Dermatoglyphic variations in five ethno-geographical cohorts of Indian populations: A Pilot Study

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Citation

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Abstract

The present study was carried out to understand the genetic relationship if any, among different Indian populations using classical dermatoglyphic markers in 250 post-graduate students. Finger print patterns were collected on a white paper using a non-spreading blue ink-pad. The other traits were recorded by direct observation. The ridges were counted and patterns were identified using glass hand-lens. Statistical analysis was done using student t-test, two-way anova (multivariate) and chi-square test of significance using ANALYSE-IT software. Phylogenetic analysis was carried out using PopGen 32 and MEGA 4 software. Significant variations were found for total ridge count between North vs. East cohort ($p<0.001$) and East vs. West cohort ($p<.001$). Interestingly, 55% of the participants from Northern cohort had dominant allele for hand clasping and thumb extension traits, while 55% participants of South cohort have recessive allele for the same. Interestingly, blood group “O” and “AB” were found significantly (($p= 0.07$) associated with “whorl” and “loop” fingerprint pattern types in each cohort.

INTRODUCTION

There is a distinct signature of ethinicity, geographical conditions, culture and language in peoples from North to South and East to West of India. Many studies have explained the genetic variations that exist within and between the populations. These variations affect all traits such as susceptibility to disease and responses to the environment. Due to social and political reasons, our national population has been divided into groups, variously called as races or ethnic groups. The north India has Hindu religious groups while eastern and southern populations are thought to be Mongolian and Dravidian [1]. They used mitochondrial, Y- chromosomal and autosomal markers to define the genetic relationships among Indian populations. Saha et al [2] also carried out a comprehensive study in five Indian populations to understand the genetic affinities among them. Although these studies have contributed significantly, our understanding on diverse ethnic groups constituting the rich socio-cultural heritage of the origin and relationships among the Indian populations is still poor. In the present study, an attempt was made to review the pre-established (genetic marker based) relationships among Indian population using classical dermatoglyphic markers, which do have a genetic component underlying [3]. Dermatoglyphic traits are those that are inherited as individual-specific traits. They are supposed to play an important role in the human biological research. These traits are useful in both population studies as well as estimating distances between the populations. The dermal ridges originate from fetal volar pads composed of mesenchymal tissue starting at the sixth to seventh week of development. Ridges become visible at about 3 months and are completed by the sixth month of prenatal development. In this study, the participants were provided with guidelines about these anthropometric markers and a well informed written consent was taken from each of the participants. Total ridge count is one of the parameters used to understand the ethno-geographic variation among different groups. Hand clasping and thumb extensions are other traits having their genetic component behind each phenotype. Studies in US have reported that thumb extension is single gene trait and about 75% individuals are with straight thumb (dominant allele). Fogle [4] have reported that only 25% Caucasian population display the recessive hitchhiker's thumb phenotype.

THE PEOPLES

Jiwaji University is situated in the North of Madhya Pradesh. It hosts students from North (Jammu & Kashmir and Himachal Pradesh), East (Manipur, ASSAM and West Bengal), West (Rajasthan and Gujarat) as well as South (Andhra Pradesh and Kerla) of India. Each of these populations has its own different geographical conditions, distinct cultural aspects, languages etc. We categorized all

the population into five cohorts as North cohort, East cohort, West cohort, Central cohort and South cohort. The people of north India are supposed to be decedents of Aryans, the Manipuri peoples belongs to mongoloid linguistic group while south Indian populations are considered to be Dravidian group. Since, the topological and climatic conditions also varies from north to south and east to west, the populations might also have underlying genetic variations in different genetic traits including, dermatoglyphic patterns pertaining to their distinct ethnic background.

MATERIALS AND METHODS

A standard questionnaire was designed to collect information for each of the participants along with a written consent. The different populations were assigned distinct codes for state representations. Since, the numbers of students representing various states were statistically not significant to be considered as individual populations, all the populations were categorized into five cohorts namely, Northern, Eastern, Western, Central and Southern cohorts to avoid the small sample size error according to their geographical locations in the map of India. The information about caste and economic status of each participant was also included into the study to make comprehensive investigation and conclusions. Ridge pattern type, total ridge count (TRC), hand clasping pattern, thumb extension and blood groups were the five variables, which were analysed in both the sexes in all the populations. Dermatoglyphic prints of all the fingers of both hands were obtained from 250 individuals in a 4-inch square box area using good quality office ink-pad on white sheets (Fig. 1). Each individual was directly observed for hand clasping and thumb extension traits (Fig. 2). Data from the two sexes were combined in both univariate and multivariate analyses. The association of different blood groups with any of the fingerprint patterns was also studied after taking fingerprints from the participants. For analysis, data from male and female sexes were combined, since both are supposed to be part of a single gene pool($_5$). The statistical comparisons were made to reach a conclusion.

Figure 1

Table 1: Total Ridge Count (TRC) variations in both sexes of sampled Indian population

Cohort	STATE(n)	TRC MALE (n)	TRC FEMALE(n)	p-value
NORTH	J&K (29)	157.23 ± 23.74 (29)	NA	-
	HP (75)	142.57± 22.19	125.00 ± 28.72	p = .004
	DL (4)	126.00	154.00 ± 13.45	p = 0.1
EAST	MN (30)	151.44 ± 32.39	126.31 ± 37.07	p = .06
	WB (5)	118.16 ± 32.16	67.33 ± 23.18	p = .047
WEST	RJ (6)	148.66 ± 16.94 (6)	NA	-
	GJ (27)	132.10 ± 17.13	131.30 ± 24.22	p =0.9
CENTER	MP (31)	136.2 0± 20.4	125.90 ± 33.7	p =0.2
	UP (18)	143.00 ± 26.08	125.00 ± 29.85	p = 0.1
SOUTH	KR+ AP (16)	153.25 ± 23.51	115.25 ±29.57	p = 0.03

Abbreviations: J&K, Jammu & Kashmir; HP, Himachal Pradesh; DL, Delhi; MN, Manipur; WB, West Bengal; RJ, Rajasthan; GJ, Gujarat; MP, Madhya Pradesh; UP, Uttar Pradesh; KR, Kerla and AP, Andhra Pradesh (n)= Number of Individuals and NA= Not available

Figure 2

Table 2: Genotypes of thumb and finger patterns and their phenotypes

Genotypes	Phenotypes
AA	Whorls on both thumbs
Aa	2 Ulnare loops or 1 ulnare loop and 1 whorl
aa	Ulnare loops on both thumbs
B-	Arches on thumbs and often other fingers
C-	Radial loops on index finger, often associated with an arch on middle finger
CC	Whorls on both the ring fingers)
Cc	2 Ulnare loops or 1 ulnare loop and 1 whorl, ulnare loop on both
dd	Radial loops on ring or little finger
E	Whorls on all fingers except for an ulnare loop on middle finger
F-	Arches on all fingers

RESULTS

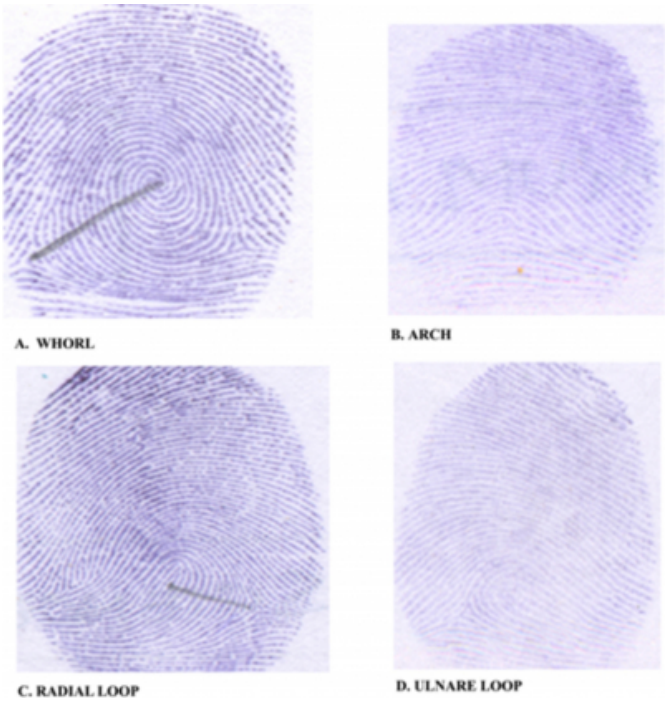
TOTAL RIDGE COUNT (TRC)

We compared the Total Ridge Count (TRC) in all the five cohorts. We found significant variations in total ridge count between North vs. East cohort ($p<0.001$) and East vs. West cohort ($p<.001$) (Table 1.) The finger print patterns were also identified and counted in all the participants of the five cohorts. There are significant variations in TRC between males and females in all the cohorts. The intra-cohort differences in TRC of males and females were not very much significant (p= 0.004, in male and females from HP; p=0.06, in males and females from MN; p=0.90, in males and females from GJ; p=0.20, in males and females from MP and p=0.002, in males and females from AP& KR), while the inter-cohort differences for TRC are more significant (North vs. East, p< 0.0001; North vs. West, p=0.39; North vs. Center, p=0.005; East vs. West, p=0.0002

and North vs. South, p=0.1). This infers that the observed inter-cohort differences in TRC might be according to the genetic differences among the studied populations, characterized by different geographical conditions, ethnicity and linguistic backgrounds. This also hints that formation of ridges and TRC, as marker used in population studies are significantly influenced by the above parameters to a greater extent, which is also revealed by phylogenetic analysis (see Fig. 3).

Figure 3

Figure 1: Various finger print patterns recorded from the sampled populations



WHORL, LOOP AND ARCH

The participants of Western cohort (Rajasthan and Gujarat samples) exhibited high percentage (6.5%) of arch bilateral pattern as compared to other cohorts. Loops (especially, ulnare loops) were more frequent in the participants of North cohort being 3.37 % on an average. Whorls showed a uniform distribution in all the five cohorts with 40% in each on an average (Fig.1Table.4)

HAND CLASPING AND THUMB EXTENSION

Regarding hand clasping trait, 52% of participants of North cohort exhibited dominant (left thumb up) allele, while rest appeared recessive (with right thumb up). Eastern and Western cohort had 45 % and 55% participants with dominant and recessive allele, respectively. The participants of Central cohort had equal (50 %) proportion of dominant and recessive alleles for this trait.

The thumb extension trait is reportedly due to a single gene. Straight thumb is dominant, with 75% of the U.S. Caucasian population displaying this trait. Only 25% of the populations were reported having the recessive hitchhiker's thumb. Hitchhiker's thumb, which is a recessive form of thumb extension trait, was also identified and noted in all the participants of five cohorts. In all cohorts, most of the participants were dominant (staright thumb) for this trait. The hitchhiker's thumb was found rare in north, west and eastern cohort. However, 29.50% of the participants from south cohort had recessive allele for thumb extension. About 80-90% of north and eastern cohorts had straight thumb that is, the dominant allele for this trait. Overall, all the cohorts showed lesser intra-cohort variations between male and female sex for this trait. But, unlike TRC recessive allele for this trait (hitchhiker's thumb) was more frequent in Dravidian population groups of south India. Interestingly, the high frequency of dominant allele in North India and recessive allele in Central and South India appears in correspondence with the high frequency of mitochondrial haplogroup HG “U” in North India while Central and South Indian population have more of HG “M”.

There are different sequence types formed unilaterly or bilaterally. The sequence types on single and both hands were examined in all the cohorts, which revealed that East cohort had 33% and 16% UUUUU (ulnare loops on all fingers) and WWWWW (whorls on all fingers) unilateral and bilateral sequence types, respectively. Overall, UUUUU and WWWWW were the sequence types being more frequent in the participants of all the cohorts. The UUUWW, pattern was found only in 9% and 5% of the participants from North and East cohort, respectively, while it was recorded 16.6% and 14.2% in the participants of Central and Southern cohort respectively. Since, on an average, 22.9% and 14.4% of the participants from all the cohorts had UUUUU and WWWWW, patterns respectively, significant genetic proximity seems to exist among all the Indian populations.

Figure 4

Table 3: Chi square ( ) analysis of thumb and finger genotypes in all the five cohorts.

Count	THUMB GENOTYPES					FINGER GENOTYPES				
COHORT	AA	Aa	aa	B-	Total	C-	CC	Cc	dd	Total
NORTH (n)	27	36	34	4	101	19	21	53	39	132
(%)	(31.7)	(23.4)	(40.8)	(5.1)		(14.5)	(50.2)	(54.4)	(12.9)	
EAST(n)	37	27	48	0	112	13	38	67	10	128
(%)	(35.1)	(26.0)	(45.3)	0		(14.0)	(48.7)	(52.7)	(12.5)	
WEST(n)	29	15	55	15	114	15	55	45	0	115
(%)	(35.7)	(26.4)	(46.1)	(5.7)		(12.6)	(43.7)	(47.4)	0	
CENTRE(n)	45	16	39	0	100	19	52	45	10	126
(%)	(31.4)	(23.2)	(40.4)	0		(13.8)	(47.9)	(51.9)	(12.3)	
SOUTH(n)	31	31	42	8	112	0	63	38	0	101
(%)	(35.1)	(26.0)	(45.3)	(5.6)		0	(38.4)	(41.6)	0	
Total (n)	169	125	218	27	539	66	229	248	59	602
X^2 statistic	53.71					133.16				
p	<0.0001					<0.0001				

Figure 6

Table 4: Two-way Anova for association of blood groups with whorl pattern in five cohorts (Analyse- it softeware).

POPOLATION COHORT	WHORLS					LOOPS				
	n	Mean	SD	SE		n	Mean	SD	SE	
NORTH	3	7.7	4.0	2.33		3	13.0	6.6	3.79	
EAST	3	10.3	5.1	2.96		3	10.0	7.8	4.51	
WEST	3	8.7	9.3	5.36		3	19.0	7.2	4.16	
CENTER	3	6.3	5.0	2.91		3	10.7	6.7	3.84	
SOUTH	3	5.0	1.0	0.58		3	6.3	8.4	4.84	
POPOLATION by BLOOD GROUP	n	Mean	SD	SE		n	Mean	SD	SE	
A	5	9.4	5.5	2.48		5	10.8	8.8	3.92	
B	5	10.2	4.3	1.91		5	15.8	8.3	3.73	
AB	5	3.2	2.2	0.97		5	8.8	4.7	2.11	
Source of variation	SSq	DF	MSq	F	p	SSq	DF	MSq	F	p
COHORT	50.9	4	12.7	0.62	0.6600	263.1	4	65.8	1.28	0.3543
BLOOD GROUP	146.8	2	73.4	3.58	0.0774	130.0	2	65.0	1.26	0.3334
Within cells	163.9	8	20.5			411.3	8	51.4		
Total	361.6	14				804.4	14			

PHENOTYPE & GENOTYPES

In the present study, finger print of each participant was studied to know the genotype for thumb and fingers (Table 2). The genotypes derived from fingerprint (pattern) phenotypes were compared for thumb and fingers among all five cohorts, which revealed significant variations ($p< 0.0001$) among different populations. About 45% of the participants were identified with “AA” genotype for thumb pattern trait in Central cohort, while 48% participants carrying had “aa” genotype for the same in East cohort (Table 3). Interestingly, 15% of the participants from West cohort had a “B “, a rare genotype for thumb, while there was none with this genotype in East and Central cohort. Similarly, a mamimum of 63% of the participants from South cohort had “CC” genotype for finger patterns, while 67% of participants from East cohort had “Cc” genotype. Thus, there exist genetic variations between cohorts showing significant ($p< 0.0001$) inter-cohort differences in frequencies of various genotypes of thumb and finger traits.

BLOOD GROUPS AND FINGERPRINT PATTERNS

Bharadwaj [6] carried out a study during 2000-2001 on 300 medical students with different ABO blood groups in a Medical College, at Ajmer, Rajasthan, India, revealed that individuals with blood group “A” have more of loops, while that of blood group “AB” had more of whorls, suggesting an association between finger print pattern and blood group. In the present study also, we examined the association of blood group types with finger print patterns in different cohorts. Ssignificant ($p= 0.07$) association was found between blood group type (ABO) and fingerprint pattern within cohorts, but not among different cohorts ($p< 0.005$). In Northern cohort, about 10 % of the participants with blood group O were having whorls while a maximum of 19% were with blood group A in the west cohort. Similarly, while 21% participant of the North cohort with blood group O had loops (ulnare +radial), 26% of the South cohort with blood group O were found associated with loops. Arch pattern was almost rare in each cohort.

Thus, our observations distinctly indicate differential associations between blood groups and finger print patterns in different Indian populations, which may likely be due to underlying genetic variations.

DISCUSSION

The primary goal of the anthropological genetics is the assessment of the effect of ethnicity and different evolutionary forces on the genetic structure and composition of the populations. They have a specific role in shaping the contemporary human variation, be it a local, regional or global population. In a study analyzing the digital patterns in the Basque valley of Deba and Spanish populations also revealed that there are individual variations in population for such dermatoglyphic patterns [7] . Dermatoglyphic markers studied in the present study were an effort to understand the genetic variations in different population groups in India through student representatives in the University campus. The total ridge count (TRC) were compared between different zones, which revealed significant difference in TRC between North vs. East ($p .0001$), North vs. Central ($p=.005$) and East vs. West ($p=.0002$) zones (Table 1). Significant variations were found in the total ridge count between the individuals from North and West of India, but only a small variation was observed in TRC between North and Central cohorts. Similarly, for hand clasping trait, we found abundance of dominant allele in North and Central India, while recessive allele was more common in

participants of South cohort. Hitchhiker's thumb trait (Fig. 2) for thumb extension was again found rare in North India while 29% of South Indian participants had this recessive allele. The frequency of genotypes derived from thumb and fingerprint patterns was also significantly ($p< 0.0001$) different in all five cohorts of Indian population (Table 3). We found maximum of 45% participants with "AA" genotype for thumb pattern trait in Central cohort while 48% participants had "aa" genotype for the same in East cohort (Table 3). Interestingly, 15% of the participants from West cohort had a "B-", a rare genotype for thumb, while there was none with this genotype in East and Central cohort. Similarly, 63% of the participants from South cohort had "CC" genotype for finger patterns while, 67% of participants from East cohort had "Cc" genotype. Significant ($p= 0.07$) intra-cohort association was found between blood group types and whorl pattern, but not for inter-cohort association between blood group types and whorl pattern. In general, blood group "O" was found associated with whorl pattern and "AB" group was associated with loop pattern in all the cohorts. Since, the finger print patterns are exhibiting a consistent association with specific blood group types in each cohort, there might be a definitive genetic basis for this association. Blood groups "O" and "AB" may be genetically associated with whorls and loops patterns, respectively in Indian populations. All the populations showed high heterozygosity for thumb extension trait (0.499) on an average while for different pattern type traits populations revealed least heterozygosity of 0.164 (see Table 5).

Our observation revealed significant variations in TRC in North vs. East cohort and East vs. West cohorts establishing underlying genetic difference among them. Like earlier studies using mitochondrial and Y-chromosomal markers, the hand clasping and thumb extension traits also indicate that there may be certain haplogroup more frequent in North than in South of India and vice-versa, as shown by high frequencies of dominant and recessive alleles for theses traits in North and South Indian populations, respectively. The strong association of blood group types with specific fingerprint patterns was an interesting finding which can be further investigated by detailed molecular studies in different population groups. The phylogenetic tree designed on the basis of dermatoglyphic markers also justified geographical proximities of different Indian populations. Thus, although the present study is based on a small numbers of individuals from the representative populations (cohorts), it does indicates that the Indian populations from North, East, West, Central and South cohort, may also be distinguished on the basis of studied dermatoglyphic markers and it also indicate some genetic association between blood group types and fingerprint patterns.

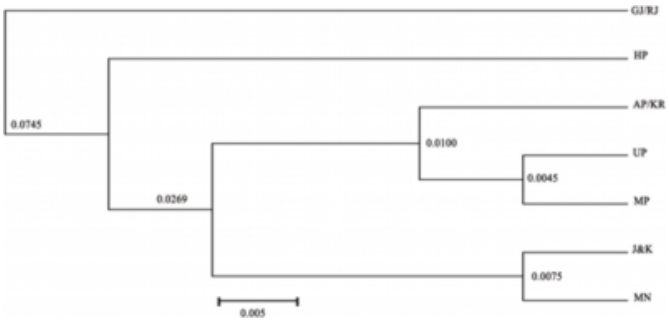
Figure 7

Table 5: Frequencies of homozygotes and hetrozygotes for three traits.

Locus	Sample Size	Ht	Hs	Gst
Hand clasping	249	0.3993	0.3951	0.0105
Thumb extension	249	0.4993	0.4503	0.0982
Pattern type	249	0.1642	0.1599	0.0258
Mean	249	0.3543	0.3351	0.0541
St. Dev		0.0296	0.0238	

Figure 8

Figure 3: Phylogenetic Neighbor joining (NJ) tree showing relationship between seven Indian populations (PopGen 32 and MEGA 4)



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