. Agriculture and allied occupations are their means of subsistence. They are located mostly in Sirohi, Udaipur and Pali districts of Rajasthan.

Saharia: Saharia are the most backward and one of the first settlers of Rajasthan. Tod (1881) mentioned them along with Minas, Bhils and Gujjars as the primitive dwellers of the region. The word Saharia appears to have been derived from the Persian World, "Sehi" meaning jungle. The Muslim rulers reckoned Saharia as inhabitants of forest. On the other hand, Census monograph 'SANWARA' gives a different view that word Saharia is derived from Persian word 'Seher' meaning desert. Saharias' customs and manner bear great resemblance to caste Hindus with whom they live in their present habitat and who consider them to be untouchable. There are 41,427 Saharia residing in Rajasthan forming 0.91 per cent of the total Scheduled Tribe population (Census of India 1981). They cultivate land and raise livestock. They reside in districts of Kota, Baran, Jhalawar, Udaipur, Dungarpur, Jaipur, Sawai - Madhopur and Churu with their main concentration (99.2%) in Kota and Baran districts. They do not have their own language; around 61 per cent of them speak Khariboli, 23 per cent Brijbhasha and 15 per cent speak Hadoti, while others have taken to local dialects.

Damor/Damaria: According to ethnographic accounts they are migrants from Gujarat. They trace their origin from Chauhan Rajputs and had a relation with the latter when Rajputana was under the Rajput rule. At that time the Damor were also chieftains of some of the small states of Rajputana. According to them, Durgaria Panwar (a Damor) was the ruler of Dungarpur and it was designated after his name. The Damor is also a clan among the Bhils but these Damors are different and claim their origin from the Rajputs (Bhasin 2004). According to 1981 Census, their population was 31,337 which is 0.71 per

cent of the total Scheduled Tribe population of Rajasthan. They inhabit the Banswara, Dungarpur, Udaipur, Churu and Ganganagar districts of Rajasthan. However, major concentration is in Dungarpur district, especially in the border area of Rajasthan and Gujarat. They are predominantly a rural community with 98.72 per cent of them living in the countryside. The Indo-Aryan language "Vagri" is their mother tongue. They recognize two sub-divisions among them, that is, Gujarati and Rajasthani. The former is treated as socially higher than the latter. Each of them is again divided into a number of exogamous clans. Land is the main economic resource of Damors and agriculture is their traditional occupation. Some of them depend on wage labour also.

Kathodi/Katkari: This tribe does not originally belong to Rajasthan. It is said that it was about 80-90 years ago that Muslim employers, the Bohras, a noted commercial community, impressed with their skill at *katha* making persuaded about 250 families to part with their parent stock of Bhils in western Khandesh district of Maharashtra (Bombay state) in search of new fortunes in the forest of Rajasthan. They were employed in the remote interiors of forests abounding in Kher trees, the raw material for manufacturing *katha* and have since come to be known as Kathodies or Katkari.

The Kathodi or Katkari is a small group comprising 2553 individuals (1236 males and 1317 females) concentrated mainly in the Udaipur district of Rajasthan (For details about the above tribal groups see Bhasin and Bhasin 1999; Bhasin 2005).

Samples Size

A total of 647 blood samples and relevant data were collected at random from apparently healthy and unrelated individuals of either sex, belonging to the six scheduled tribes of Rajasthan that is, Bhil and Kathodi tribes of Udaipur districts (206 samples), Garasia tribe of Sirohi district (125 samples); Damor of Dungarpur district (104 samples); Mina of Sawai Madhopur district (101 samples) and Saharia scheduled tribe of Baran district (111 samples). All the blood samples were collected in EDTA -vials, kept on ice and transported to the laboratory for analysis.

Laboratory Analysis

Red cells were tested for A1A2BO, MNSs, Rhesus, Duffy, Lewis, Kell and Kidd blood group systems using Orthodiagnosics, USA and Diamed, AG, Switzerland make antiseras, following the manufacturer's instructions and standard serological techniques after Bhasin and Chahal (1995). The isozyme polymorphic system Glucose Phosphate Isomerase (GPI) was typed as per the methods listed in Haris and Hopkinson (1976). Glucose- 6- Phosphate Dehydrogenase (G-6-PD) deficiency screening was done by fluorescence spot test after Beutler (1966), and 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). The hemoglobin variant has been observed on the cathodal portion of the gel, as per the electrophoretic technique described by Scott and Fowler (1982).

Statistical Analysis

The allele/haplotype frequency calculations have been done after Bhasin and Chahal (1995) and chi-square test was performed to test for Hardy-Weinberg equilibrium among populations for particular marker used in the study.

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

Allele/ Haplotype Frequency Distribution

Population wise observed and expected phenotype numbers and allele/haplotype frequencies calculated from the observed numbers, for the studied polymorphic genetic markers among Bhil, Garasia, Damor, Kathodi, Mina and Saharia tribes are given in Tables 1 and 2 respectively. In no systems except Rhesus, Duffy, G-6-PD deficiency and hemoglobin variants where pronounced natural selection operates, did the expected phenotype numbers calculated assuming Hardy-Weinberg equilibrium show any statistically significant variation from the observed phenotype numbers.

Among the studied tribes, Saharia, Mina, Kathodi and Damor show higher frequency of allele *ABO* *B (30.6, 28.7, 27.4 and 22.9% respectively) as compared to allele *ABO**A (16.3, 15.1, 20.6 and 20.3% respectively). Frequency of both the alleles are same among Damor (that is, 22.4%), whereas a higher *ABO**A (21.2%) than *ABO**B (19.9%) was observed among Bhil tribe.

Table 1: Observed and expected phenotype numbers for 12 polymorphic markers among six tribes of Rajasthan

System and phenotype	Observed and expected phenotype numbers											
	Bhil		Garasia		Damor		Kathodi		Meena		Saharia	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
<i>A1A2BO</i>												
O	34	36.6	37	38.2	32	33.5	28	27.4	31	31.9	31	31.3
A1	26	27.9	32	33.1	24	25.2	24	23.4	16	15.8	20	20.2
A2	3	3.2	4	4.1	3	3.1	2	1.9	3	3.1	2	2
B	27	29.1	36	37.1	31	32.5	37	36.1	39	40.8	46	46.4
A1B	14	7.9	13	10.9	11	8.4	8	10.1	10	7.2	11	9.9
A2B	2	1.1	3	4	3	1.2	1	1	2	1.5	1	1.1
Total	106	105.9	125	127.4	104	103.9	100	99.9	101	100.3	111	110.9
<i>MNSs</i>												
MMSS	5	4.1	9	6.4	6	4.2	1	2.5	7	4.9	8	4.4
MMSs	14	14	15	20.2	15	15.1	14	12.8	14	16.4	14	17.2
MMss	16	12	19	16.1	17	13.6	17	16.6	17	13.8	16	17
MNSS	8	5.9	10	8	6	5.9	7	4.8	7	6.9	6	5.5
MNSs	16	23.7	24	28.2	18	22.9	20	21.3	19	22.9	17	23.5
MNss	19	23.1	26	24.5	19	22.4	22	23	17	18.9	32	24.7
NNSS	2	2.8	3	2.5	3	2	2	2.3	3	2.5	3	1.8
NNSs	12	9.8	9	9.8	9	8.7	8	8.6	9	8.1	7	7.9
NNss	14	11.1	10	9.3	12	9.2	9	7.9	8	6.6	8	8.9
Total	106	106.6	125	124.9	104	104.1	100	99.9	101	100.6	111	110.9

Table 1: Contd...

System and phenotype	Observed and expected phenotype numbers											
	Bhil		Garasia		Damor		Kathodi		Meena		Saharia	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
<i>Rhesus (RH)</i>												
CCDEE	0	0	0	0	0	0	0	0	0	0	0	0.1
CCDEe	0	0	1	1.1	0	0	0	0	0	0	4	4.2
CCDee	42	42.9	41	45	38	40.6	37	31.3	37	30.9	37	39.2
CCdEE	0	0	0	0	0	0	0	0	0	0	0	0
CCdEe	0	0	0	0	0	0	0	0	0	0	0	0
CCdee	0	0.1	0	0	0	0	0	0	0	0	0	0
CcDEE	0	0	1	0.3	0	0	0	0	0	0	3	1.3
CcDEe	20	18.5	28	24.6	21	17.5	17	15	21	15.7	26	25.3
CcDee	30	29.5	38	33.7	32	30.3	30	33.1	32	31.4	28	23.2
CcdEE	0	0	0	0	0	0	0	0	0	0	0	0
CcdEe	0	0	0	0	0	0	0	0	0	0	0	0
Ccdee	1	1.1	1	1	1	0.9	1	1.1	0	0	0	0
ccDEE	2	1.9	3	3.2	2	1.9	2	1.9	1	1.6	3	3.7
ccDEe	5	6.6	5	9.3	3	6.7	6	8.2	2	6.2	6	7.1
ccDee	2	1.8	2	1.9	1	0.9	3	4	3	2.3	2	1.7
ccdEE	0	0	0	0	0	0	0	0	0	0	0	0
ccdEe	0	0	0	0	0	0	0	0	0	0	0	0
ccdee	4	3.6	5	4.8	6	5.2	4	5.3	5	1.7	2	1.7
Total	106	106.1	125	124.9	104	103.9	100	99.8	101	98.8	111	107.5
<i>Duffy (FY)</i>												
FY A	35	32.6	44	34.2	38	37.5	33	34.9	36	26.5	39	28.5
FY B	32	31.9	38	38	28	28	28	27.9	24	23.9	27	27
FY AB	37	39.4	42	51.8	35	35.5	36	33.9	41	50.5	45	55.5
FY NIL	2	2	1	0.9	3	2.9	3	3	0	0	0	0
Total	106	106	125	125	104	103.9	100	99.9	101	101	111	111
<i>Kell (KEL)</i>												
KEL K+	4	-	3	-	3	-	1	-	0	-	5	-
KEL K-ve	102	-	122	-	101	-	99	-	101	-	106	-
Total	106	-	125	-	104	-	100	-	101	-	111	-
<i>Lewis (LE)</i>												
LE A	12	8.7	20	15.9	13	9.5	14	14.1	16	14.1	16	12.3
LE B	61	61	65	64.9	59	58.9	54	56.2	46	46	59	58.9
LE AB	3	6.1	6	10.1	3	6.5	3	6.9	5	6.9	4	7.7
LE -ve	30	29.9	34	33.9	29	29	29	29	34	33.9	32	31.9
Total	106	105.9	125	124.9	104	103.9	100	101	101	101	111	110.9
<i>Kidd (JK)</i>												
JK A	64	-	71	-	63	-	60	-	58	-	68	-
JK B&JK -ve	42	-	54	-	41	-	40	-	43	-	43	-
Total	106	-	125	-	104	-	100	-	101	-	111	-
<i>Haptoglobin (HP)</i>												
HP 1-1	8	5.9	8	6.1	7	4.7	8	5.1	8	5.5	5	3.8
HP 2-1	34	38.2	39	42.9	30	34.7	29	34.9	31	36.1	31	33.4
HP 2-2	64	61.9	78	76.1	67	64.7	63	60.1	62	59.4	75	73.8
Total	106	106	125	125	104	104	100	100	101	101	111	111
<i>Transferrins (TF)</i>												
TF C-C	103	103	124	124	102	102	95	95.1	101	101	111	111
TF C-B	2	1.9	0	0	1	0.9	3	2.9	0	0	0	0
TF C-D	1	0.9	1	1	1	0.9	2	1.9	0	0	0	0
Total	106	104.9	125	125	104	103.9	100	99.9	101	101	111	111
<i>Glucose Phosphate Isomerase (GPI)</i>												
GPI 1-1	66	66	58	58.1	96	96	81	81.1	76	76	50	50
GPI 1-3	0	0	2	1.9	0	0	1	0.9	0	0	1	0.9
GPI 1-4	0	0	1	0.9	0	0	0	0	0	0	2	1.9
GPI 1-7	0	0	0	0	0	0	2	1.9	0	0	0	0
Total	66	66	61	60.9	96	96	84	83.9	76	76	53	52.9
<i>Glucose 6 Phosphate Dehydrogenase (G6PD) Deficiency</i>												
G6PD Normal	92	-	113	-	94	-	81	-	93	-	98	-
G6PD Def.	14	-	12	-	10	-	19	-	8	-	13	-
Total	106	-	125	-	104	-	100	-	101	-	111	-
<i>Haemoglobin (HB) Variants</i>												
HB AA	83	-	63	-	102	-	80	-	87	-	80	-
HB Variants	9	-	11	-	5	-	19	-	0	-	0	-
Total	92	-	74	-	107	-	99	-	87	-	80	-

Table 2: Allele/haplotype frequency of 12 polymorphic markers among six tribes of Rajasthan

System and alleles	Allele frequencies/per cent distribution					
	Bhill	Garasia	Damor	Kathodi	Meena	Saharia
<i>A1A2BO</i>						
<i>ABO*AI</i>	18.7	19.5	17.7	18.8	12.5	14.6
<i>ABO*A2</i>	2.5	2.9	2.6	1.8	2.6	1.7
<i>ABO*B</i>	19.9	22.4	22.9	27.4	28.7	30.6
<i>ABO*O</i>	58.8	55.3	56.8	52.3	56.2	53.1
Total	99.9	100	100	100	100	99.9
χ^2 Value	5.97	0.77	3.47	0.49	1.29	0.13
<i>MNSs</i>						
<i>MNS*MS</i>	19.6	22.5	20.2	15.7	22	19.8
<i>MNS*Ms</i>	33.7	35.9	36.1	40.8	36.9	39.2
<i>MNS*NS</i>	14.3	14.4	13.9	15.3	15.6	12.6
<i>MNS*Ns</i>	32.4	27.3	29.8	28.2	25.5	28.4
Total	100	100	100	100	100	100
χ^2 Value	6.68	4.35	4.01	2.35	3.47	8.75
<i>Rhesus (RH)</i>						
<i>RH*CDE</i>	0	0.7	0	0	0	3.5
<i>RH*CDDe</i>	60.9	57.9	60.4	53.7	62.9	59.4
<i>RH*cDE</i>	0	0	0	0	0	0
<i>RH*Cde</i>	2.7	2.1	2.1	2.3	0	0
<i>RH*cDE</i>	13.7	16.1	13.5	13.5	12.4	18.5
<i>RH*cDe</i>	4.2	3.6	1.8	7.5	5.2	6.2
<i>RH*cdE</i>	0	0	0	0	0	0
<i>RH*cde</i>	18.5	19.6	22.3	23.6	19.6	12.5
Total	100	99.9	100	99.9	100	99.9
χ^2 Value	11.64*	5.11	3.2	3.03	11.64*	2.74
<i>Duffy (FY)</i>						
<i>FY*A</i>	43.4	44.1	45.4	44.3	51.3	50.7
<i>FY*B</i>	42.9	46.9	37.6	38.4	48.7	49.3
<i>FY*-ve</i>	13.7	8.9	16.9	17.3	0	0
Total	100	100	100	99.9	100	100
χ^2 Value	0.33	4.64*	0.015	0.23	5.15*	5.84*
<i>Kell (KEL)</i>						
<i>KEL*K</i>	1.9	1.2	1.5	0.5	0	2.3
<i>KEL*-ve</i>	98.1	98.8	98.5	99.5	100	97.7
Total	99.9	100	100	100	100	100
χ^2 Value	-	-	-	-	-	-
<i>Lewis (LE)</i>						
<i>LE*A</i>	7.35	11	8	8.9	11	9.5
<i>LE*B</i>	39.5	36.8	39.2	37.3	30.9	36.9
<i>LE*-ve</i>	53.2	52.2	52.8	53.9	58	53.7
Total	100	100	100	99.9	100	100
χ^2 Value	2.72	2.77	3.24	3.55	0.77	2.94
<i>Kidd (JK)</i>						
<i>JK*A</i>	37.1	34.3	37.2	36.8	34.8	37.8
<i>JK*B&JK*_ve</i>	62.9	65.7	62.8	63.2	65.2	62.2
Total	100	100	100	100	100	100
χ^2 Value	-	-	-	-	-	-
<i>Haptoglobin (HP)</i>						
<i>HP*1</i>	23.6	22	21.2	22.5	23.3	18.5
<i>HP*2</i>	76.4	78	78.8	77.5	76.7	81.5
Total	100	100	100	100	100	100
χ^2 Value	1.28	1.03	0	2.84	2.09	0.59
<i>Transferrins (TF)</i>						
<i>TF*C</i>	98.6	99.6	99	97.5	100	100
<i>TF*B</i>	0.9	0	0.5	1.5	0	0
<i>TF*D</i>	0.5	0.4	0.5	1	0	0
Total	100	100	100	100	100	100
χ^2 Value	0	0	0	0	—	—

Table 2: Contd...

System and alleles	Allele frequencies/per cent distribution					
	Bhill	Garasia	Damor	Kathodi	Meena	Saharia
<i>Glucose Phosphate Isomerase (GPI)</i>						
<i>GPI*1</i>	100	97.5	100	98.2	100	97.2
<i>GPI*3</i>	0	1.6	0	0.6	0	0.9
<i>GPI*4</i>	0	0.8	0	0	0	1.9
<i>GPI*7</i>	0	0	0	1.2	0	0
Total	100	100	100	100	100	100
χ^2 Value	-	0	-	0	-	0
<i>Glucose 6 Phosphate Dehydrogenase (G6PD) Deficiency</i>						
<i>G6PD*N</i>	86.8	90.4	90.4	81	92.1	88.3
<i>G6PD*def.</i>	13.2	9.6	9.6	19	7.9	11.7
Total	99.9	100	100	100	100	100
<i>Haemoglobin (HB) Electrophoretic Variants</i>						
<i>HB*A</i>	90.2	85.5	95.3	80.8	100	100
<i>HB*variants</i>	9.8	14.9	4.7	19.2	0	0
Total	100	99.9	100	100	100	100

The *ABO*A2*, though present among all the studied tribes exhibit less than 3 per cent frequency.

For the MNSs system, the studied tribes shows highest frequency of *MNS*Ms* haplotype (ranges 33.67 to 40.78 %) followed by *MNS*Ns* (ranges 25.5 to 32.4%), *MNS*MS* (ranges 15.7 to 22.5 %) and *MNS*NS* (ranges 12.6 to 15.6 %). The incidence of *MN*M* allele in the studied population varies from 53.3 per cent among Bhil to 59.0 per cent among Mina, whereas allele *S remain less than 40 per cent (ranges 31.0 % among Kathodi to 37.6% among Mina).

The studied tribes do not show much variability in the distribution of Rhesus system haplotype. The frequency of the most common haplotype *RH*CDe* is highest among all six tribes (varies from 53.69 % among Kathodi to 62.87 % among Mina), followed by haplotype *RH*cde* (varies from Saharia - 12.45 % to Kathodi- 23.60 %), *RH*cDE* (ranges Minas- 12.38 % to Saharias 18.46 %) and *RH*cDe* (ranges Minas- 1.78 % to Kathodi- 7.46 %), except among Saharia where frequency of haplotype *RH*cDE* is higher (18.46 %) then the haplotype *RH*cde* (12.49 %). Haplotype *RH*CDE* is observed only among Garasia and Saharia (0.73 and 3.49 % respectively).

The Duffy System allele *FY* A* frequency (varies from 43.37 % among Bhil to 51.26 % among Mina) is higher than the allele *FY*B* (varies from 38.35 % among Kathodi to 49.32 % among Saharia) among all the studied groups, except Garasia where frequency of *FY* B* (46.92 %) is slightly higher than the *FY* A* frequency (that is, 44.14 %). The rare *FY*null* allele has

been observed in a comparatively high frequency among Bhil (13.7 %), Garasia (8.9 %), Damor (16.9 %) and Kathodi (17.3 %) tribes.

The Lewis blood group distribution show a high frequency of allele *LE*null* (ranges 52.15% among Garasia to 58.02 % among Mina) among all the studied tribe, followed by allele *LE*B* (Mina- 30.98 % to Bhils 39.46 %). The frequency of allele *LE*A* has been observed comparatively low (varies from 7.35 % among Bhil to 11.01 % among Garasia).

The Kell blood group system rare allele *KEL*K* though in low frequency (varies from 0.51 % among Kathodi to 2.28 % a Saharia) has been observed among all the studied tribes except Mina.

The Kidd blood group distribution among the studied tribe shows a very low variability. The allele *JK*A* varies from 34.27 % among Garasia to 37.76 % among Saharia.

The Haptoglobin serum protein allele *HP*1* frequency (varies from 18.5 % among Saharia to 23.6 % among Bhil) is lower than the *HP*2* allele among all the studied tribes.

Transferrin serum protein, rare alleles *TF*B* and *TF*D* has been observed among Bhil (0.94 and 0.5 % respectively), Damor (0.48 and 0.5 % respectively) and Kathodi (1.50 and 1.0 % respectively) tribes. Among Garasia only *TF*D* has been found in the low frequency (0.4 %), whereas among Mina and Saharia, no variant other than the common *TF*C* was encountered.

In glucose phosphate isomerase enzyme polymorphism, apart from the common *GPI 1-1* variant, three rare variants *GPI 3-1*, *GPI 4-1* and *GPI 7-1* have been observed in three tribes. The

allele *GPI*3* has been found in Garasia (1.6 %), Kathodi (0.6 %) and Saharia (0.9 %) whereas allele *GPI*4* could be detected only among Garasia (0.8 %) and Saharia (1.2 %). The third rare allele *GPI*7* has been observed among Kathodi (1.19 %) tribe only. The other three populations -Bhil, Damor and Mina were found to be monomorphic for common variant GPI 1-1.

The glucose-6-phosphate dehydrogenase (G-6-PD) deficiency, which provides selective advantage against falciparum malaria, has been observed in quite high frequency among all the studied tribes that is, Kathodi -19.00 %; Bhil -13.20 %; Saharia 11.71 %; Damor -9.61 %; Garasia -9.60 % and Mina -7.92 %.

Haemoglobin electrophoretic variants are observed in quite high frequencies among Kathodi (19.2 %), Garasia (14.9 %), Bhil (9.8 %) and Damor (4.7 %) tribes, whereas no variant observed among Mina and Saharia tribes.

Statistical Inferences

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 studied tribes, 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 twelve loci is presented in Table 3. The average heterozygosity for the present sample has been found 36.7 % which is more than three times the values recorded by Nei and Roychoudhury (1974) for various ethnic groups

(10 %) using random loci. But this difference is not real and is attributable to the fact that only

Table 3: Heterozygosity among the six tribes of Rajasthan-Estimates by population based on 12 polymorphic loci.

S. No.	Populations	Heterozygosity(H)
1	Bhil	0.367
2	Garasia	0.413
3	Damor	0.352
4	Kathodi	0.389
5	Meena	0.329
6	Saharia	0.354
	Mean	0.367

polymorphic loci were considered in the present study. Therefore, the two values given above are in good agreement. The present value fit well in the heterozygosity range 0.21 to 0.37 calculated more recently on world population by Cavalli-Sforza et al. (1994) using various polymorphic loci.

The average heterozygosity among all the studied tribes is comparatively high and shows a little variation from one tribal population to the other, Garasia being the most heterozygous population group (41. %3) and Mina being the least heterozygous (32.9 %).

Genetic Differentiation: The Wahlund's variance (Wahlund 1928) and a set of gene diversity measures developed by Nei (1973) have been used to analyze the genetic differentiation among the studied tribes.

The value of Wahlund's variance (f) calculated from 14 di-allelic loci are listed in Table 4. The high value of f is evident for HB* variants and G6PD*Def (that is, 0.041 and 0.015 respectively), which suggests that natural

Table 4: Mean allele frequency variance and Wahlund's variance among six tribes of Rajasthan

S.No.	Allele	Mean (P)	Variance (σ^2)	Wahlund's variance (f)
1	C	0.61	0.0008	0.0034
2	D	0.79	0.0016	0.0003
3	E	0.15	0.0012	0.0089
4	M	0.57	0.0004	0.0019
5	S	0.34	0.0006	0.0028
6	LE*A	0.09	0.0002	0.0027
7	FY*A	0.46	0.0012	0.0049
8	K	0.01	0	0.006
9	JK*A	0.36	0.0002	0.0009
10	HP*1	0.22	0.0003	0.002
11	TF*B	0.01	0	0.008
12	GPI*3	0.01	0	0.0085
13	HB*variants	0.1	0.0031	0.0415
14	G6PD* def	0.11	0.0016	0.015
	Mean	0.0.30	0.0008	0.0076

Table 5: Estimates of Nei’s measures of gene diversity among six tribes of Rajasthan.

S.No.	Locus	Gene diversity in the total population HT	Intra population of gene diversity Hs	Inter population gene diversity DST	Co-efficient of gene diversity GST
1	A1A2BO	0.6263	0.5971	0.0292	0.0467
2	Rhesus	0.5887	0.5858	0.003	0.005
3	MNSs	0.7202	0.7187	0.0016	0.0022
4	LE	0.5652	0.5638	0.0013	0.0024
5	FY	0.5811	0.5726	0.0085	0.0146
6	KEL	0.0242	0.0241	0.0001	0.005
7	JK	0.4625	0.4621	0.0003	0.0007
8	HP	0.3413	0.3407	0.0006	0.0017
9	TF	0.0174	0.0173	0.0001	0.0055
10	GPI	0.0234	0.0231	0.0003	0.0109
11	HB	0.1868	0.1814	0.0053	0.0285
12	G6PD	0.2088	0.2062	0.0026	0.0125
	Mean	0.3622	0.3558	0.0044	0.0113

Table 6: Nei’s standard genetic distance among six tribes of Rajasthan

Populations	Bhil	Garasia	Damor	Kathodi	Meena	Saharia
Bhil	0					
Garasia	0.001375	0				
Damor	0.000848	0.001926	0			
Kathodi	0.002664	0.002801	0.001504	0		
Meena	0.004883	0.002727	0.005497	0.005976	0	
Saharia	0.005357	0.003108	0.006045	0.006242	0.002364	0

selection may be operating and leading to this higher differentiation of these genes among the studied populations. Differentiation with respect to other genes has been observed insignificant and it appears that there has been a little effect of population subdivision of these gene or late divergence of these populations from one another.

The gene diversity (HT) among the six studied tribes (0.3621) has been analyzed into its two components, that is, intra- population gene diversity (Hs = 0.3577) and inter population gene

diversity (DST = 0.0044) (Table 5). This shows that the gene diversity between population groups is smaller than the gene diversity within the population groups, indicating the fact that only a small fraction of the total gene diversity is due to the differences between the population groups. Further, it also suggests that the populations under investigation are at an early stage of genetic differentiation.

The coefficient of gene diversity, (GST) value among six tribes of present study is comparatively high at A1A2 BO, Duffy, HB and G-6-PD

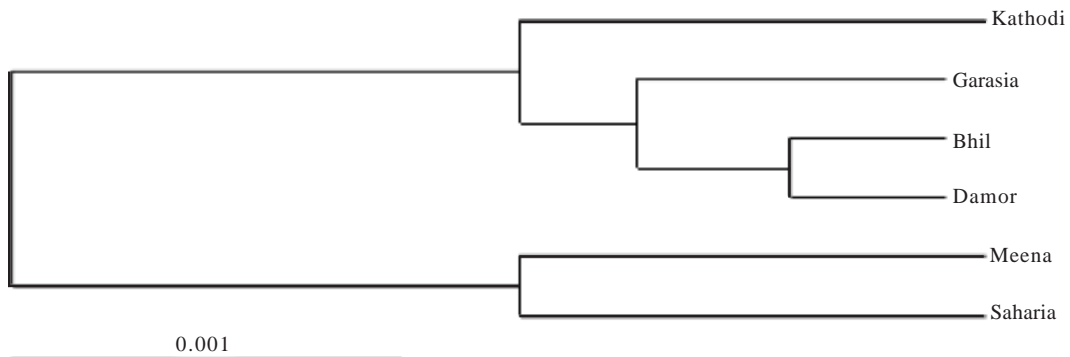


Fig. 1. Unrooted UPGMA – Tree of Nei’s standard genetic distances among six tribes of Rajasthan

loci (that is, 0.0125 to 0.0467), whereas, little differentiation has been recorded at MNSs, Lewis, Kidd and HP loci. Moderate GST has been exhibited by loci Rhesus and Kell.

Genetic Distance: Nei's standard distance matrix for the present study is presented in Table 6. It has been observed that the genetic distance measure (D) is comparatively low between Bhil, Damor, Garasia and Kathodi, when compared to Mina and Saharia tribes, who show less distance among them.

The overall 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 clear from the figure that the studied tribes make two main clusters, one of Mina and Saharia, other of Bhil, Damor, Garasia and Kathodi. Within the cluster Bhil and Damor are closest joined by Garasia and then Kathodi.

CONCLUSION

From the above results it can be concluded that the genetic structure and genetic affinity of the studied populations partially support the ethnographic view that there might have existed two main stems of tribal population, that is, Mina and Bhil tribes in ancient Rajasthan. The Saharias exhibit genetic proximity to Mina and higher genetic distance with other studied tribes and might have a necessarily early origin from the Mina stem. The second cluster of Damor, Garasia and Kathodi show genetic affinity to Bhil tribe, the reason might be their phylogenetic origin involving Bhil stem, which contradicts with the ethnographic history of at least Damor and Garasia tribes. The other plausible reason could be gene flow between these populations due to the geographic proximity. A common situation observed in India by many studies is that genetic makeup of the populations show more affinity if they are geographically close rather due to the ethnic or socio-cultural affinity.

ACKNOWLEDGEMENTS

Thanks to The Secretary, Department of Environment and Forests, Govt. of India, New Delhi, India, for providing financial assistance to Prof. Dr. M. K. Bhasin (Principal Investigator) for the Project "Human Settlements, Human Activities and Health Status among Tribal Groups

of Northern India with Special Reference to Rajasthan" and Prof. Dr. S.M.S. Chahal (Department of Human Biology, Punjabi University, Patiala) for his help in the analysis of some genetic markers of the present study.

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