Genetic Diversity among Coastal Populations of Maharashtra, Goa and Odisha, India

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ABSTRACT India has served as a gateway between continents, with waves of human migration leaving rich cultural and linguistic diversity in their wake. Studies of genetic variation provide inferences about the nature and intensity of forces that have modulated our evolutionary course. The researchers analyzed genetic diversity using 5 genetic markers (ABO, MN, Rh, Se and tasters/non-tasters) in seven populations sampled from Maharashtra, Goa (western coastal zone) and Odisha (eastern coastal zone) of India. The genetic distance estimated by the DISPAN program revealed that geographic segregation has led to genetic divergence among the population of similar ethnicity while population inhabiting same geographical region had higher genetic affinity despite their ethnic origin. ABO locus among all showed maximum genetic divergence between the populations. However, more studies referring to the coastal populations of India could provide new insights into the processes of admixture, selection and drift which lead to population dispersal and differentiation.

INTRODUCTION

India has served as major corridor for the dispersal of modern humans out of Africa ~2,000000 years ago (Cann 2001), owing to its geographical location at the tri-junction of the African, the northern Eurasian and the Oriental realm (Gadgil et al. 1997). The evolutionary antiquity of Indian ethnic groups and gene flow due to subsequent migrations has resulted in a rich tapestry of socio-cultural, linguistic and biological diversity of the subcontinent (Indian Genome Variation Consortium 2008). The tendency to isolate and subjugate the subordinate cultures has augmented such diversity, which is further nurtured by the ecological regimes variegation (Gadgil and Guha 1992).

Despite distinct religious communities, hierarchical castes and sub-castes and isolated tribal groups, inbreeding in human populations arising primarily from marriages between individuals related by ancestry or ethnicity have apparently hampered the gene flow between different factions resulting into isolated endogamous groups. Extensive literature has however demonstrated high degree of heterogeneity among Indian population (Cavalli-Sforza et al. 1964; Papin et al. 1996). The divergence in population genetic structure and sub-structure due to distinct genetic ancestry within or between racial/ethnic groups thereby results in population stratification. Furthermore, selective forces either favour the conservation of existing phenotypes or promote the emergence of new phenotypes leading to rapid divergence of traits between species and the depression of polymorphism within species (Vallender et al. 2004). Thereby, analyses of allele frequency of polymorphic loci such as ABO blood group, phenylthiocarbamide (PTC), taster, secretor etc. offer valuable inroads into understanding of phylogenetic relationships between the populations. Also, accuracy of evolutionary analysis of populations requires the analysis of a large number of genetic polymorphisms belonging to many loci (Bowcock et al. 1991).

Thus, the genetic diversity among people of India has long been of interest for understanding the origin and evolution of the people of the Indian subcontinent (Mountain et al. 1995; Majumder 1998; Basu et al. 2003; Cordaux et al. 2004), enabling us to understand the nature and intensity of actions of various forces that have modulated our evolutionary course. Despite numerous studies from different regions of India, the genetic variations among the coastal populations have not been studied much.

Objective of the Study

The present study was undertaken to assess the extent of genetic diversity and proximity in contemporary endogamous populations...
by estimating heterozygosity, genetic distance
and genetic identity among the populations of
Maharashtra, Goa from western coastal zone and
Odisha from eastern coastal zone.

MATERIAL AND METHODS

Area and People

The present study includes data on the popu-
lation groups from western and eastern coastal
zones of India namely Maratha, Kunbi, Bhandari
and Kharavi from district Ratnagiri, Mahara-
ashtra; Kharavi and Bhandari form South Goa dis-
trict, Goa; and Nolia from district Ganjam, Odis-
ha respectively. The data was collected in differ-
ent phases during 2009-2011. Bhandari inhabi-
ting western coastal region of Maharashtra and
Goa derive their name from the Sanskrit word
‘bhandar’ as in ancient times they were deployed
as special guards for treasuries. Drawing toddy
from palm tree to manufacturing liquor is their
traditional economic resource. However post-
independence, steadily growing population and
disproportionate increase in palm tree have com-
pelled them to do agriculture and other commer-
cial pursuits. Bhandari included in the O.B.C cat-
egory under Constitutional status, is an endog-
amous group following monogamy as a rule of
marriage (Singh 2004).

Maratha is the dominant caste of Maharash-
tra mostly involved in agriculture. They produce
food grains and other commodities for the con-
sumption of the family and the surplus, if left is
sold in the market. Those who do not own land
works as agricultural labourers or industrial work-
ners for wages. It is an endogamous group and
speaks Marathi which belongs to Indo- Europe-
ian language group (Singh 2004).

The ‘Kharavi’ community of Maharashtra
and Goa belong to Hindu religion despite the
fact that after the Portuguese conquest of Goa in
1510 AD a large number of them were converted
into Christianity. They reside along the coastal
belt and are engaged in the traditional profes-
sion of constructing boats, their maintenance and
fishing (Shaikh et al. 2011).

Nolias known as ‘sea people’ of Odisha sus-
tain themselves by fishing and related activities.
Except small children, every member in the house-
hold contributes in production activities. Adult
men go into the sea, women and children help
them on the beach and old people does mending
of the fishing net and training young ones for
fishing. They are Telugu fisherman who migrat-
ed to Ganjam district of Odisha in the end of
nineteenth century and are now constitutionally
categorised as OBC (Kapoor et al. 2010).

Kunbi in Maharashtra is a generic term which
refers to individuals who depend on agriculture
for their livelihood (Singh 2004). They belong to
the Hindu religion and claim to have been war-
rriors and land lord. They speak Marathi Lan-
guage and make more than 30% population of
Maharashtra (Tekade et al. 2011).

Data Collection

Study purpose was explained to all the vol-
unteers prior to data collection and written con-
sent was obtained from each subject. The study
protocol was duly approved by the institutional
ethical clearance committee. The blood samples
were collected by finger prick with sterile lancet
after cleaning the puncture site with 70% ethyl
alcohol. ABO, Rh and MN blood groups typing
of each individual was determined by standard
agglutination method on glass slides using re-
agents Anti-A1, Anti-B, Anti-D, Anti-M and Anti-
N respectively. The secretor status was deter-
mined by using the haemagglutination inhibition
test (Bhasin and Chahal 1996). Harris and Kal-
mus (1949) serial dilution method was used to
assess the taste sensitivity to PTC.

Data Analysis

Considering 4 alleles for ABO gene (O, A1, A2
and B) and 2 alleles for Rh gene (D, d), MN gene
(M,N), Secretor gene (Se, se) and Taster gene
(T,t), the allele frequencies were calculated for
each population (Bhasin and Chahal 1996). The
estimated allele frequencies of the genetic mark-
ers were further analysed to assess standard
genetic distance (Nei 1972) and average het-
erozygosity (Nei 1978) using the genetic distance
and phylogenetic analysis DISPAN program (Ota
1993). The parameter D measures the accumulat-
ed allele differences per locus or codon differ-
ences per unit length of DNA. The coefficient of
gene differentiation (Gst) was used to estimate
the level of gene flow or extent of gene diversity
between the populations relative to the total
population, expressed as

\[ G_{st} = \frac{D_{st}}{H_{t}} \]
where, $D_{ST}$ and $H_e$ are the average gene diversity between populations and for total population respectively. The standard errors of average heterozygosity and Nei’s genetic distance were computed for each population. The phylogenetic tree (dendrogram) was constructed by using the neighbor-joining (NJ) method (Saitou and Nei 1987) and the unweighted pair group method with arithmetic mean (UPGMA) (Sneath and Sokal 1973) from distance matrices. Bootstrap resampling 1,000 (Efron 1982; Felsenstein 1985) was performed to test the percentage of a group’s occurrence. Genetic Identity ($I$) was calculated (Hedrick 2005) as:

$$I = \frac{\sum_{i=1}^{n} p_i^x p_i^y}{\sum_{i=1}^{n} p_i^x + \sum_{i=1}^{n} p_i^y}$$

Where, $p_i^x$ and $p_i^y$ are the frequencies of the ‘$i$’th allele in two populations.

**RESULTS**

The phenotype frequency of genetic markers namely A1A2BO, Rh and MN blood groups, ABH secretion in saliva and taster trait were analysed to infer the allele frequency among the endogamous populations inhabiting Maharashtra, Goa and Odisha (Tables 1, 2 and 3). Generally, the frequency of O allele was highest followed by A1, B and A2 in all the populations under study. Incidence of O allele was higher among Maratha (0.66), A1 among Bhandari (Maharashtra, 0.29), B allele among Nolias (0.27) and A2 allele among Kunbi (0.15) as compared to the other populations. The frequency estimates of Rh alleles indicate higher value for Rh (D) than Rh(d) for all population, being highest among Kharavi of Maharashtra (0.86). Similarly, the allele frequency for secretor (Se) and taster allele (T) was higher for Bhandari (0.59) and Kunbi (0.60) of Maharashtra respectively.

Table 4 displays the average heterozygosity in the populations analysed for multiple loci. The average heterozygosity which indicates the degree of within-population variation was observed to be higher for Kunbi population (0.46).

![Table 1: ABO blood group frequencies among different endogamous populations of Maharashtra, Goa and Odisha](image)

<table>
<thead>
<tr>
<th>Populations</th>
<th>Phenotype</th>
<th>Allele frequencies</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A1</td>
<td>A2</td>
</tr>
<tr>
<td>Maharashtra</td>
<td>Maratha</td>
<td>143</td>
</tr>
<tr>
<td></td>
<td>Kunbi</td>
<td>127</td>
</tr>
<tr>
<td></td>
<td>Bhandari</td>
<td>109</td>
</tr>
<tr>
<td></td>
<td>Kharavi</td>
<td>131</td>
</tr>
<tr>
<td>Goa</td>
<td>Kharavi</td>
<td>137</td>
</tr>
<tr>
<td></td>
<td>Bhandari</td>
<td>137</td>
</tr>
<tr>
<td>Odisha</td>
<td>Nolia</td>
<td>126</td>
</tr>
</tbody>
</table>

![Table 2: MN blood group and Rh gene frequencies among different endogamous population of Maharashtra, Goa and Odisha](image)

<table>
<thead>
<tr>
<th>Populations</th>
<th>Phenotype</th>
<th>Allele frequencies</th>
<th>Phenotype</th>
<th>Allele frequencies</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>M</td>
<td>N</td>
<td>MN</td>
<td>M</td>
</tr>
<tr>
<td>Maharashtra</td>
<td>Maratha</td>
<td>143</td>
<td>41(0.31)</td>
<td>14(0.11)</td>
</tr>
<tr>
<td></td>
<td>Kunbi</td>
<td>127</td>
<td>55(0.43)</td>
<td>43(0.34)</td>
</tr>
<tr>
<td></td>
<td>Bhandari</td>
<td>109</td>
<td>48(0.44)</td>
<td>28(0.26)</td>
</tr>
<tr>
<td></td>
<td>Kharavi</td>
<td>131</td>
<td>58(0.44)</td>
<td>21(0.16)</td>
</tr>
<tr>
<td>Goa</td>
<td>Kharavi</td>
<td>137</td>
<td>60(0.44)</td>
<td>31(0.23)</td>
</tr>
<tr>
<td></td>
<td>Bhandari</td>
<td>137</td>
<td>61(0.45)</td>
<td>38(0.28)</td>
</tr>
<tr>
<td>Odisha</td>
<td>Nolia</td>
<td>122</td>
<td>55(0.40)</td>
<td>15(0.11)</td>
</tr>
</tbody>
</table>
The extent of gene diversity as expressed by heterozygosity indices ($H_S$, $H_T$, $D_{ST}$) and coefficient of gene differentiation ($G_{ST}$) have been furnished in Table 5. The value for $H_S$ showed within population genetic variability to be highest for ABO locus (0.576) and lowest for Rh locus (0.349). Between populations gene diversity was also higher for ABO locus (0.0125) but lowest for MN locus (0.00002). By comparison, the measure of genetic differentiation ($G_{ST}$) revealed maximum genetic divergence between population relative to the combined population for ABO locus (0.021) followed by taster (0.018) and secretor trait (0.011) though the differentiation was not so pronounced.

In Maharashtra (Table 6), the distance was found to be higher between Kunbi and Kharavi (1.94%) followed by Maratha (1.88%) however, the latter seemed to be more closely related to Bhandari and Kharavi (0.0029). Kharavi and Bhandari from Goa suggested higher genetic affinity (0.00008). While geographic differentiation has led to divergence in the population belonging to similar ethnic background that is,
Kharavi (0.0030) and Bhandari (0.0025) from Maharashtra were at greater distance from their respective stock inhabiting Goa. The genetic identity matrix presented in Table 7 also confers to the analysis of genetic proximity.

The dendrogram drawn on the basis of genetic distance matrix as per UPGMA method, consists of three major clades constituted by Nolia, Kunbi and Bhandari (Goa), Kharavi (Goa) Bhandari (Maharashtra), Kharavi (Maharashtra) and Maratha (Fig. 1). Nolias demonstrated earliest divergence followed by Kunbi as compared to the other populations. Clade comprised of Bhandari (Goa), Kharavi (Goa), Bhandari (Maharashtra), Kharavi (Maharashtra) and Maratha depicts greater affinity to each other. Within this broad cluster there are two sub-clusters: the first formed by Bhandari (Goa) and Bhandari (Maharashtra); and the second by Kharavi (Goa) and Maratha.

**Table 7: Genetic identity matrix among different populations of Maharashtra, Goa and Odisha**

<table>
<thead>
<tr>
<th></th>
<th>Maharashtra</th>
<th>Goa</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kunbi</td>
<td>0.9812</td>
<td></td>
</tr>
<tr>
<td>Bhandari</td>
<td>0.9971</td>
<td>0.9957</td>
</tr>
<tr>
<td>Kharavi</td>
<td>0.9971</td>
<td>0.9806</td>
</tr>
<tr>
<td>Kharavi</td>
<td>0.9999</td>
<td>0.9886</td>
</tr>
<tr>
<td>Bhandari</td>
<td>0.9930</td>
<td>0.9959</td>
</tr>
<tr>
<td>Odisha</td>
<td>Nolia</td>
<td>0.9907</td>
</tr>
</tbody>
</table>

**DISCUSSION**

The multiple waves of migration from time immemorial have supplemented the contemporary ethnically, culturally, linguistically and genetically diverse populations. Despite the anthropological and archaeological evidences contentious issues about the origin and divergence of populations in the Indian subcontinent remains inexplicable. Reddy et al. (1987) showed that anthropometric pattern of variation documents the importance of geographic proximity of micro-differentiation under the Indian social setup. Genetic measures inclusive of genetic distance, heterozygosity and genetic differentiation permit analysis of divergence and affinity among populations.

In the present study, the average heterozygosity for all the population was high ranging from 0.456 for Maratha to 0.509 for Kunbi. The low gene differentiation 0.004 to 0.021 for MN
and A1A2BO locus respectively concord with the finding of low (0.26-1.70%) genetic differentiation in Indian populations by Papiha et al. (1982) asserted on the basis of analysis of genetic markers consisting of 11 blood groups and red cell enzyme systems in 14 endogamous groups of north-west India. Mukherjee et al. (1979) analysed 16 biomarker among nine endogamous population of Maharashtra (Nava Budha, Maratha, Deshastha Rigvedi Brahmin, Chitpavan Brahmin, Chandrasenya Kayastha Prabhu, Parsis, Bhil, Pawara and Katkari). The genetic divergence between these groups was small as compared to the within group heterogeneity and the average heterozygosity per gene per locus ranged 20–22%. In the present study, intra population gene diversity $H_s$ were quite high compared to inter-population gene diversity. Previous studies on Indian population have also revealed higher intra-population diversity (Bamshad et al. 1998; Tekade et al. 2011). This suggests the differences in genetic structure are more likely to be due to their breeding structure, differential migration and ethnic affiliation.

It has been observed that many genetic studies have been carried on the different populations representing different part of India and the genetic composition of the Indian people has been examined according to the existing social structure. The coastal populations or fishing communities of Western coastal zone and Eastern coastal zone have not been studied so far. Such studies can throw light on the various processes of admixture, selection and drift which lead to population dispersal and differentiation and might be of special interest to cultural biologist, anthropologists, historians, human genetist and geographers.

ACKNOWLEDGMENTS

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