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Anthropogenetic Profile of "denotified" Tribes (Vimukt Jatis) of Punjab (North-West India) and its Social Implication

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INTRODUCTION

The “denotified” tribes, also known as the Vimukt Jatis, are the tribes that were originally listed under the Criminal Tribes Act of 1871, as Criminal Tribes and "addicted to the systematic commission of non-bailable offences." Once a tribe became "notified" as criminal, all its members were required to register with the local magistrate, failing which they would be charged with a crime under the Indian Penal Code.

The Act was repealed in August 1949 and former "criminal tribes" were “denotified” in 1952, when the Act was replaced with the Habitual Offenders Act 1952 of Government of India, and in 1961 state governments started releasing lists of such tribes. At the time of the independence in 1947, there were 13 million people in 127 communities who faced constant surveillance, search and arrest without warrant if any member of the group was found outside the prescribed area.

The creation of these categories should be seen in the context of colonialism. The British authorities listed them separately by creating a category of castes or tribes labeled as criminal. The first Census of India was conducted in 1871 and at that time there was no consensus or any definition of "tribe". The terms "Tribe" and "Caste" were used interchangeably for these communities. In this colonial context, the term "Tribe" connoted the notions of primitiveness and backwardness and hence the assumption that these tribes needed to be civilized or transformed.

Today, there are 313 Nomadic Tribes and 198 “denotified” tribes in India, yet the legacy of the Act continues to haunt the majority of 60 million people belonging to these tribes, especially as their notification over a century ago has meant not just alienation and stereotyping by the police and the media, but also economic hardships. A large number of them can still only subscribe to a slightly altered label, the "Vimukt jatis" (or the Ex-Criminal Tribes).

Located on the North-West border of India, Punjab has been the gateway of the country for the entry of different racial/ethnic stocks over millennia. Historically, the people of Punjab are supposed to be progeny of a mixture of several proto- and post-Harappa invaders who entered this land from the West from time to time, and of original autochthonous settlers of the area (Rose, 1919).

Officially, presently there is no tribe in Punjab. However, there are seven “denotified” tribes inhabiting the state namely, the Bauria, Bazigar, Bangala, Barad, Gandhila, Nat and Sansi. Most of these have their pockets of concentration though few are distributed all over Punjab. Their total population as per the Census of India 2001 was 436,809, the Bazigar having the highest population (208,442), followed by the Sansi (105,337), Bauria (102,232), Barar (8,679), Bangali (7,765), Gandhila (3,283) and Nat (1,071). The distribution of these “denotified” tribes in Punjab is shown in Table 1.

Table 1. The “denotified” tribes and their distribution in Punjab (Census of India, 2001).

“Denotified” tribe	Population	District(s) of Punjab
Bauria	102,232	Faridkot, Bathinda, Mansa, Moga, Ferozepur, Muktsar, Sangrur, Ludhiana, Kapurthala
Bazigar	208,442	Whole State
Bangali	7,765	Ropar, Gurdaspur, Amritsar, Ludhiana, Bathinda, Sangrur, Jalandhar, Kapurthala, Muktsar, Hoshiarpur
Barar	8,679	Hoshiarpur, Gurdaspur, Jalandhar, Amritsar
Gandhila	3,283	Patiala
Nat	1,071	Amritsar, Ferozepur, Sangrur, Ludhiana, Jalandhar
Sansi	105,337	Gurdaspur, Hoshiarpur, Jalandhar, Ludhiana, Patiala, Sangrur
Total	436,809	All districts

The “denotified” tribes (Vimukt Jatis) of Punjab had been struggling since India’s independence, first to remove the tag of criminality attached to them during the British colonial regime and second, to acquire the status of Schedule Tribe (ST). It is ironic that they had been wrongly placed in the category of Scheduled Caste (SC) in Punjab and they see this as an attempt to denigrate them.

The Vimukt Jatis had been contesting for Scheduled Tribe (ST) status for long so that they have a stake in reservation quota for jobs, admissions, scholarships and other benefits announced from time to time by the government for the ST. Since as of now they are clubbed with the Scheduled Castes of Punjab, the so-called ‘creamy SC layer’ (e.g. the Ramdasia, Balmiki etc.) takes all the benefits meant for SC. In fact, the illiteracy and backwardness of the Vimukt Jatis are coming in their way to garner the benefits of any govermental reservation policy.

The present study is a biological anthropology approach to establish the genetic profile of the Vimukt Jatis of Punjab. As a detailed social anthropological study is already available on the Vimukt Jatis of Punjab which indicate a tribal status for them (Singh, 2010), it would be interesting to examine if the results from the present anthropogenetic approach corroborate this finding. That is, the present study is an attempt to provide genetic basis to the findings of the social-anthropological inquiry already reported in literature on the Vimukt Jatis of Punjab. This will help make the case of the Vimukt Jatis, a socially disadvantaged group of people, for a tribal status more rational and logical thereby helping them get their true identity validated, enabling them get the financial and other benefits due to them.

Social anthropological evidence

The “denotified” tribes have been relevant to other communities of Punjab, directly or indirectly, but they neither adopted the Punjabi culture nor mixed with them till they were settled forcibly by the colonial British government. Even then the “denotified” tribes maintained distance from the other communities. These people were suspected to pose threat to the law and order, as thieves and burglars. Thus they were interned in the reformatories – industrial and agricultural settlements – where they were compelled to work for their living.

After remaining in denial over the existence of Scheduled Tribes in Punjab, the Punjab government has now been handed a report of a survey conducted by the Punjabi University, Patiala (Singh, 2010) that concludes that seven ex-criminal (“denotified”) tribes and Gurjar fulfill the parameters of "tribe" laid down by the Union Government and the social anthropologists. It states that the conditions under which the “denotified” tribes live in are dismal compared to the major Scheduled Caste communities of Punjab such as Adharmis and Balmikis, but even then the former have been denied the benefits of any reservation policy.

Physical (biological) anthropological evidence

With only a couple of serological observations on the ABO blood groups (Sidhu and Sidhu, 1980, 1988) in the Bazigar and Sansi and a solitary report on the RH(D) blood groups in the Bazigar (Sidhu and Sidhu, 1988), the “denotified” Tribe populations of Punjab are little represented on the genetic map of the state.

AIM AND OBJECTIVES

The main aim of the present investigation was to anthropogenetically characterize the “denotified” tribes of Punjab using original data from 10 different genetic markers and 5 anthropometric measurements and use the results thus generated to address the problem of their tribal status scientifically and rationally. The two main objectives of the present investigation were as follows.

1. To characterize genetically the 7 "denotified" tribes (Vimukt Jatis) of Punjab viz., the Bazigar, Sansi, Bauria, Barad, Bangala, Gandhila and Nat using original allele frequency data from a battery of serological and DNA markers. Their anthropometric profile will also be investigated.

2. To ascertain the tribal character, if any, of the "denotified" tribes (Vimukt Jatis) of Punjab using the present genetic data and that reported in the literature on common markers on different non-tribal and tribal populations of North and Central India, respectively.

METHODOLOGY

The anthropometric measurements such as stature and those required for the calculation of the cephalic index i.e. maximum head breadth and maximum head length, and nasal index i.e. nasal breadth and nasal height were taken in the field on a total of 1,154 male and female subjects belonging to seven "denotified" tribes of Punjab viz., the Bazigar, Sansi, Bauria, Bangala, Barad, Gandhila and Nat (Table 2), following standard anthropometric techniques as given in Martin and Saller (1957) and Singh and Bhasin (1989). Ethical clearance for the present project was obtained from the Institutional Ethical Committee of the Punjabi University, Patiala.

Table 2. Village and district wise sampling and sample sizes for the present study.

"Denotified" tribe	Village	District	Sample size	
			Genetic analysis	Anthropometry
Bazigar	Arnetu	Patiala	68	
	Sanour	Patiala	64	
	Bahadurgarh	Patiala	28	
	Amargarh	Sangrur	72	
		Total	**232**	**303**
Sansi	Dudhad	Patiala	15	
	Langroi	Patiala	23	
	Mithu Majra	Patiala	14	
	Bagrian	Sangrur	25	
	Kheri Jattan	Sangrur	34	
	Rohti Channa	Patiala	20	
	Kakrala	Patiala	28	
	Samadgarh	Sangrur	63	
		Total	**222**	**241**
Bauria	Leelan Megh Singh	Ludhiana	198	
	Sherpur Kalan	Ludhiana	2	
		Total	**200**	**202**
Bangala	Doraha	Ludhiana	68	

	Dugri		37	
		Total	**105**	**105**
Barar	Piplanwala	Hoshiarpur	37	
	Saila Khurd		30	
	Singdiwala		07	
	Banga	Shaheed Bhagat Singh Nagar	43	
		Total	**117**	**114**
Gandhila	Arnetu (n=89)	Patiala		
	Sadharanpur		13	
	Bakraha		12	
		Total	**114**	**134**
Nat	Bhedpura	Patiala	10	
	Dhablan		07	
	Mehmadpur		04	
	Shutrana		02	
	Aakad		02	
	Wazirpur	Sangrur	07	
	Chuharpur		03	
	Khunimajra	Rupnagar	22	
	Bhankarpur	Sahibzada Ajit Singh Nagar	04	
		Total	**55**	**55**
		Grand total	**1055**	**1154**

Anthropometry

The following 5 anthropometric measurements were taken on subjects belonging to seven "denotified" tribes of Punjab following the standardized techniques as given by Martin and Saller (1957) and Singh and Bhasin (1989). Stature (height vertex) was measured with the help of an anthropometric rod. For head and nose measurements, respectively, spreading and sliding calipers were used.

1. Stature: It was taken as the vertical distance from the highest point on the head (vertex) of the subject to the floor in the Frankfort horizontal (F-H) plane.
2. Head length: It was measured as the distance from the most prominent point in the mid-sagittal plane of forehead (glabella) to the most prominent point on external Occipital protuberance of the subject.
3. Head breadth: It was taken as the greatest transverse diameter on the head of the subject from euryon to euryon (a bilaterally paired point that forms the terminus of the line of greatest breadth of the skull).
4. Nasal height: It was measured as a distance from the point of deepest concavity of the soft tissue contour of the root of the nose (nasion) of the subject to the point where the lowest border of the nose meets the outer contour of the lip (subnasale).
5. Nasal breadth: It was measured as the distance between two alar points on the nose of the subject.

The head and nose measurements so obtained were used to calculate the following two indices.

Cephalic Index (C.I.) = (Head Breadth / Head Length) X 100
Nasal Index (N.I.) = (Nasal Breadth /Nasal Height) X 100

After obtaining the prior informed consent (Appendix-I), 3-5 ml blood sample was collected in sterile EDTA.K_2 vial from a total of 1,051 randomly chosen, unrelated, healthy adult male and female subjects belonging to the seven "denotified" tribes of Punjab viz. the Bazigar (n=232), Sansi (n=222), Bauria (n=200), Bangala (n=105), Barad (n=117), Gandhila (n=114) and Nat (n=61) (Table 2). The samples were collected from various districts of Punjab in different field works transported personally to the laboratory in the Department of Human Genetics, Punjabi University, Patiala for their detailed laboratory analyses.

Serological analyses

In the laboratory, the red cells were typed for A1A2BO and RH(D) blood groups by the tube method using Anti-A, Anti-A1, Anti-B and Anti-D, following standard serological techniques (Dunsford and Bowley, 1967).

DNA genotyping

For the genetic analysis, genomic DNA was extracted from the collected blood samples using the inorganic method of Miller et al. (1988) and it was subjected to quality and quantity checks using a spectrophotometer. Each DNA sample was genotyped for a battery of 8 Alu Ins/Del loci (*APO*, *CD4*, *PV92*, *TPA25*, *FXIIIB*, *ACE*, *PLAT*, *D1*) following the primer sequences and annealing temperatures listed in Table 3. Genotyping involved amplification of the DNA by polymerase chain reaction (PCR) using locus-specific primers for 8 *Alu* Ins/Del loci. The amplified PCR products were run on 2% agarose gel with Ethidium Bromide (EtBr) as a stain dye. The results were visualized in a UVP Gel Doc-It Imaging System and recorded (Figs. 1-8).

Table 3. Primer sequences and annealing temperatures for the studied *Alu* Ins/Del loci.

Marker	Primer sequence	Annealing temperature	Reference
ACE	F : 5’– CTGGAGACCACTCCCATCCTTTCT - 3’ R : 5’– GATGTGGCCATCACATTCGTCAGAT - 3’	58° C	Majumder *et al.* (1999)
APO	F : 5’– AAGTGCTGTAGGCCATTTAGATTAG - 3’ R : 5’–AGTCTTCGATGACAGCGTATACAGA - 3’	50° C	Majumder *et al.* (1999)
CD4	F : 5’-AGGCCTTGTAGGGTTGGTCTGATA - 3’ R : 5’- TGCAGCTGCTGAGTGAAAGAACTG-3’	63° C	Majumder *et al.* (1999)
D1	F : 5’-TGCTGATGCCCAGGGTTAGTAAA - 3’ R : 5’TTTCTGCTATGCTCTTCCCTCTC -3’	56.8° C	Majumder *et al.* (1999)
FXIIIB	F : 5’ TCAACTCCATGAGATTTTCAGAAGT - 3’ R : 5’- CTGGAAAAATGTATTCAGGTGAGT -3’	54.4° C	Majumder *et al.* (1999)
PLAT	F : 5’-GTG AAA AGC AAG GTCTAC CAG - 3’ R : 5’- TGCAGCTGCTGAGTAAAGAATG-3’	59° C	Stoneking et al. (1999)
PV92	F:5’AACTGGGAAAATTTGAAGAGAAAGT - 3’ R : 5’GAC ACC GAG TTC ATC TTG AC -3’	52.5° C	Majumder *et al.* (1999)
TPA25	F : 5’- GTAAGAGTTCCGTAACAGGAC AGCT- 3’ R : 5’- CCCCACCCTAGGAGAACTTCT CTTT-3’	54° C	Majumder *et al.* (1999)

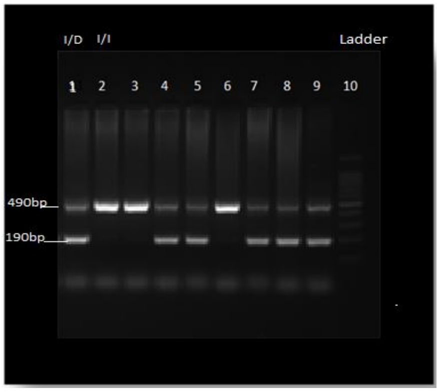


Fig. 1. Gel image of genotypes of *Alu* ACE

Allele	Genotype	Band size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	490bp	2, 3, 6
Deletion (D)	Heterozygous (I/D)	490bp, 190bp	1, 4, 5, 7, 8, 9
-	Homozygous deletion (D/D)	190bp	-

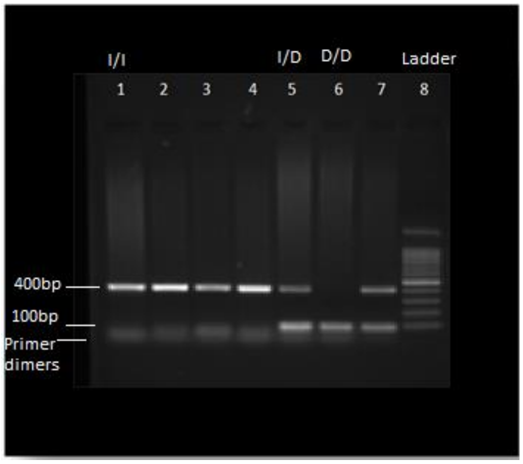


Fig. 2. Gel image of genotypes of *Alu* APO

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	400bp	1, 2, 3, 4
Deletion (D)	Heterozygous (I/D)	400bp, 100bp	5, 7
	Homozygous deletion (D/D)	100bp	6

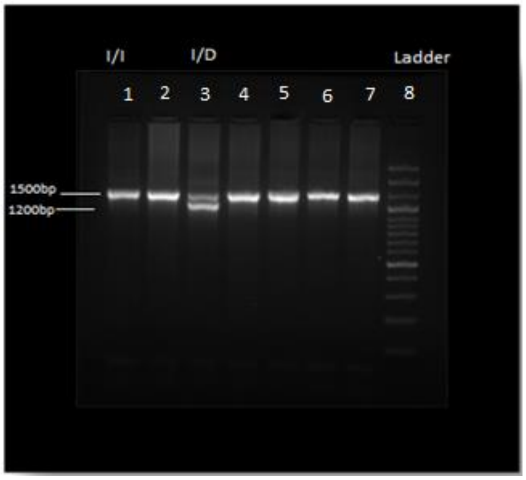


Fig. 3. Gel image of genotypes of *Alu* CD4

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	1500bp	1, 2, 4, 5, 6, 7
Deletion (D)	Heterozygous (I/D)	1500bp, 1200bp	3
	Homozygous deletion (D/D)	1200bp	-

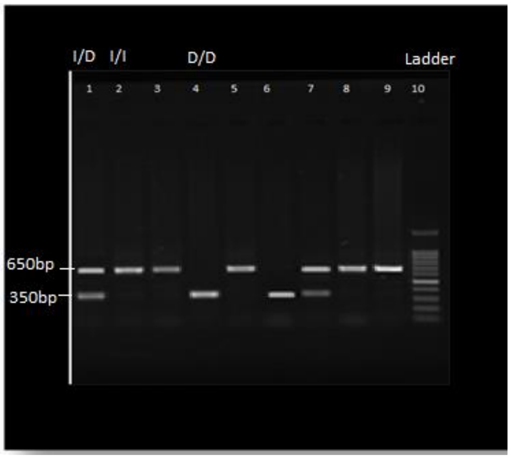


Fig. 4. Gel image of genotypes of *Alu* D1

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	650bp	2, 3, 5, 8, 9
Deletion (D)	Heterozygous (I/D)	650bp, 350bp	1, 7
	Homozygous deletion (D/D)	350bp	4, 6

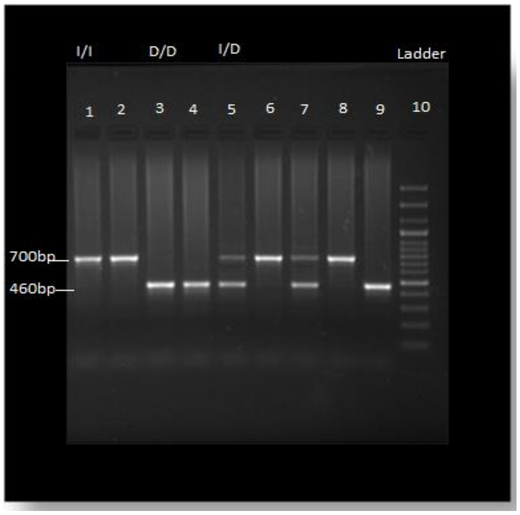


Fig. 5. Gel image of genotypes of *Alu* FXIIIB

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	700bp	1, 2, 6, 8
Deletion (D)	Heterozygous (I/D)	700bp, 460bp	5, 7
-	Homozygous deletion (D/D)	460bp	3, 4, 9

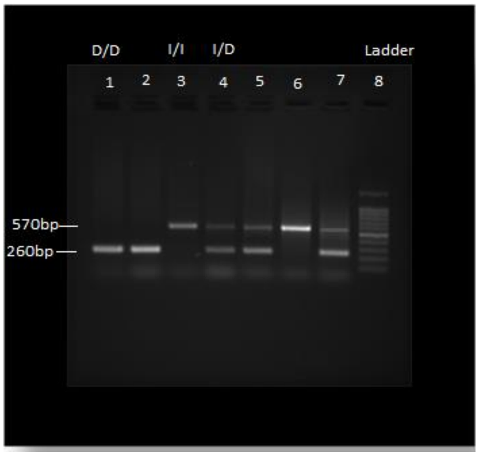


Fig. 6. Gel image of genotypes of *Alu* PLAT

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	570bp	3, 6
Deletion (D)	Heterozygous (I/D)	570bp, 260bp	4, 5, 7
-	Homozygous deletion (D/D)	260bp	1, 2

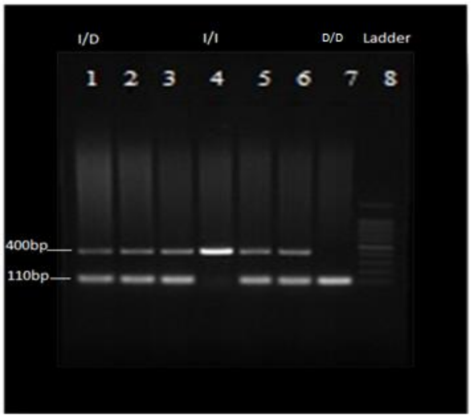


Fig. 7. Gel image of genotypes of *Alu* PV92

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	400bp	4
Deletion (D)	Heterozygous (I/D)	400bp, 110bp	1, 2, 3, 5, 6
-	Homozygous deletion (D/D)	110bp	7

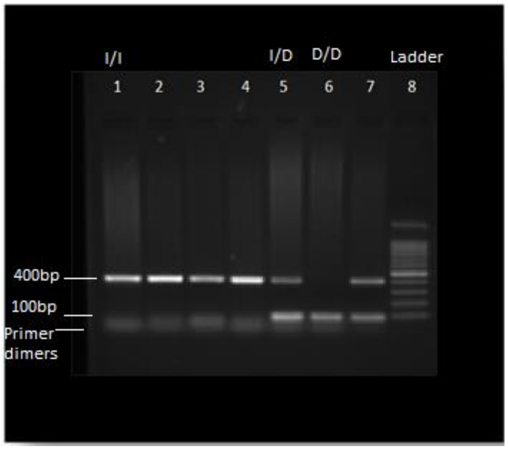


Fig. 8. Gel image of genotypes of *Alu* TPA25

Allele	Genotype	Band Size	Lane number(s)
Insertion (I)	Homozygous insertion (I/I)	400bp	1, 2, 3, 4
Deletion (D)	Heterozygous (I/D)	400bp, 100bp	5, 7
	Homozygous deletion (D/D)	100bp	6

Statistical Analyses

Allele frequencies were calculated in the ABO blood group system following Yasuda (1984), in the RH(D) blood group system by the square root method and in the DNA markers by the gene counting method (Mourant *et al.*, 1976). Deviations from the Hardy–Weinberg equilibrium were studied by the goodness-of-fit chi-square (χ^2_{HW}) test using phenotype/genotype data. Contingency χ^2 test was used to study overall inter-group differences using phenotype counts of A1A2BO and RH(D) loci and genotype counts for Alu Ins/Del markers. To assess the extent of gene differentiation among the present "denotified" ” tribes of Punjab, the Nei’s (1973) measure of gene differentiation was calculated. To seek genomic affinities among the present "denotified" ” tribes of Punjab, the pair wise estimates of genetic distance (*D*) (Nei, 1972) were calculated and dendrograms were constructed by UPGMA method (Sneath and Sokal, 1973) using PHYLIP 3.695 Software

RESULTS

Anthropometric Analysis

Five anthropometric measurements (Stature, head breadth, head length, nasal height and nasal breadth) were taken on a total of 1154 male and female subjects belonging to 7 "denotified" tribes of Punjab viz., the Gandhila, Barad, Bangala, Bazigar, Sansi, Bauria and Nat, using the standard anthropometric instruments and techniques (Martin and Saller, 1957; Singh and Bhasin, 1989).

Head and nose measurements were used to calculate cephalic index (C.I.) and nasal index (N.I.), respectively. Tables 4-11 present the results of the anthropometric investigation in the present study.

Stature, Nasal Index and Cephalic Index

Descriptive statistics for the stature, nasal index and cephalic index such as mean, standard deviation (S.D.) and standard error (S.E.) are given in Table 4.

Table 4. Descriptive statistics of the Stature, Nasal Index and Cephalic Index in various "denotified" tribes of Punjab, North West India.

"Denotified" tribe	Gender	n	Stature (mm)			Nasal Index (N.I.)			Cephalic Index (C.I.)		
			Mean	S.D.	S.E.	Mean	S.D.	S.E.	Mean	S.D.	S.E.
Gandhila	Male	26	1563.8	70.0	13.7	79.6	9.1	1.8	77.1	3.9	0.8
	Female	108	1577.1	73.3	7.1	82.5	9.1	0.9	76.5	3.8	0.4
	Total	134	1574.5	72.6	6.3	81.9	9.1	0.8	76.6	3.9	0.3
Barad	Male	38	1532.1	86.0	14.0	80.5	11.8	1.9	79.6	3.7	0.6
	Female	76	1536.3	63.1	7.2	79.0	9.6	1.1	79.2	2.9	0.3
	Total	114	1534.9	71.2	6.7	79.5	10.4	1.0	79.3	3.2	0.3
Bangala	Male	27	1714.2	56.0	10.8	76.5	8.1	1.6	78.2	4.3	0.8
	Female	78	1542.6	52.1	5.9	74.1	7.6	0.9	83.1	3.2	0.4
	Total	105	1586.7	92.1	9.0	74.7	7.8	0.7	81.9	4.1	0.4
Bazigar	Male	84	1678.6	63.2	6.9	78.7	9.3	1.0	75.4	3.4	0.4
	Female	219	1538.5	53.9	3.6	75.7	8.7	0.6	78.2	3.1	0.2
	Total	303	1577.4	84.5	4.9	76.5	8.9	0.5	77.5	3.4	0.2
Bauria	Male	55	1650.9	68.2	9.2	73.8	8.4	1.1	78.6	3.3	0.5
	Female	147	1537.3	54.1	4.5	70.5	8.4	0.7	80.7	3.5	0.3
	Total	202	1568.1	77.0	5.4	71.4	8.5	0.6	80.1	3.5	0.3
Sansi	Male	72	1596.9	88.2	10.4	84.9	4.8	0.6	78.6	3.4	0.4
	Female	169	1571.6	71.8	5.5	71.5	5.2	0.4	79.0	4.1	0.3
	Total	241	1579.1	77.8	5.0	75.5	7.9	0.5	78.9	3.9	0.3

Nat	Male	11	1677.3	39.8	12.0	72.4	8.9	2.7	76.9	4.0	1.2
	Female	44	1532.6	54.3	8.2	68.4	7.1	1.1	77.7	5.0	0.8
	Total	55	1561.5	77.8	10.5	69.2	7.6	1.0	77.5	4.8	0.7

Stature

Table 5 presents gender wise classification of the stature as proposed by Martin and Saller (1957). Based on the results of the stature observed in the present "denotified" tribes of Punjab, the subjects were classified into different categories as shown in Table 6. Short stature was common only in the Barad with a total (male + female) frequency of 40.3%. The Gandhila, Bazigar and Sansi showed an overall preponderance for lower medium stature while the Bauria and Nat were observed to have medium type of stature and tall stature was observed to be common in the Bangala. No subject was classified under pygmy and giant stature types in the present "denotified" tribes of Punjab.

Table 5. Classification of stature according to Martin and Saller (1957).

Class	Stature range (mm)	
	Males	Females
Pygmy	Under 1290	Under 1209
Very Short	1300 - 1499	1210 – 1399
Short	1500 – 1599	1400 – 1489
Lower Medium	1600 – 1639	1490 – 1529
Medium	1640 – 1669	1530 – 1559
Upper Medium	1670 – 1699	1560 – 1589
Tall	1700 – 1799	1590 – 1679
Very Tall	1800 – 1999	1680 – 1869
Giant	2000 and above	1870 and above

Table 6. Distribution of subjects of seven "denotified" tribes of Punjab according to stature type.

“Denotified” tribe	Gender	Stature type						
		Very Short	Short	Lower Medium	Medium	Upper Medium	Tall	Very Tall
Gandhila (n=134)	Male	00 (0.0%)	04 (3.0%)	04 (3.0%)	03 (2.2%)	05 (3.7%)	09 (6.7%)	01 (0.75%)
	Female	00 (0.0%)	09 (6.7%)	30 (22.4%)	26 (19.4%)	19 (14.2%)	23 (17.2%)	01 (0.75%)
	Total	00 (0.0%)	13 (9.7%)	34 (25.4%)	29 (21.6%)	24 (17.9%)	32 (23.9%)	02 (1.5%)
Barad (n=114)	Male	01 (0.9%)	20 (17.5%)	11 (9.6%)	04 (3.5%)	00 (0.0%)	02 (1.7%)	00 (0.0%)
	Female	02 (1.7%)	26 (22.8%)	22 (19.3%)	15 (13.2%)	07 (6.1%)	04 (3.5%)	00 (0.0%)
	Total	03 (2.6%)	46 (40.3%)	33 (28.9%)	19 (16.7%)	07 (6.1%)	06 (5.2%)	00 (0.0%)
Bangala (n=105)	Male	00 (0.0%)	00 (0.0%)	02 (1.9%)	04 (3.8%)	03 (2.8%)	17 (16.2%)	01 (0.95%)
	Female	01 (0.95%)	10 (9.5%)	20 (19.0%)	19 (18.1%)	15 (14.3%)	13 (12.4%)	00 (0.0%)
	Total	01 (0.95%)	10 (9.5%)	22 (20.9%)	23 (21.9%)	18 (17.1%)	30 (28.6%)	01 (0.95%)
Bazigar (n=303)	Male	00 (0.0%)	08 (2.6%)	13 (4.3%)	14 (4.6%)	15 (4.9%)	31 (10.2%)	01 (0.3%)
	Female	00 (0.0%)	42 (13.9%)	55 (18.1%)	49 (16.2%)	40 (13.2%)	32 (10.6%)	03 (1.0%)
	Total	00 (0.0%)	50 (16.5%)	68 (22.4%)	63 (20.8%)	55 (18.1%)	63 (20.8%)	04 (1.3%)
Bauria (n=202)	Male	02 (1.0%)	09 (4.4%)	13 (6.4%)	10 (5.0%)	08 (3.9%)	12 (5.9%)	01 (0.5%)
	Female	00 (0.0%)	28 (13.9%)	31 (15.3%)	36 (17.8%)	29 (14.4%)	22 (10.9%)	01 (0.5%)
	Total	02 (1.0%)	37 (18.3%)	44 (21.7%)	46 (22.8%)	37 (18.3%)	34 (16.8%)	02 (1.0%)
Sansi (n=241)	Male	00 (0.0%)	08 (3.3%)	16 (6.6%)	13 (5.4%)	18 (7.5%)	15 (6,2%)	02 (0.8%)
	Female	00 (0.0%)	25 (10.4%)	44 (18.3%)	44 (18.3%)	28 (11.6%)	24 (10.0%	04 (1.7%)
	Total	00 (0.0%)	33 (13.7%)	60 (24.9%)	57 (23.6%)	46 (19.1%)	39 (16.2%)	06 (2.5%)
Nat (n=55)	Male	00 (0.0%)	00 (0.0%)	00 (0.0%)	05 (9.1%)	03 (5.5%)	03 (5.5%)	00 (0.0%)
	Female	01 (1.8%)	07 (12.7%)	12 (21.8%)	12 (21.8%)	08 (14.5%)	04 (7.3%)	00 (0.0%)
	Total	01 (1.8%)	07 (12.7%)	12 (21.8%)	17 (30.9%)	11 (20.0%)	07 (12.8%)	00 (0.0%)

Nasal Index

Table 7 presents the classification of nose type based on mean Nasal Index (NI) proposed by Martin and Saller (1957).

Table 7. Different nose types on the basis of Nasal Index (NI) according to Martin and Saller (1957).

Nose type	Nasal Index Range (mm)
Leptorrhine	< 69.9
Mesorrhine	70 – 84.9
Platyrrhine	85 – 99.9
Hyperplatyrrhine	> 100

Table 8 shows the frequency distribution of different nose types in seven "denotified" tribes of Punjab. The table shows that mesorrhine nose type was commonly found in all of them with a frequency distribution ranging from 66.7% in the Bangala to 50.0% in the Bauria except for the Nat (38.2%). The frequency distribution of different nose types in the present Bangala, Bazigar, Bauria and Sansi "denotified" tribes of Punjab followed a sequence pattern mesorrhine > leptorrhine > platyrrhine > hyperplatyrrhine. While for the Gandhila and Barad the sequence pattern observed was mesorrhine > platyrrhine > leptorrhine > hyperplatyrrhine. Hyperplatyrrhine showed the lowest frequency in all the studied "denotified" tribes of the present study and the nose type was found absent in both the Sansi and Nat.

Table 8. Frequency distribution of nose types in 7 "denotified" tribes of Punjab, North West India.

"Denotified" tribe	Nasal index (NI)	Nose type	Male	%	Female	%	Total	%
Gandhila	< 69.9	Leptorrhine	3	2.2	9	6.7	12	8.9
	70 – 84.9	Mesorrhine	15	11.2	59	44.0	74	55.2
	85 – 99.9	Platyrrhine	8	6.0	36	26.9	44	32.9

	> 100	Hyperplatyrrhine	0	0.0	4	3.0	4	3.0
	Total		26	19.4	108	80.6	134	100
Barad	< 69.9	Leptorrhine	7	6.1	17	15.0	24	21.1
	70 – 84.9	Mesorrhine	21	18.4	37	32.5	58	50.9
	85 – 99.9	Platyrrhine	9	7.9	20	17.5	29	25.4
	> 100	Hyperplatyrrhine	1	0.9	2	1.7	3	2.6
	Total		38	33.3	76	66.7	114	100
Bangala	< 69.9	Leptorrhine	4	3.8	23	21.9	27	25.7
	70 – 84.9	Mesorrhine	21	20.0	49	46.7	70	66.7
	85 – 99.9	Platyrrhine	2	1.9	6	5.7	8	7.6
	> 100	Hyperplatyrrhine	0	0.0	0	0.0	0	0.0
	Total		27	25.7	78	74.3	105	100
Bazigar	< 69.9	Leptorrhine	13	4.3	53	17.5	66	21.8
	70 – 84.9	Mesorrhine	51	16.8	133	43.9	184	60.7
	85 – 99.9	Platyrrhine	20	6.6	31	10.2	51	16.8
	> 100	Hyperplatyrrhine	0	0.0	2	0.6	2	0.6
	Total		84	27.7	219	72.3	303	100
Bauria	< 69.9	Leptorrhine	18	8.9	69	34.2	87	43.1
	70 – 84.9	Mesorrhine	32	15.8	69	34.2	101	50.0
	85 – 99.9	Platyrrhine	4	2.0	9	4.5	13	6.4
	> 100	Hyperplatyrrhine	1	0.5	0	0.0	1	0.5
	Total		55	27.2	147	72.8	202	100
	< 69.9	Leptorrhine	16	6.6	43	17.9	59	24.5
	70 – 84.9	Mesorrhine	47	19.5	108	44.8	155	64.3

Sansi	85 – 99.9	Platyrrhine	9	3.7	18	7.5	27	11.2
	> 100	Hyperplatyrrhine	0	0	0	0	0	0
	Total		72	29.8	169	70.2	241	100
Nat	< 69.9	Leptorrhine	6	10.9	26	47.3	32	58.2
	70 – 84.9	Mesorrhine	3	5.5	18	32.7	21	38.2
	85 – 99.9	Platyrrhine	2	3.6	0	0.0	2	3.6
	> 100	Hyperplatyrrhine	0	0.0	0	0.0	0	0.0
	Total		11	20.0	44	80.0	55	100

Cephalic Index

Table 9 presents the classification of head types based on Cephalic Index (C.I.) as proposed by Martin and Saller (1957).

Table 9. Different head types on the basis of Cephalic Index (C.I.) according to Martin and Saller (1957).

Head type	Cephalic Index range (mm)
Dolichocephalic	< 74.9
Mesocephalic	75 – 79.9
Brachycephalic	80 – 84.9
Hyperbrachycephalic	> 85

The distribution frequency for different head types in present “denotified” tribes of Punjab is given in Table 10 according to which mesocephalic head was observed in the highest frequency among the Gandhila, Barad, Bazigar, Sansi and Nat ranging from as high as 57.4% in the Bazigar to 45.4% in the Nat. However, brachycephalic head type was observed in highest frequency in the Bangala (44.8%) and Bauria (42.1%). The sequence pattern for distribution of different head types in order of high to low frequency was observed to be similar in the Gandhila and Nat (mesocephalic > doliococephalic >brachycephalic > hyperbrachycephalic). While a similar pattern as mesocephalic >brachycephalic > dolicocephalic > hyperbrachycephalic was observed in the Barad, Bazigar and Sansi. The Bauria and Bangala showed a different pattern from rest of the five populations, the sequence pattern observed in former two populations was brachycephalic > mesocephalic > hyperbrachycephalic > dolicocephalic and brachycephalic > hyperbrachycephalic > mesocephalic > dolicocephalic.

Table 10. Distribution of head types in 7 "denotified" tribes of Punjab, North West India.

"Denotified" tribe	Cephalic Index (CI)	Head type	Male	%	Female	%	Total	%
Gandhila	< 74.9	Dolichocephalic	10	7.5	35	26.1	45	33.6
	75 – 79.9	Mesocephalic	10	7.5	52	38.8	62	46.3
	80 – 84.9	Brachycephalic	5	3.7	19	14.2	24	17.9
	> 85	Hyperbrachycephalic	1	0.7	2	1.5	3	2.2
	Total		26	19.4	108	80.6	134	100
Barad	< 74.9	Dolichocephalic	4	3.5	6	5.3	10	8.8
	75 – 79.9	Mesocephalic	21	18.4	35	30.7	56	49.1
	80 – 84.9	Brachycephalic	9	7.9	34	29.8	43	37.7
	> 85	Hyperbrachycephalic	4	3.5	1	0.9	5	4.4
	Total		38	33.3	76	66.7	114	100
Bangala	< 74.9	Dolichocephalic	6	5.7	2	1.9	8	7.6
	75 – 79.9	Mesocephalic	15	14.3	8	7.6	23	21.9
	80 – 84.9	Brachycephalic	4	3.8	43	41.0	47	44.8
	> 85	Hyperbrachycephalic	2	1.9	25	23.8	27	25.7
	Total		27	25.7	78	74.3	105	100
Bazigar	< 74.9	Dolichocephalic	34	11.2	29	9.6	63	20.8
	75 – 79.9	Mesocephalic	43	14.2	131	43.2	174	57.4

	80 – 84.9	Brachycephalic	7	2.3	57	18.8	64	21.1
	> 85	Hyperbrachycephalic	0	0.0	2	0.7	2	0.7
	Total		84	27.7	219	72.3	303	100
Bauria	< 74.9	Doliochocephalic	7	3.4	6	3	13	6.4
	75 – 79.9	Mesocephalic	27	13.4	56	27.7	83	41.1
	80 – 84.9	Brachycephalic	19	9.4	66	32.7	85	42.1
	> 85	Hyperbrachycephalic	2	1	19	9.4	21	10.4
	Total		55	27.2	147	72.8	202	100
Sansi	< 74.9	Dolichocephalic	22	9.1	15	6.2	37	15.3
	75 – 79.9	Mesocephalic	41	17.0	71	29.5	112	46.5
	80 – 84.9	Brachycephalic	9	3.7	70	29.1	79	32.8
	> 85	Hyperbrachycephalic	0	0.0	13	5.4	13	5.4
	Total		72	29.8	169	70.2	241	100
Nat	< 74.9	Dolichocephalic	3	5.5	11	20.0	14	25.5
	75 – 79.9	Mesocephalic	6	10.9	19	34.5	25	45.4
	80 – 84.9	Brachycephalic	2	3.6	11	20.0	13	23.6
	> 85	Hyperbrachycephalic	0	0.0	3	5.5	3	5.5
	Total		11	20.0	44	80.0	55	100

Table 11 presents gender wise distribution of stature, head and nose type in male and female subjects of the seven “denotified” tribes of Punjab. As inferred from the mean stature in male subjects of the seven “denotified” tribes, the short stature type was found most common in the Gandhila, Barad and Sansi populations followed by medium stature type in the Bauria males and upper medium in the Bazigar and Nat males. In contrast to this the female subjects of the “denotified” tribes showed a preponderance of medium stature in all except Gandhila and Sansi females among which upper medium stature was most commonly found. The mesorrhine nose type was most commonly observed for all “denotified” tribes of Punjab except for the Nat females in which leptorrhine nose type was most commonly observed and mesocephalic head type was most commonly observed in all “denotified” tribes of Punjab except in the Bauria and Bangala females in which brachycephalic head type was found to be most common.

Table 11. Gender wise distribution of the stature, head type and nose type in 7"denotified" tribes of Punjab.

"Denotified" tribe	Gender	Mean Stature (mm)	Stature type	Mean Nasal Index	Nose type	Mean Cephalic Index	Head type
Gandhila	Male	1563.8	Short	79.6	Mesorrhine	77.1	Mesocephalic
	Female	1577.1	Upper medium	82.5	Mesorrhine	76.5	Mesocephalic
Barad	Male	1532.1	Short	80.5	Mesorrhine	79.6	Mesocephalic
	Female	1536.3	Medium	79.0	Mesorrhine	79.2	Mesocephalic
Bangala	Male	1714.2	Tall	76.5	Mesorrhine	78.2	Mesocephalic
	Female	1542.6	Medium	83.6	Mesorrhine	83.1	Brachycephalic
Bazigar	Male	1678.6	Upper medium	78.7	Mesorrhine	75.4	Mesocephalic
	Female	1538.5	Medium	75.7	Mesorrhine	78.2	Mesocephalic
Bauria	Male	1650.9	Medium	73.8	Mesorrhine	78.6	Mesocephalic
	Female	1537.3	Medium	70.5	Mesorrhine	80.7	Brachycephalic
Sansi	Male	1596.9	Short	84.9	Mesorrhine	78.6	Mesocephalic
	Female	1571.6	Upper medium	71.5	Mesorrhine	79.0	Mesocephalic
Nat	Male	1677.3	Upper medium	72.4	Mesorrhine	76.9	Mesocephalic
	Female	1532.6	Medium	68.4	Leptorrhine	77.7	Mesocephalic

A1A2BO and RH(D) blood groups

The results of serological analysis are presented in Table 12-13. No typing could be done for the Barad population due to haemolysis of blood during the transportation from field area to the laboratory. Table 12 shows the observed phenotype numbers of A1A2BO blood groups for six "denotified" tribes of Punjab investigated. The frequency of phenotype B was observed high in the Gandhila (38.05%), Sansi (52.61%) and Bauria (52.74%) whereas the phenotype O showed high frequency in the Bangala (49.52%), Nat (42.00%) and Bazigar (42.96%). Phenotype A2 was found in low proportions in all "denotified" tribes of Punjab (range 0.88% in Gandhila - 6.67% in Bangala) barring the Bauria. The phenotype A2B was not observed in the Bangala and Bauria while it was found in low frequency in the Bazigar (0.43%) and Sansi (1.61%). Hardy Weinberg Chi-square test revealed that barring the Nat (χ^2=10.4621, $p<0.05$, statistically significant) all studied populations were in genetic equilibrium with respect to the distribution of A1A2BO blood groups. One possible reason for genetic disequilibrium in the Nat may be the genetic drift due to its small sample size.

Table 12. Distribution of the A1A2BO blood groups in "denotified" tribes of Punjab.

"Denotified" tribe	Number tested	A1	A2	B	A1B	A2B	O	χ^2_{HW} (d.f. 2)
Gandhila	113	25 (22.12)	01 (0.88)	43 (38.05)	21 (18.58)	02 (1.77)	21 (18.58)	3.1844
Bangala	105	22 (20.95)	07 (6.67)	22 (20.95)	02 (1.90)	00 (0.00)	52 (49.52)	1.8993
Nat	50	11 (22.00)	01 (2.00)	13 (26.00)	02 (4.00)	02 (4.00)	21 (42.00)	10.4621*
Bazigar	233	30 (12.88)	03 (1.29)	85 (36.48)	16 (6.87)	01 (0.43)	98 (42.06)	2.0255
Sansi	249	26 (10.44)	09 (3.61)	131 (52.61)	21 (8.43)	04 (1.61)	58 (23.29)	1.5513
Bauria	201	17 (8.46)	00 (0.00)	106 (52.74)	10 (4.98)	00 (0.00)	68 (33.83)	0.0087

Figures in parentheses are percentages
*Statistically significant ($p \leq 0.05$)

For RH(D) blood group system (Table 13). The absence of RH(D)- phenotype is considered to be a tribal characteristic in populations of India which in the present study was the case observed in the Nat "denotified" tribe. However, RH(D)- phenotype was detected in other 5 "denotified" tribes of Punjab, albeit in low frequency, ranging from 1.77% (Gandhila) to 8.03% (Sansi).

Table 13. Distribution of the RH(D) blood groups in "denotified" tribes of Punjab.

“Denotified” tribe	Number tested	RH(D) +	RH(D) –
Gandhila	113	111 (98.23)	02 (1.77)
Bangala	105	99 (94.29)	06 (5.71)
Nat	50	50 (100.00)	00 (0.00)
Bazigar	233	222 (95.28)	11 (4.72)
Sansi	249	229 (91.97)	20 (8.03)
Bauria	201	190 (94.53)	11 (5.47)

Figures in parentheses are percentages.

Distribution of allele frequencies for the A1A2BO blood groups for the studied six “denotified” tribes of Punjab are presented in Table 14. The frequency of the *B* allele was found to be high in all the "denotified" tribes of Punjab ranging from 0.1235 in the Bangala to 0.3888 in the Sansi and the frequency of allele *A1* was observed in a range of 0.0695 in the Bauria to 0.2243 in the Gandhila while, *A2* was detected in low frequency (range 0.0097 in the Bazigar to 0.0461 in the Bangala) in all but the Bauria "denotified" tribe of Punjab. Overall the distribution pattern of A1A2BO locus allele frequencies observed in the "denotified" tribes of Punjab was 0>B>A1>A2. At the RH(D) locus, the frequency of *d* allele was observed low in the "denotified" tribes of Punjab ranging from 0.1330 (Gandhila) to 0.2834 (Sansi) while the allele was lacking in the Nat.

Table 14. Distribution of the allele frequencies of the A1A2BO and RH(D) blood group systems in six "denotified" tribes of Punjab.

“Denotified” tribe	Allele frequencies					
	A1A2BO				RH(D)	
	A1	*A2*	*B*	*O*	*D*	*d*
Gandhila	0.2243	0.0099	0.3437	0.4221	0.8670	0.1330

Bangala	0.1226	0.0461	0.1235	0.7078	0.7609	0.2391
Nat	0.1411	0.0155	0.1856	0.6578	1.0000	0.0000
Bazigar	0.1029	0.0097	0.2471	0.6402	0.7827	0.2173
Sansi	0.0986	0.0357	0.3888	0.4769	0.7166	0.2834
Bauria	0.0695	0.0000	0.3494	0.5811	0.7661	0.2339

Contingency χ^2 test

Contingency χ^2 test was conducted to study overall inter-group variation among the six "denotified" tribes of Punjab with respect to A1A2BO and RH(D) blood group systems and the results are presented in Tables 15 and 16, respectively. The contingency χ^2 for A1A2BO blood groups (χ^2=130.2237, $p<0.05$ at 25 d.f.) demonstrated statistically significant heterogeneity among the six "denotified" tribes of Punjab. However, the contingency χ^2 test for RH(D) blood groups (χ^2 = 9.5794, $p>0.05$ at 5 d.f.) revealed no such inter-group differences demonstrating genetic homogeneity among the six "denotified" tribes of Punjab for RH(D) blood groups distribution.

Table 15. Contingency Chi Square test for the A1A2BO blood group system among six "denotified" tribes of Punjab

Phenotype	Number	Gandhila	Bangala	Nat	Bazigar	Sansi	Bauria	Chi square (d.f. 25)
A1	Obs. No.	25	22	11	30	26	17	130.2237
	Exp. No.	15.56	14.46	6.88	32.10	34.30	27.68	
A2	Obs. No.	01	07	01	03	09	00	
	Exp. No.	2.49	2.31	1.10	5.14	5.49	4.44	
B	Obs. No.	43	22	13	85	131	106	
	Exp. No.	47.52	44.16	21.03	98.00	104.73	84.54	
A1B	Obs No.	21	02	02	16	21	10	
	Exp. No.	8.55	7.95	3.78	17.64	18.85	15.21	
A2B	Obs. No.	02	00	02	01	04	00	
	Exp. No.	1.07	0.99	0.47	2.20	2.35	1.90	
0	Obs. No.	21	52	21	98	58	68	
	Exp. No.	37.78	35.11	16.72	77.91	83.26	67.21	

Obs. No. = Observed number, Exp. No. = Expected number

Table 16. Contingency Chi Square test for the RH(D) blood group system among six "denotified" tribes of Punjab.

Phenotype	Number	Gandhila	Bangala	Nat	Bazigar	Sansi	Bauria	Chi square (d.f. 5)
RH(D) +	Obs. No.	111	99	50	222	229	190	9.5794
	Exp. No.	107.06	99.48	47.37	220.75	235.91	190.43	
RH(D) -	Obs. No.	02	06	00	11	20	11	
	Exp. No.	5.94	5.52	2.63	12.25	13.09	10.57	

Obs. No. = Observed number, Exp. No. = Expected number.

Heterozygosity

In the present study the heterozygosity (*h*), a measure of genetic variation, was estimated at the A1A2BO and RH(D) loci in the six “denotified” tribes of Punjab following Nei (1973) and the results are presented in Table 17. For A1A2BO locus *h* was found to be high for all the seven “denotified" tribes of Punjab ranging from 0.4666 in the Bangala to 0.6533 in the Gandhila with an average of 0.5495. For RH(D) locus, heterozygosity was observed nil in the Nat while in the remaining “denotified” tribes of Punjab the range was 0.2306 in the Gandhila to 0.4062 in the Sansi with an average of 0.2832. The average heterozygosity (*H*) for both A1A2BO and RH(D) varied from 0.2564 in the Nat to 0.5084 in the Sansi.

Table 17. Heterozygosity (*h*) values at the A1A2BO and RH(D) loci in six "denotified" tribes of Punjab.

“Denotified” tribe	Heterozygosity (*h*)		Average Heterozygosity (*H*)
	A1A2BO	RH(D)	
Gandhila	0.6533	0.2306	0.4420
Bangala	0.4666	0.3639	0.4153
Nat	0.5127	0.0000	0.2564
Bazigar	0.5184	0.3402	0.4293
Sansi	0.6105	0.4062	0.5084
Bauria	0.5354	0.3584	0.4469
Average	0.5495	0.2832	0.4164

Gene diversity and differentiation

Nei's gene diversity estimates (Nei, 1973) for the A1A2BO and RH(D) in the seven “denotified” tribes of Punjab are presented in Table 18. For A1A2BO locus the total gene diversity (H_T) was high 0.5715 and most of it was attributed to the intra-populational gene diversity (H_S) 0.5495 than the inter-populational gene diversity (D_{ST}) 0.0220. For RH(D) locus total genetic diversity was found moderate (H_T) 0.3009 , and like A1A2BO locus, most of it was due to intra-populational gene diversity (H_S) 0.2832 while only a small fraction (0.0177) was due to inter-populational gene diversity (D_{ST}). The coefficient of gene differentiation (G_{ST}) at A1A2BO locus was 0.0386 which was less than that obtained at RH(D) locus (0.0588), with an average of 0.0487 at both serological loci.

Table 18. Coefficient of gene differentiation (G_{ST}) at the A1A2BO and RH(D) loci in 6 "denotified" tribes of Punjab, North West India

Locus	Total gene diversity of the population (H_T)	Intra-populational gene diversity (H_S)	Inter-populational gene diversity (D_{ST})	Coefficient of gene differentiation (G_{ST})
A1A2BO	0.5715	0.5495	0.0220	0.0386
RH(D)	0.3009	0.2832	0.0177	0.0588
Average	0.4362	0.4164	0.0199	0.0487

Genetic Distance

To study genetic relationships among the present "denotified" tribes of Punjab, the Nei's measure of genetic distance (*D*) was estimated from the allele frequencies and the results are presented in Table 19. The *D* value varied from a low of 0.0058 between the Bazigar and Nat, suggesting close genomic affinities between them to as high as 0.1526 between the Gandhila and Bangala suggesting little affinities between them.

Table 19. Pair wise genetic distance (*D)* among various "denotified" tribes of Punjab.

"Denotified" tribe	Gandhila	Bangala	Nat	Bazigar	Sansi	Bauria
Gandhila	-					
Bangala	0.1526	-				
Nat	0.0964	0.0064	-			
Bazigar	0.0770	0.0202	0.0058	-		
Sansi	0.0279	0.1324	0.0847	0.0504	-	
Bauria	0.0521	0.0725	0.0405	0.0160	0.0133	-

An UPGMA dendrogram was constructed using this distance matrix (Table 19) and is presented in Fig. 9. The figure shows that the present "denotified" tribes of Punjab were placed into two sub-clusters, each with three "denotified" tribes - one cluster comprised the Sansi, Bauria and Gandhila while the other included the Bazigar, Nat and Bangala.

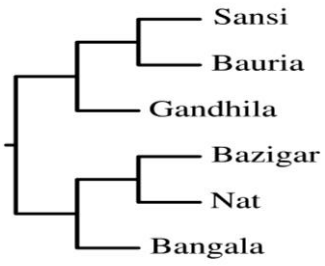


Fig. 9. UPGMA Tree depicting genetic affinities among the six "denotified" tribes of Punjab based on blood groups data.

Alu Ins/Del POLYMORPHISMS

Distribution of *Alu* Ins/Del genotype counts

The observed genotype numbers for the 8 *Alu* Ins/Del loci studied in the 7 "denotified" tribes of Punjab were tested for genetic equilibrium by Hardy–Weinberg (HW) χ^2 goodness of fit test and for inter-group heterogeneity by the contingency χ^2 test (Table 20). The results showed that the distribution of genotypes of *Alu ACE, APO, FXIIIB* and *PV92* were in Hardy–Weinberg equilibrium (HWE) in all the seven "denotified" tribes investigated. Overall statistically significant departures were observed for 11 out of total 56 HWE tests. Notably as many as 6 of the 11 departures were found at *D1* locus, while *CD4* locus showed significant departures in the Bazigar and Sansi, *PLAT* locus showed such departures in the Gandhila and Barad and *TPA25* locus showed it only in the Gandhila. Further, to rule out fluke findings as a result of expected genotype number obtained as less than 5, Yates' correction was applied for *CD4* locus in the Sansi and for *PLAT* locus in the Barad. Contingency χ^2 test was carried out at each of the eight loci with respect to seven populations and the χ^2 values were found to be statistically significant ($p \leq 0.05$ at 12 d. f.) for all of them (Table 10).

Table 20. Observed genotype numbers, allele frequencies, H.-W. Chi-square ($\chi^2_{\text{H-W}}$) and Contingency χ^2 for eight *Alu* Ins/Del loci in the seven "denotified" tribes of Punjab

Marker locus	"Denotified" tribe	Number tested	Genotype numbers observed			Allele frequencies		$\chi^2_{\text{H-W}}$ (d.f. 1)	Contingency χ^2 (d.f. 12)
			I/I	*I/D*	*D/D*	*I*	*D*		
APO	Gandhila	92	79	12	1	0.9239	0.0761	0.0723	154.4945*
	Barad	104	51	47	6	0.7163	0.2837	1.3056	
	Bangala	78	44	25	9	0.7244	0.2756	3.0380	
	Bazigar	200	160	35	5	0.8875	0.1125	2.1803	
	Bauria	198	82	95	21	0.6540	0.3460	0.7181	
	Sansi	190	165	25	0	0.9342	0.0658	0.9422	
	Nat	60	45	12	3	0.85	0.15	1.7542	
ACE	Gandhila	100	14	52	34	0.4000	0.6000	0.6945	78.8431*
	Barad	96	55	32	9	0.7396	0.2604	1.7404	
	Bangala	96	48	44	4	0.7292	0.2708	2.4711	
	Bazigar	192	72	87	33	0.6016	0.3985	0.5755	
	Bauria	189	60	90	39	0.5556	0.4444	0.2411	
	Sansi	192	63	102	27	0.5937	0.4063	1.9670	
	Nat	58	29	26	3	0.7241	0.2759	0.8636	

CD4	Gandhila	86	73	11	2	0.9128	0.0872	1.6485	64.6330*
	Barad	100	88	10	2	0.9300	0.0700	2.8086	
	Bangala	85	83	2	0	0.9882	0.0118	0.0120	
	Bazigar	194	154	26	14	0.8608	0.1392	35.0145*	
	Bauria	195	186	9	0	0.9770	0.0230	0.1088	
	Sansi	197	189	6	2	0.9746	0.0254	16.3156$^{\#}$*	
	Nat	61	47	12	2	0.8688	0.1312	0.4735	
D1	Gandhila	98	48	18	34	0.5612	0.4388	38.5341*	116.7084*
	Barad	98	12	18	68	0.2143	0.7857	20.2480*	
	Bangala	104	18	24	62	0.2885	0.7115	19.9370*	
	Bazigar	195	81	42	72	0.5231	0.4769	62.9800*	
	Bauria	195	30	42	123	0.2615	0.7385	38.1653*	
	Sansi	201	87	24	90	0.4925	0.5075	116.446*	
	Nat	58	5	22	31	0.2759	0.7241	0.1484	
FXIIIB	Gandhila	96	18	52	26	0.4583	0.5417	0.7934	41.1978*
	Barad	94	34	50	10	0.6277	0.3723	1.7905	
	Bangala	96	46	36	14	0.6667	0.3333	2.3437	
	Bazigar	201	54	105	42	0.5299	0.4701	0.4731	
	Bauria	192	57	84	51	0.5157	0.4843	2.9591	
	Sansi	180	69	81	30	0.6083	0.3917	0.5578	
	Nat	61	13	29	19	0.4508	0.5492	0.0970	
PLAT	Gandhila	91	24	61	6	0.5989	0.4011	14.2167*	144.6662*
	Barad	101	9	24	68	0.2080	0.7920	6.8334$^{\#*}$	
	Bangala	97	8	47	42	0.3247	0.6753	1.0656	
	Bazigar	195	48	87	60	0.4692	0.5308	2.1213	
	Bauria	191	35	88	68	0.4136	0.5864	0.4810	
	Sansi	197	18	99	80	0.3426	0.6574	2.6313	
	Nat	60	28	29	3	0.7083	0.2917	1.7288	

PV92	Gandhila	95	9	43	43	0.3210	0.6790	0.1390	56.1548*
	Barad	95	36	50	9	0.6421	0.3579	2.0010	
	Bangala	96	20	52	24	0.4792	0.5208	0.6971	
	Bazigar	183	36	88	59	0.4372	0.5628	0.0952	
	Bauria	195	21	99	75	0.3616	0.6384	1.9390	
	Sansi	188	41	88	59	0.4521	0.5479	0.5722	
	Nat	60	13	29	18	0.4583	0.5417	0.0423	
TPA25	Gandhila	94	26	62	6	0.6064	0.3936	13.6951*	52.7877*
	Barad	96	32	40	24	0.5417	0.4583	2.4834	
	Bangala	96	40	42	14	0.6354	0.3646	0.2982	
	Bazigar	194	78	96	20	0.6495	0.3505	1.4628	
	Bauria	190	42	95	53	0.4710	0.5290	0.0021	
	Sansi	191	57	105	29	0.5733	0.4267	2.9190	
	Nat	60	22	32	6	0.6333	0.3667	1.3200	

*Statistically significant (p≤0.05)

#* Yates' correction applied

Distribution of *Alu* Ins/Del allele frequencies

Out of the eight *Alu* Ins/del loci, 7 are insertion polymorphisms while 1 locus (*CD4*) is a deletion polymorphism and All of them were polymorphic in the present material of the seven "denotified" tribes of Punjab. The allele frequencies were calculated by the gene counting method (Mourant et al., 1976) and are listed in Table 10. It was observed that the *APO* (*I*) allele was found with high frequency ranging from 0.6540 in the Sansi to 0.9342 in the Bauria. Whereas, *CD4* (*D*) allele was observed with low frequency in all the seven "denotified" tribes, ranging from 0.0118 in the Bangala to 0.1392 in Bazigar. *ACE* (*I*) allele was found with moderate to high frequency as 0.4000 in the Gandhila to 0.7396 in the Barad. For *PLAT* (*I*) allele the range was observed from as low of 0.2080 in the Barad to as high of 0.7083 in Nat. Similarly, D1 (*I*) allele was found in the range of 0.2143 in the Barad to 0.5612 in Gandhila. The (I) allele of *FXIIIB* (ranging from 04508 in the Nat to 0.6667 in the Bangala) and *TPA25* (ranging from 04710 in the Bauria to 0.6495 in the Bazigar) was found to have moderate frequencies in the present populations. Fig. 10 demonstrates the distribution of insertion/deletion allele frequency at 8 *Alu* loci studied in the seven "denotified" tribes of Punjab.

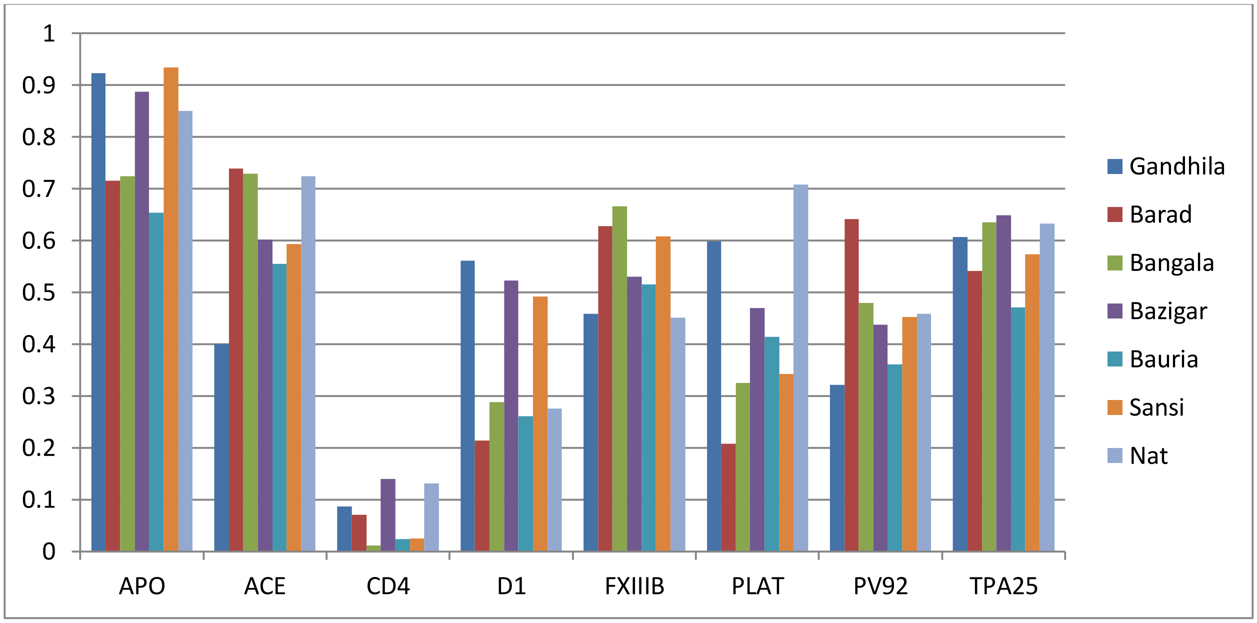


Fig. 10. Distribution of insertion/deletion allele frequency for eight Alu loci studied in seven "denotified" tribes of Punjab.

Heterozygosity (*h*)

Heterozygosity estimates were obtained from eight *Alu* Ins/Del markers in the seven denotified tribes of Punjab following the method of Nei (1973) and the results are presented in Table 21. Considerably high heterozygosity estimates were found at 6 *Alu* loci viz., *ACE* (range 0.3852-0.4582), *D1* (range 0.3367-0.4999), *PLAT* (range 0.3294-0.4981), *PV92* (range 0.4054-0.4991), *TPA25* (range 0.4553-0.4987), *FXIIIB* (range 0.4444-0.4995) across all seven populations investigated, while low amount of heterozygosity was observed at *CD4* locus (range 0.0232-0.2396). The average heterozygosity (*H*) was considerably high for all the seven "denotified" tribes ranging from 0.3721 in the Sansi to 0.4202 in the Bazigar.

Table 21. Locus wise distribution of Nei's heterozygosity (*h*) and average heterozygosity (*H*) in 7 "denotified" tribes of Punjab

"Denotified" tribe	Heterozygosity (*h*)								Average heterozygosity (*H*)
	APO	*ACE*	*CD4*	*D1*	*FXIIIB*	*PLAT*	*PV92*	*TPA25*	
Gandhila	0.1406	0.4800	0.1592	0.4925	0.4965	0.4804	0.4360	0.4774	0.3953
Barad	0.4064	0.3852	0.1302	0.3367	0.4674	0.3294	0.4596	0.4965	0.3764
Bangala	0.3993	0.3950	0.0232	0.4105	0.4444	0.4386	0.4991	0.4633	0.3842
Bazigar	0.1997	0.4794	0.2396	0.4990	0.4982	0.4981	0.4921	0.4553	0.4202
Bauria	0.4525	0.4938	0.0451	0.3863	0.4995	0.4851	0.4617	0.4983	0.4153
Sansi	0.1230	0.4824	0.0495	0.4999	0.4765	0.4505	0.4054	0.4892	0.3721
Nat	0.2550	0.3995	0.2280	0.3995	0.4952	0.4132	0.4965	0.4644	0.3939

Nei's gene diversity analysis

Gene diversity estimates (H_S, H_T and D_{ST}) and the coefficient of gene differentiation (G_{ST}) at eight *Alu* Ins/Del loci in the seven "denotified" tribes of Punjab following Nei (1973) are presented in Table 22. The results showed that the total gene diversity (H_T) in the present populations ranged between 0.1297 (*CD4*) and 0.4972 (*PLAT*) with an average of 0.4181. Most of it was attributable to intra-subpopulational gene diversity (H_S) with an average of 0.3988 (ranging from 0.1250 at *CD4* to 0.4825 at *FXIIIB*). By comparison, the inter-subpopulational gene diversity (D_{ST}) was rather low ranging from 0.0047 at *CD4* to 0.0550 at *PLAT* loci. The coefficient of gene differentiation (G_{ST}) was quite high ranging from 0.0146 for *TPA25* to 0.1106 for *PLAT* with an average of 0.0540, demonstrating a high degree of gene differentiation among the seven "denotified" tribes of Punjab.

Table 22. Gene diversity estimates (H_S, H_T, D_{ST}) and the coefficient of gene differentiation (G_{ST}) at eight *Alu* loci in the 7 "denotified" tribes of Punjab.

Locus	Total gene diversity of the population (H_T)	Intra-subpopulational gene diversity (H_S)	Inter-subpopulational gene diversity (D_{ST})	Coefficient of gene differentiation (G_{ST})
APO	0.3042	0.2823	0.0219	0.0720
ACE	0.4709	0.4450	0.0259	0.0550
CD4	0.1297	0.1250	0.0047	0.0362
D1	0.4682	0.4321	0.0361	0.0771
FXIIIB	0.4948	0.4825	0.0123	0.0249
PLAT	0.4972	0.4422	0.0550	0.1106
PV92	0.4950	0.4772	0.0178	0.0360
TPA25	0.4848	0.4777	0.0071	0.0146
Average	0.4181	0.3955	0.0226	0.0540

Genetic distance

The pair wise standard genetic distances (*D*) were estimated from the observed allele frequencies using the method of Nei (1972) and the results are listed in Table 23. It was evident from this table that the genetic distance between the Bazigar and Sansi was lowest (0.0088), suggesting their genetic closeness while *D* value was highest (0.1227) between the Barad and Gandhila, suggesting their little genetic affinities. A tree depicting genomic relationships among seven "denotified" tribes of Punjab based on Alu Ins/Del markers is depicted in Fig. 11

Table 23. Pair wise genetic distance (*D)* among the various "denotified" tribes of Punjab based on Alu Ins/Del markers.

"Denotified" tribe	Gandhila	Barad	Bangala	Bazigar	Bauria	Sansi	Nat
Gandhila	-						
Barad	0.1227	-					
Bangala	0.0794	0.0121	-				
Bazigar	0.0175	0.0592	0.0326	-			
Bauria	0.0535	0.0230	0.0222	0.0393	-		
Sansi	0.0317	0.0419	0.0231	0.0088	0.0347	-	
Nat	0.0477	0.0735	0.0470	0.0301	0.0440	0.0512	-

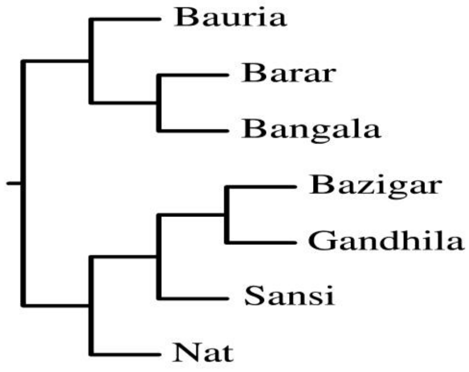


Fig. 11. UPGMA Tree depicting genomic relationships among seven "denotified" tribes of Punjab based on Alu Ins/Del markers.

DISCUSSION

Stature, Nasal Index and Cephalic Index

Table 24 presents the mean stature (mm) of the present “denotified” tribes of Punjab as well as various other tribal and non tribal populations from India. Most of the data reported was for males, whereas very little data was available on females. It was evident that 7 out of the 9 tribes reported from Central India had lower medium stature (reported for males) and the mean stature ranged from 1611.6 mm in the Kol to 1631.9 mm in the Oraon tribe (Gautam and Adak, 2008). The males of Halba tribe (mean 1613.1 mm) from Central India and females of Santhal tribe (mean 1510.4) from East India also had lower medium stature (Ghosh and Malik, 2006).

With respect to their mean stature, out of the present seven "denotified" tribes of Punjab, none was observed to have lower medium stature. Short stature was common in males of the Sansi, Gandhila and Barad. These present results were similar to that reported in males of Santhal tribe (1598.4 mm) from West Bengal, and the Majhi (1584.3 mm) and Korwa tribes (1551.2 mm) from Central India. Medium stature was commonly observed among Bauria males (1650.9 mm) and the upper medium stature was common in the Bazigar (1678.6 mm) and Nat males (1677.3 mm) while tall stature was most common in the Bangala males (1714.2 mm) similar to that reported from Jat Sikh males (1704.0 mm) from Punjab and Gujjar males (1723.1 mm) from North India.

The medium stature was commonly observed among females of the Bauria (1537.3 mm), Nat (1532.6 mm), Bazigar (1538.8 mm), Bangala (1542.6 mm) and Barad (1536.8 mm) "denotified" tribes of Punjab. These results were similar to those reported for the Santhal females tribe (1510.4 mm). Upper medium stature was common in the Gandhila (1577.1 mm) and Sansi (1571.6 mm) females which was similar to that reported for the Jat Sikh females (1579.1 mm) (Table 24).

As for the nose types, the present findings suggest that the mesorrhine (medium nose) was common in the males of the seven "denotified" tribes of Punjab with mean Nasal Index (NI) ranging from 72.4 (Nat) to 84.9 (Sansi). Similar results were observed in the females (except for the Nat females who had leptorrhine (fine nose) type of nose with mean NI 68.4) with mean NI ranging from 70.5 in the Bauria to 83.6 in the Bangala (Table 24). These findings were similar to nose type of various caste and tribal populations reported from North, West India and Central India (Table 24).

As for the head types, the mean Cephalic Index (CI) observed in 7 "denotified" tribes of Punjab demonstrated that mesocephalic head type was common in males and females with mean CI ranging from 75.4 to 79.6. Whereas, brachycephalic head type was observed only in the

Bangala (mean CI = 83.1) and the Bauria (mean CI = 80.7) females (Table 24). The present results on mesocephaly preponderance were similar to that reported from Bhil, Barelia, Halba and Gond tribes from Central (Bhargav and Kher, 1961; Ghosh and Malik, 2006; Chatterjee *et al.*, 2015) as well as to the populations from West (Uttekar *et al.*, 2013; Jadhav *et al.*, 2011; Jaiswal *et al.*, 2016) India. While the Brachycephalic head type observed common among the present Bangala and Bauria females was similar to that reported from North India populations (Anupama *et al.*, 2010, Seema and Verma, 2016).

Table 24. Mean stature, NI and CI in seven "denotified tribes" of Punjab and in various other tribal and non tribal populations of India.

Population	Area	Mean Stature (mm)		Mean Nasal Index (NI)		Mean Cephalic Index (CI)		Reference
		Male	Female	Male	Female	Male	Female	
Gandhila	North India	1563.8	1577.1	79.6	82.5	71.1	76.5	Present study
Barad	North India	1532.1	1536.3	80.5	79.0	79.6	79.2	Present study
Bangala	North India	1714.2	1542.6	76.5	83.6	78.2	83.1	Present study
Bazigar	North India	1678.6	1538.5	78.7	75.7	75.4	78.2	Present study
Bauria	North India	1650.9	1537.3	73.8	70.5	76.6	80.7	Present study
Sansi	North India	1596.9	1571.6	84.9	71.5	78.6	79.0	Present study
Nat	North India	1677.3	1532.6	72.4	68.4	76.9	77.7	Present study
Jat Sikh	North India	1704.0	-					Singh *et al.* (1988)
Jat Sikh	North India	-	1579.1					Sidhu *et al.* (1982)
Bania	North India	-	1542.8					
Bania	North India			70.0				Singla (2005)
Jat Sikh	North India			72				
Majhabi-Sikh	North India			76.5				
Brahmin	North India			70.2	69.9			Kaushal *et al.* (2013)
Mazhabi Sikh	North India			76.5	68.9			
Muslim	North India			67.0	69.4			
Punjabi	North India	-	-	-	-	84.4	82.1	Mahajan *et al.*

Population								(2009)
Punjabi Population	North India	-	-	-	-	80.5	84.3	Seema and Verma (2016)
Bania	North India	1687.1	1551.8	-	-	-	-	Kumar and Patnaik (2013)
Koli	North India	1526.5	-					Krishan and Kumar (2007)
Gujjar	North India	1723.1	-					Krishan (2008)
Indian population	North India	1688.6	1563.9					Asha and Prabha (2011)
UP Population	North India			75.8	72.1			Ray *et al.* (2016)
Indian population	South India	1696.2	1568.2					Asha and Prabha (2011)
Santhal Tribe	East India	1598.4	1510.4	79.7	79.4	73.4	75.9	Ghosh and Malik (2006)
Orissa Population	East India					77.3	78.4	Patro *et al.* (2014)
Bhil Tribe	Central India					76.9		Bhargav and Kher (1960)
Barela Tribe	Central India					79.8		Bhargav and Kher (1961)
Bhil Tribe	Central India	1614.2	-					Gautam and Adak (2008)

Gond Tribe	Central India	1623.5	-	79.9		77.5		Gautam and Adak (2008)
Kol Tribe	Central India	1611.6	-					Gautam and Adak (2008)
Korku Tribe	Central India	1624.5	-					Gautam and Adak (2008)
Majhi Tribe	Central India	1584.3	-					Gautam and Adak (2008)
Oraon Tribe	Central India	1631.9	-					Gautam and Adak (2008)
Sonr Tribe	Central India	1620.6	-					Gautam and Adak (2008)
Korwa Tribe	Central India	1551.2	-					Gautam and Adak (2008)
Saharia Tribe	Central India	1627.8	-					Gautam and Adak (2008)
Halba Tribe	Central India	1613.1		81.7				Chatterjee *et al.* (2015)
Ahirwar	Central India			81	82.4	73.7	73.4	Singh and Purkit (2006)
Dhangi	Central India			76.5	76.2	71.9	71.6	
Bhopal	Central India	-	-			81.2	80.3	Nair *et al.* (2014)
Reva	Central India					75.8	79.2	Mishra *et al.* (2014)
Gujarat Population	West India	1659.2	-			81.2	80.4	Jadhav and Shah (2004)
Gujarat Population	West India					-	82.5	Uttekar *et al.* (2013)
Bheel Meena	West India	-	-	83.0	79.7	-	-	Gangrade (2012)

Rabari	West India					80.8	-	Jadhav *et al.* (2011)
Bhil	West India					80.8	-	
Sindhi	West India					77.8	-	
Siddi	West India					78.8	-	
Sindhi	West India					82.8	-	
Patel	West India					81.0	-	
Kharwa	West India					79.8	-	
Bania	West India					77.0	78.0	Jaiswal *et al.* (2016)
Brahmin	West India					75.7	78.3	
Jat	West India					76.7	78.8	
Meena	West India					77.0	78.6	
Others	West India					78.1	77.3	
Jat	West India			68.1				Choudhary *et al.* (2012)
Sindhi	West India			70.7				

A1A2BO and RH(D) blood group systems

Table 25 presents the distribution of A1+A2, B, O and RH allele frequencies in different caste and tribal populations of India. In the present study the average frequencies of A1+A2 (range 0.0695-0.2342), B (range 0.1235-0.3888) and O (range 0.4221-0.7071) alleles for six (out of seven) "denotified" tribes of Punjab were 0.1459, 0.2730 and 0.5809, respectively. These frequencies were not comparable with the allele frequency data of other caste populations of Punjab, viz., the Jat Sikh (0.216, 0.239, 0.545) and the Khatri (0.283, 0.320, 0.442) (Kaur *et al.*, 1981). On the other hand, the present ABO results were similar to the A, B, O allele frequencies of the scheduled caste population of Punjab reported by Kaur *et al.* (1981) (0.196, 0.274, 0.530) and the Balmiki (0.1840, 0.2560, 0.5600), Dhanak (0.1570, 0.3230, 0.5200), Ravidasi (0.1850, 0.2870, 0.5790) and Ramdasi (0.1710, 0.2460, 0.5690) Scheduled Castes of Punjab (Sidhu, 2003). The present results were also similar to the 7 nomadic tribal populations of Rajasthan with average values being 0.209, 0.286, 0.505, respectively for A1+A2, B and O alleles (Sachdev, 2012) as well as the tribal Bhil of Rajasthan (Alisha, 2017) with frequencies 0.2008, 0.2143 and 0.5848, respectively for A1+A2, B and O alleles (Table 25).

The average Rh(D) + allele frequency was observed high (range 0.7166-1.0000) in the present "denotified" tribes of Punjab. The results were similar to those reported in were reported for four Scheduled Caste populations viz., the Balmiki (0.8330), Dhanak (0.8420), Ravidasi (0.8270) and Ramdasi (0.8450) (Sidhu, 2003) and the Jat Sikh (0.8451) of Punjab (Kaur, 2017) as well as with 7 nomadic tribal populations of West (range 0.8650-1.000; Sachdev, 2012), while the tribal Bhil surprisingly showed moderate frequency for Rh(D)+ allele (0.6914) (Alisha, 2017) (Table 25).

Table 25. Distribution of ABO and RH(D) allele frequencies in different caste and tribal populations of India

Population	Region	Distribution of allele frequencies					Reference
		A/ A1+A2	*B*	*O*	*D*	*D*	
Gandhila	North India	0.2342	0.3437	0.4221	0.8670	0.1330	Present study
Bangala	North India	0.1687	0.1235	0.7078	0.7609	0.2391	
Nat	North India	0.1566	0.1856	0.6578	1.0000	0.0000	
Bazigar	North India	0.1126	0.2471	0.6402	0.7827	0.2173	

Sansi	North India	0.1343	0.3888	0.4769	0.7166	0.2834	
Bauria	North India	0.0695	0.3494	0.5811	0.7661	0.2339	
Jat Sikh	North India	0.2160	0.3490	0.5450			Kaur *et al.* (1981)
Khatri	North India	0.2830	0.3200	0.4420			
Scheduled Castes	North India	0.1960	0.2740	0.5340			
Jat Sikh	North India	0.1560	0.2440	0.5998	0.8451	0.1549	Kaur (2017)
Balmiki	North India	0.1840	0.256	0.5600	0.8330	0.1670	Sidhu (2003)
Dhanak	North India	0.1570	0.323	0.5200	0.8420	0.1580	
Ravidasi	North India	0.1850	0.287	0.5790	0.8270	0.1730	
Ramdasi	North India	0.1710	0.246	0.5690	0.8450	0.1550	
Brahmin	North India	0.1988	0.3100	0.4906	0.7261	0.2739	Mukhopadhyay and Kshatriya (2004)
Rajput	North India	0.2561	0.3288	0.4151	0.7838	0.2161	
Malha	North India	0.0400	0.3560	0.6040	0.9000	0.1000	Jaggi *et al.* (2014)
Banjara	North India	0.2860	0.3600	0.3540	0.5940	0.4060	
Kumhar	North India	0.2200	0.3680	0.4120	0.6610	0.3390	
Saini	North India	0.2310	0.3220	0.4470	0.8000	0.2000	
Syed	North India	0.2833	0.1781	0.5476	0..6559	0.3441	
Sheikh	North India	0.2386	0.2079	0.5592	0.5631	0.4369	Hussain *et al.* (2013)
Pathan	North India	0.2098	0.1953	0.6020	0.6616	0.3384	
Shia	North India	0.1654	0.2952	0.5419	0.5835	0.4165	
Sherwani	North India	0.1995	0.2163	0.5925	0.5687	0.4313	
Ansari	North India	0.2115	0.2576	0.5370	0.5959	0.4041	
Buksa	North India	0.2839	0.1904	0.5256	0.8833	0.1167	Singh *et al.* (2013)
Hindu	East India	0.1900	0.2100	0.6000	-	-	Chakraborty (2011)
Muslim	East India	0.1800	0.1900	0.6300	-	-	
Banjara	West India	0.1950	0.2610	0.5440	0.8950	0.105	Sachdev (2012)
Natt	West India	0.2190	0.3550	0.4260	0.8910	0.1.9	
Sapara	West India	0.2100	0.2610	0.5720	0.8360	0.164	
Bawariya	West India	0.0880	0.340	0.5720	0.8650	0.135	
Sansui	West India	0.2580	0.3340	0.4080	1.0000	Nil	
Bhopa	West India	0.2750	0.2090	0.5720	0.8650	0.135	
Gujjar	West India	0.1910	0.2200	0.5890	1.0000	Nil	
Rajput	West India	0.1955	0.2288	0.5757	0.7263	0.2737	Alisha *et al.* (2017)
Bhil	West India	0.2008	0.2143	0.5848	0.6914	0.3086	

Alu Ins/Del polymorphisms

Table 26 presents the distribution of allele frequencies of six *Alu* loci (*ACE, APO, CD4, D1, PV92, FXIIIB*) in the present "denotified" tribes and various other tribal and caste populations reported from North (Kaur *et al.*, 2002; Panjaliya *et al.*, 2012, 2013; Majumder *et al.*, 1999; Chakrabarti *et al.*, 2002), Central (Mukherjee *et al.*, 2000) and West (Dada *et al.*, 2011; Kshatriya *et al.*, 2011) India.

The frequency *APO* (I) allele was observed varying from moderate to high in the present "denotified" tribes of Punjab (range 0.6540-0.9342) as observed in other populations reported from North (range 0.4400-0.9460), Central (range 0.4810-0.7140) and West (range 0.6290-0.9480) India. The frequency of *CD4* (D) allele was observed low in seven "denotified" tribes (range 0.0118-0.1392) of Punjab as well as in other populations reported from North (range nil-0.1650), Central (range 0.0180-0.1011) and West (range 0.0170-0.2320) India. The overall allele frequency distribution pattern of the present denotified tribes of Punjab was found similar to the Indo-European speaking tribes of West India (Kshatriya *et al.*, 2011).

The higher heterozygosity (range 0.3721-0.4202) with respect to eight *Alu* loci reflected greater genetic variability in the seven "denotified tribes of Punjab". The coefficient of gene differentiation (G_{ST}=5.4%) in the present "denotified" tribes of Punjab depicted the extent of genetic heterogeneity prevalent in the present study populations. Gene differentiation (G_{ST}) recorded in the present study was much greater than that reported among various caste populations of Punjab viz., the Jat Sikh, Brahmin, Khatri and Scheduled Castes (G_{ST}=1.3%) (Kaur *et al.*, 2002) and various endogamous populations of Haryana (G_{ST}=2.7%, Yadav and Arora, 2011). Various studies on some tribal populations of India have reported G_{ST} values ranging from 2.5% (Mukherjee *et al.*, 2000) followed by 4.9% reported among tribal populations from West India (Dada *et al.*, 2011) to as high as 6.8% reported by on various tribal and caste populations of India (Majumder *et al.*, 1999). Thus the present value of G_{ST} (5.4%) was much higher than caste populations but similar to G_{ST} values reported among tribal populations of India.

Table 26. Distribution of insertion/deletion allele frequencies of common six *Alu* markers in 7 "denotified" tribes of Punjab and various other populations reported from India.

Population	Area	Allele frequency						Reference
		ACE	APO	D1	CD4*	FXIIIB	PV92	
Gandhila[1]	North India	0.4000	0.9239	0.5612	0.0872	0.4583	0.3210	Present study
Bangala[1]	North India	0.7292	0.7244	0.2885	0.0118	0.6667	0.4792	
Barad[1]	North India	0.7396	0.7163	0.2143	0.0700	0.6277	0.6421	
Bazigar[1]	North India	0.6016	0.8875	0.5231	0.1392	0.5299	0.4372	
Bauria[1]	North India	0.5556	0.6540	0.2615	0.0230	0.5157	0.3616	
Sansi[1]	North India	0.5937	0.9342	0.4925	0.0254	0.6083	0.4521	
Nat[1]	North India	0.7241	0.8500	0.2759	0.1312	0.4508	0.4583	
Jat Sikh[1]	North India	0.5150	0.8866	0.3775	0.1650	0.6100	0.3655	Kaur *et al.* (2002)
Brahmin[1]	North India	0.4895	0.9062	0.4687	0.0834	0.5418	0.3541	
Khatri[1]	North India	0.6250	0.8750	0.5104	0.0625	0.5937	0.4062	
Scheduled Castes[1]	North India	0.4791	0.9062	0.3645	0.0521	0.6875	0.5000	
Brahmin[2]	North India	0.7200	0.6150	0.4400	0.1100	0.4850	0.5500	Panjaliya *et al.* (2012) and Panjaliya *et al.* (2013)
Rajput[2]	North India	0.5750	0.7400	0.4900	0.1400	0.6500	0.4750	
Gujjar[2]	North India	0.3800	0.4400	0.5700	0.1300	0.5700	0.3600	
Jat Sikh[2]	North India	0.6200	0.8100	0.5000	0.1600	0.6700	0.3000	
Brahmin[3]	North India	0.5930	0.8890	0.3700	0.1150	0.5930	0.3330	Majumdar *et al.* (1999)
Chamar[3]	North India	0.7000	0.7200	0.5000	0.0000	0.7800	0.5400	

Muslim[3]	North India	0.6430	0.9460	0.4640	0.0370	0.5000	0.3150	
Rajput[3]	North India	0.5380	0.9020	0.3070	0.0200	0.7040	0.3370	
Katharia Tharu[3]	North India	0.5690	0.8470	0.4170	0.0140	0.7920	0.6940	Chakrabarti *et al.* (2002)
Rana Tharu[3]	North India	0.6230	0.7260	0.4430	0.0290	0.8210	0.8210	
Toto[4]	North East India	0.5670	0.8500	0.3330	0.0000	0.9140	0.9330	
Ho[4]	North East India	0.7310	0.8490	0.4520	0.0000	0.8020	0.5650	
Mizo[5]	North East India	0.6030	0.8450	0.2860	0.0000	0.6480	0.8620	
Paite[5]	North East India	0.6750	0.9050	0.3150	0.0000	0.5420	0.7790	Meitei *et al.* (2010)
Meitei[5]	North East India	0.5440	0.9170	0.2630	0.0340	0.6330	0.6760	
Kom[5]	North East India	0.2590	0.9060	0.4540	0.0000	0.7860	0.4370	
Thadou[5]	North East India	0.7780	0.9170	0.3970	0.0400	0.3970	0.8170	
Kabui[5]	North East India	0.5610	0.7930	0.2690	0.0000	0.7840	0.8680	
Aimol[5]	North East India	0.5870	0.9230	0.3500	0.0000	0.6640	0.8820	

Manipur Muslim[5]	North East India	0.5730	0.8240	0.2800	0.0000	0.4760	0.4400	
Manipur Bamon[5]	North East India	0.5910	0.7220	0.3510	0.0000	0.6200	0.6330	
Zeme[5]	North East India	0.4710	0.5290	0.2170	0.4530	0.6100	0.8350	Panmei *et al.* (2016)
Liangmai[5]	North East India	0.4510	0.7750	0.2200	0.1110	0.5933	0.8680	
Rongmei[5]	North East India	0.5090	0.7280	0.2790	0.1880	0.5740	0.7440	
Muria[6]	Central India	0.5310	0.7140	0.3470	0.1011	0.7860	0.5200	Mukherjee *et al.* (2000)
Halba[6]	Central India	0.6460	0.6910	0.4270	0.0940	0.6980	0.5630	
Kamar[6]	Central India	0.6400	0.6490	0.3420	0.0180	0.7460	0.5540	
Chinda Bhunjia[6]	Central India	0.7960	0.4810	0.6200	0.0380	0.7310	0.4070	
Chakhutia Bhunjia[6]	Central India	0.6490	0.6220	0.2890	0.0900	0.7500	0.4120	
Rajput[7]	West India	0.6130	0.8940	0.3360	0.0380	0.7090	0.4220	Dada *et al.* (2011)
Bhil[7]	West India	0.5100	0.8800	0.2340	0.0358	0.7150	0.4050	
Saharia[7]	West India	0.5780	0.8000	0.3120	0.0709	0.6290	0.4330	
Mina[7]	West India	0.4160	0.6290	0.3260	0.0170	0.5830	0.5230	
Garasia[7]	West India	0.7300	0.9230	0.4610	0.0800	0.5190	0.4030	
Damaria[7]	West India	0.5440	0.9480	0.3100	0.2320	0.4210	0.2960	

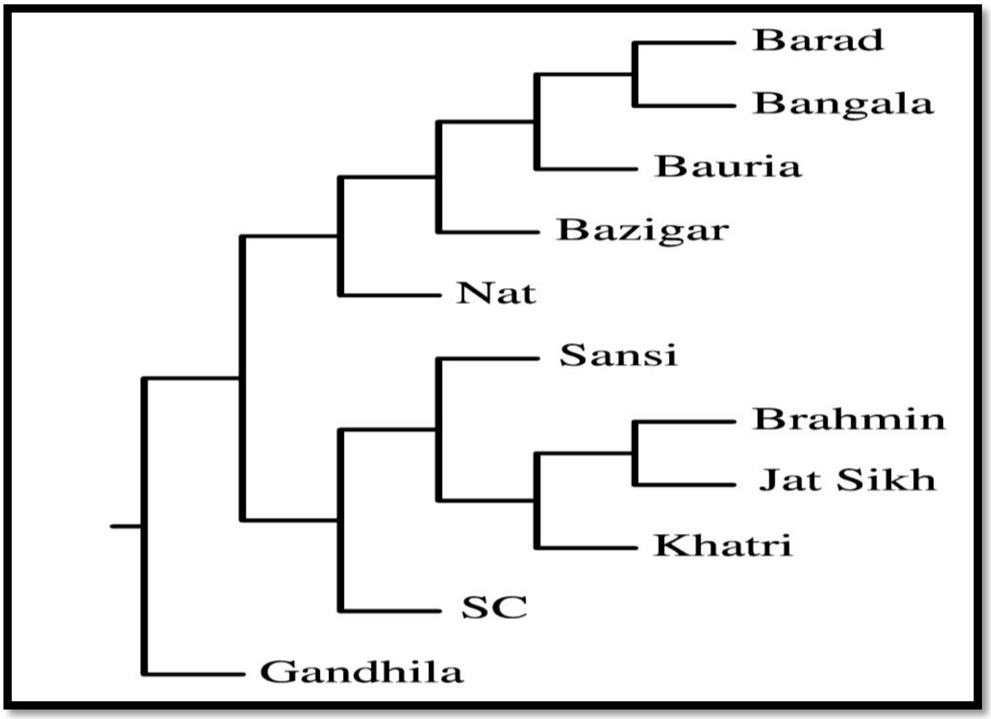
Vasava[8]	West India	0.7500	0.8020	0.3140	0.1180	0.5380	0.5290	Kshatriya *et al.* (2011)
Gamit[8]	West India	0.6900	0.7300	0.3040	0.0500	0.4010	0.4120	
Konkana[8]	West India	0.4710	0.7840	0.3230	0.1150	0.4510	0.5120	
Mota Chaudhary[8]	West India	0.5800	0.6910	0.3040	0.1060	0.2200	0.3060	
Pavagadhi Chaudhary[8]	West India	0.5610	0.7890	0.3540	0.0730	0.5730	0.4880	
Nana Chaudhary[8]	West India	0.6180	0.7750	0.4000	0.0500	0.6270	0.3730	
Dhodia[8]	West India	0.6380	0.8320	0.3510	0.0480	0.4100	0.4780	
Dubla[8]	West India	0.7240	0.8130	0.3170	0.0620	0.5900	0.4900	

*Denotes the frequency of deletion allele

[1]=Punjab, [2]=Jammu, [3]=Uttar Pradesh, [4]=West Bengal, [5]=Manipur, [6]=Madhya Pradesh, [7]=Rajasthan, [8]=Gujarat

Genetic affinities of the "denotified" tribes of Punjab with other caste populations of state

The genetic affinities of the seven investigated "denotified" tribes of Punjab with other caste populations of the state viz., the Jat Sikh, Brahmin, Khatri and Scheduled Castes (Kaur *et al.,* 2002) were studied using 7 *Alu* Ins/Del loci viz., *ACE, APO, CD4, D1, FXIIIB, PV92, PLAT.* The UPGMA tree (Fig. 12) depicting the hierarchial clustering between populations clearly presented that the five out of the seven "denotified" tribes viz., the Barad, Bangala, Bazigar, Bauria and Nat formed a separate cluster while, the Sansi was observed clustered with the caste populations reported from Punjab (Kaur *et al.,* 2002). Interestingly Gandhila was separated from this major cluster. The MDS plot (Fig. 13) clearly separated the "denotified" tribes of Punjab from the caste populations suggesting no genetic closeness between the "denotified" tribes and caste populations reported from Punjab.



SC = Scheduled Castes

Fig.12. UPGMA tree depicting genetic affinities of the seven denotified tribes with other caste populations reported from Punjab based on 7 *Alu* loci.

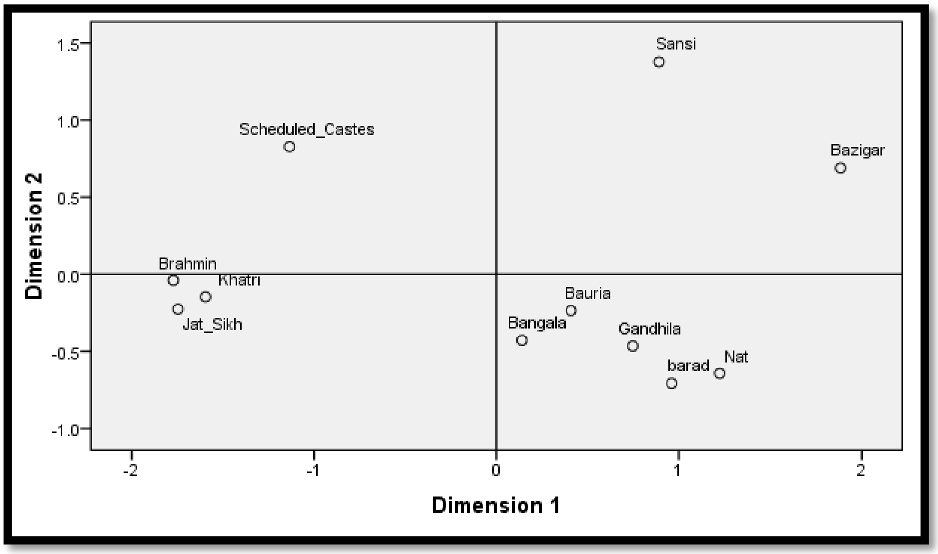


Fig.13. MDS plot demonstrating genetic affinities of the seven "denotified" tribes of Punjab with other caste populations reported from the state based on 7 *Alu* loci.

Genetic affinities of the investigated seven "denotified" tribes of Punjab with different populations reported from India

The genetic affinities of the seven investigated "denotified" tribes with various caste and tribal populations from North (Kaur *et al.*, 2002; Panjaliya *et al.*, 2012, 2013; Majumder *et al.*, 1999; Chakrabarti *et al.*, 2002), Central (Mukherjee *et al.*, 2000) and West (Dada *et al.*, 2011; Kshatriya *et al.*, 2011) India were studied using data on 6 common *Alu* Ins/Del loci viz., *ACE, APO, CD4, D1, FXIIIB, PV92* (Table 23).

As per the UPGMA tree (Fig. 14) four "denotified" tribes viz., the Bangala, Bauria, Barad and Nat were observed clustered with Indo-European speaking tribes (Vasava, Gamit, Dubla, Dhodia, Konkana) of West India (Kshatriya *et al.*, 2011) while the remaining three, the Gandhila, Bazigar and Sansi were observed clustered together and close to the MC (Mota Choudhary) tribe from West India (Kshatriya *et al.*, 2011). The MDS plot (Fig. 15) showed that the "denotified" tribes were clustered away from the caste populations from North India and appeared relatively close to the Indo-European speaking tribal populations from West India (Kshatriya *et al.*, 2011).

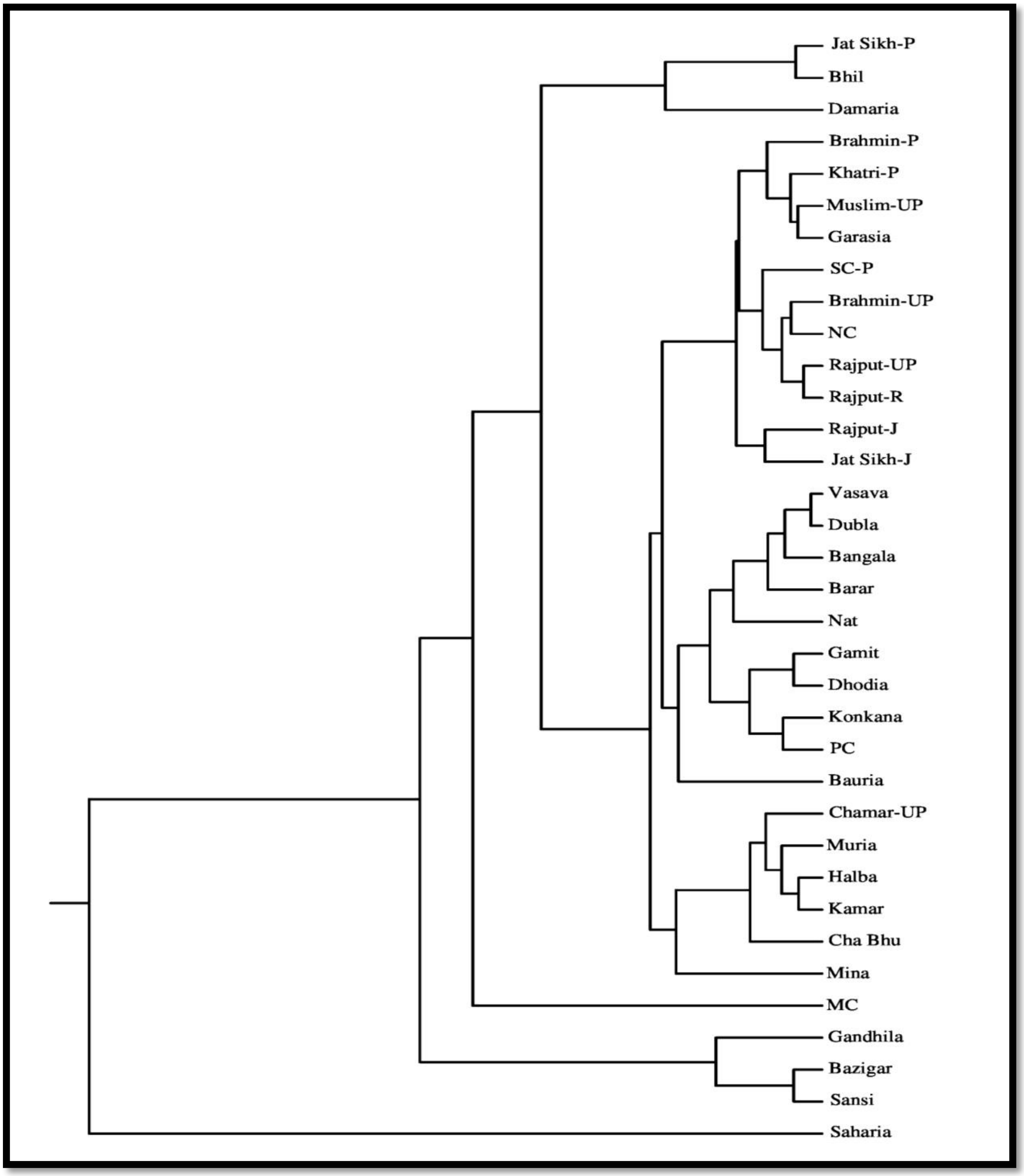


Fig.14. UPGMA tree depicting genetic affinities of the seven "denotified" tribes of Punjab with various caste and tribal populations of India.

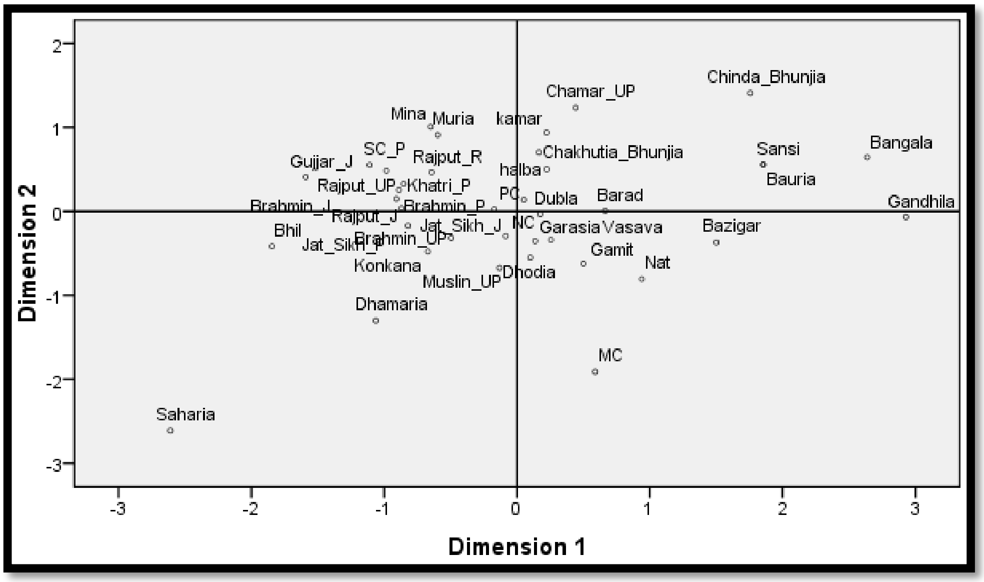


Fig. 15. MDS plot genetic affinities of the even "denotified" tribes of Punjab with various caste and tribal populations of India.

CONCLUSIONS

(i) Short stature was predominantly observed in males of the Sansi, Gandhila, and Barad "denotified" tribes of Punjab which was similar to that reported in males of Santhal tribe of West Bengal as well as the Majhi and Korwa tribes of Central India. The medium stature was commonly observed among females of the Bauria, Nat, Bazigar, Bangala and Barad "denotified" tribes of Punjab, similar to that reported from females of the Santhal tribe.

(ii) The present results suggested the preponderance of mesorrhine (medium nose) in the males of the seven "denotified" tribes of Punjab, barring the Nat females. These results were similar to the findings reported on predominance of mesorrhine in different tribal and non tribal populations from North, Central and West India.

(iii) Mesocephalic head type was found to be common in males of the 7 "denotified" tribes of Punjab as well as in females of 5 (Gandhila, Barad, Bazigar, Sansi and Nat) out of 7 "denotified" tribes of Punjab demonstrated the preponderance of mesocephaly. These results were similar to that reported in the Bhil, Barelia, Santhal and Gond tribes of

Central and East India. The brachycephalic head type was common in the present Bangala and the Bauria females, a finding which was similar to that reported in population of West India.

(iv) The average frequencies of A, B, O alleles for six (out of seven) "denotified" tribes of Punjab were similar to the scheduled caste populations of Punjab (Kaur *et al.*, 1981; Sidhu *et al.*, 2003) as well as to 7 nomadic tribal populations of Rajasthan (Sachdev, 2012) and the tribal Bhil of Rajasthan (Alisha, 2017).

(v) The Rh(D)+ allele frequency in the present study six "denotified" tribes (range 0.8156) was similar to the value reported in the Scheduled Castes (0.836; Sidhu, 2003) and Jat Sikh (0.8451; Kaur, 2017) of Punjab as well as to the Rajputs (0.7260; Alisha, 2017) and 7 nomadic tribal populations of Rajasthan (range 0.8650-1.0000; Sachdev, 2012).

(vi) In case of 8 *Alu* Ins/Del markers studied in the seven "denotified" tribes of Punjab, the average allele frequency distribution pattern was similar to the Indo-European speaking tribes of South Gujarat, West India (Kshatriya *et al.*, 2011).The frequency of *APO* (I) allele was observed varying from moderate to high in the seven "denotified" tribes (range 0.6540-0.9342) of Punjab similar to the tribal population reported from West India (range 0.6290-0.9480). The frequency of *CD4* (D) allele was observed low in seven "denotified" tribes (range 0.0118-0.1392) of Punjab which was similar to the caste and tribal populations reported from North (range nil-0.1650), Central (range 0.0180-0.1011) and West (range 0.0170-0.2320) India.

(vii) The coefficient of gene differentiation value estimated in the present "denotified" tribes of Punjab (G_{ST} = 5.4%) demonstrated great genetic heterogeneity in the present study populations. The G_{ST} value recorded in present "denotified" tribes of Punjab was greater than that reported in caste populations (the Jat Sikh, Brahmin, Khatri and Scheduled Castes) of the state (G_{ST} = 1.3%) (Kaur *et al.*, 2002) but similar to G_{ST} value (4.9%) reported among tribal populations from West India (Dada *et al.*, 2011).

(viii) The UPGMA tree of populations of Punjab (Fig. 12) demonstrated that the Gandhila separated at an early stage of evolution from the remaining six "denotified" tribes. The Barad, Bangala, Bazigar, Bauria and Nat formed a subcluster while, the Sansi was observed clustered with the caste populations reported from Punjab (Kaur *et al.*, 2002). The MDS plot (Fig.13) clearly separated the “denotified” tribes of Punjab from the caste populations, suggesting no genetic closeness between them.

(ix) The UPGMA tree (Fig. 14) and MDS plot (Fig. 15) of the genetic affinity of the seven “denotified” tribes of Punjab with various caste and tribal populations of India, clearly showed that the “denotified” tribes were clustered away from the caste populations of North India and appeared relatively close to the Indo-European speaking tribal populations of West India.

SUMMARY

There are seven “denotified” tribes inhabiting the state namely, the Bauria, Bazigar, Bangala, Barad, Gandhila, Nat and Sansi. Their total population as per the Census of India 2001 was 436,809, the Bazigar having the highest population (208,442), followed by the Sansi (105,337), Bauria (102,232), Barar (8,679), Bangali (7,765), Gandhila (3,283) and Nat (1,071).

The “denotified” tribes (Vimukt Jatis) of Punjab had been struggling since India’s independence, first to remove the tag of criminality attached to them during the British colonial regime and second, to acquire the status of Schedule Tribe (ST). It is ironic that they had been wrongly placed in the category of Scheduled Caste (SC) in Punjab and they see this as an attempt to denigrate them. The Vimukt Jatis had been contesting for Scheduled Tribe (ST) status for long so that they have a stake in reservation quota for jobs, admissions, scholarships and other benefits announced from time to time by the government for the ST. Since as of now they are clubbed with the Scheduled Castes of Punjab, the so-called ‘creamy SC layer’ (e.g. the Ramdasia, Balmiki etc.) takes all the benefits meant for SC.

The present study is a biological anthropology approach to establish the genetic profile of the Vimukt Jatis of Punjab. As a detailed social anthropological study is already available on the Vimukt Jatis of Punjab which indicate a tribal status for them (Singh, 2010), it would be interesting to examine if the results from the present anthropogenetic approach corroborate this finding. That is, the present study is an attempt to provide genetic basis to the findings of the social-anthropological inquiry already reported in literature on the Vimukt Jatis of Punjab. This will help make the case of the Vimukt Jatis, a socially disadvantaged group of people, for a tribal status more rational and logical thereby helping them get their true identity validated, enabling them get the financial and other benefits due to them. The main findings of the present project are listed below.

1. The stature was predominantly observed short in males of the Sansi, Gandhila, and Barad "denotified" tribes of Punjab which was similar to that reported in males of Santhal tribe of West Bengal as well as the Majhi and Korwa tribes of Central India. The medium stature was commonly observed among females of the Bauria, Nat, Bazigar, Bangala and Barad "denotified" tribes of Punjab, similar to that reported from females of the Santhal tribe. The present results suggested the preponderance of mesorrhine (medium nose) in the males of the seven "denotified" tribes of Punjab, barring the Nat females. These results were similar to the findings reported on predominance of mesorrhine in different tribal and non tribal populations from North, Central and West India. Mesocephalic head type was found to be common in males of the 7 "denotified" tribes of Punjab as well as in females of 5 (Gandhila, Barad, Bazigar, Sansi and Nat) out of 7 “denotified” tribes of Punjab demonstrated the preponderance of mesocephaly. These results were similar to that reported in the Bhil, Barelia, Santhal and Gond tribes of Central and East India. The brachycephalic head type was common in the present Bangala and the Bauria females, a finding which was similar to that reported in population of West India.
2. As for the average frequencies of A, B, O alleles for six (out of seven) "denotified" tribes of Punjab, these were similar to the scheduled caste populations of Punjab (Kaur *et al.*, 1981; Sidhu *et al.*, 2003) as well as to 7 nomadic tribal populations of Rajasthan (Sachdev, 2012) and the tribal Bhil of Rajasthan (Alisha, 2017). The Rh(D)+ allele frequency in the present study six "denotified" tribes (range 0.8156) was similar to the value reported in the Scheduled Castes (0.836; Sidhu, 2003) and Jat Sikh (0.8451; Kaur, 2017) of Punjab as well as to the Rajputs (0.7260; Alisha, 2017) and 7 nomadic tribal populations of Rajasthan (range 0.8650-1.0000; Sachdev, 2012).
3. In case of 8 *Alu* Ins/Del markers studied in the seven “denotified” tribes of Punjab, the average allele frequency distribution pattern was similar to the Indo-European speaking tribes of South Gujarat, West India (Kshatriya *et al.*, 2011).The frequency of *APO* (I) allele was observed varying from moderate to high in the seven “denotified” tribes (range 0.6540-0.9342) of Punjab similar to the tribal population reported from West India (range

0.6290-0.9480). The frequency of *CD4* (D) allele was observed low in seven "denotified" tribes (range 0.0118-0.1392) of Punjab which was similar to the caste and tribal populations reported from North (range nil-0.1650), Central (range 0.0180-0.1011) and West (range 0.0170-0.2320) India.

4. The coefficient of gene differentiation (G_{ST}) value estimated in the present "denotified" tribes of Punjab (5.4%) showed great genetic heterogeneity in the present study populations of the state. The G_{ST} value recorded in present "denotified" tribes of Punjab was greater than that reported in caste populations (the Jat Sikh, Brahmin, Khatri and Scheduled Castes) of the state (G_{ST} = 1.3%) (Kaur *et al.*, 2002) but similar to G_{ST} value (4.9%) reported among tribal populations from West India (Dada *et al.*, 2011).
5. The assessment of the genetic affinities of the "denotified" tribes of Punjab with other caste populations of state (Fig. 12) demonstrated that the Gandhila separated at an early stage of evolution from the remaining six "denotified" tribes. The Barad, Bangala, Bazigar, Bauria and Nat formed a subcluster while, the Sansi was observed clustered with the caste populations reported from Punjab (Kaur *et al.*, 2002). The MDS plot (Fig.13) clearly separated the "denotified" tribes of Punjab from the caste populations, suggesting no genetic closeness between them.
6. The UPGMA tree (Fig. 14) and MDS plot (Fig. 15) of the genetic affinity of the seven "denotified" tribes of Punjab with various caste and tribal populations of India, clearly demonstrated that these "denotified" tribes were clustered away from the caste populations of North India and appeared relatively close to the Indo-European speaking tribal populations of West India.

Like the social anthropological evidence already available on the "denotified" tribes (Vimukt Jatis) of Punjab indicating a tribal status for them (Singh, 2010), the present physical (biological) anthropological project on these populations also corroborate their affinities with various tribal populations of West India than the caste populations of Punjab. Thus it is suggested/recommended that the Bauria, Bazigar, Bangala, Barad, Gandhila, Nat and Sansi populations of Punjab should be provided the scheduled tribe (ST) status in the state to so that they have a stake in reservation quota for jobs, admissions, scholarships and other benefits provided by the Central government for the ST enabling these illiterate and backward populations of Punjab get social justice.

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Appendix-I

Consent Form and General Information Sheet

Study Title: "Anthropogenetic Profile of "denotified" Tribes (Vimukt Jatis) of Punjab (North-West India) and its Social Implication"

Participant: Name ________________ Caste ______________ Gender _____________

Age _____ (in years) Place ________________ Marital Status ___________

Please read the following before putting your signature below:	[**X**]
• I have genuinely informed the investigator about my current health status that I am not under any serious medical condition which includes suffering from any genetic or psychological disorder.	[ ]
• I am free to participate or not to participate in this study.	[ ]
• I have been given the opportunity to ask questions and reply was given for all the questions to my satisfaction.	[ ]
• I have been informed by the investigators about the process including the nature, objective and known and likely inconveniences related to this study and I have understood them.	[ ]
• By signing this form, I give my free and informed consent to take part in this study as outlined in the information sheet and this consent form.	[ ]
• I give permission for any blood that is left over after the tests to be stored and used for further laboratory tests for medical research.	[ ]
• By signing this form I have not given up my legal rights.	

____ Date: ___ / ___ /_______

Signature/Thumb Impression of Participant (or Legal Representative)

________________________________ ________________________________

Name and Signature of Investigator Name and Signature of the Witness