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# Genetic differentiation among four groups of fishermen of the Eastern coast, India

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**Summary.** The four endogamous groups of fishermen living around the city of Puri, located on the eastern coast of India, were studied for blood groups, red cell enzymes and serum proteins (11 loci). Only 1·3% of the total diversity among the groups studied is due to differences between them ($G_{ST} = 0{\cdot}013$). The genetic distances between populations were estimated using Edwards and Cavalli-Sforza's method. The pattern of genetic distance reflects the geographical distribution of these groups. In general, these observations support the patterns of variation based on anthropometric and dermatoglyphic variables.

## 1. Introduction

Over two million fishermen, both marine and inland, live along the 3000 mile long coast of Peninsular India. These communities are divided into numerous endogamous groups; they speak different languages, have different social backgrounds, and are of different geographic origin. For example, some groups prefer consanguineous marriages, while in others such marriages are strictly prohibited. Excessive population densities and consequent dwindling of resources often led these people to emigrate in pursuit of a better niche for fishing, and thus come in contact with alien populations. Such a situation is evident in some parts of the coastal Andhra Pradesh. Until recently, however, little attention has been paid to the study of these groups. In order to fill this gap a project was begun in 1977 among the three migrant groups of fishermen living around Puri, located on the eastern coast of India (figure 1). The population structure, demography, and biological variation in these groups have already been reported (Reddy 1981, 1982 a and b, 1983 a, b and c, 1984; Reddy, Chopra and Mukherjee 1987; Reddy, Chopra, Karmakar and Malhotra 1988). In the present paper, we examine the nature of genetic variation among these people based on blood groups, red cell enzymes, and serum proteins. Comparable data on a local group of fishermen called Kevto, who fish in the Chilka Lake, about 60 km inland from Puri town, are also presented. The genetic affinities between the marine fishermen groups will be evaluated in the light of known ethnohistorical and geopraphical backgrounds and with reference to patterns observed using anthropometrics and quantitative finger and palmar dermatoglyphics.

### *Population backgrounds*

Three of the four groups considered in the present study namely, Vadabalija of Penticotta (VADP), Vadabalija of Vadapeta (VADV), and Jalari (JALP) are migrants in Puri and speak Telugu, a language different from the local Oriya. While the VADP migrated some 35 years ago from 48 villags of Visakapatnam, East Godavari and West Godavari districts of Andhra Pradesh (Figure 1), the VADV and JALP migrated some

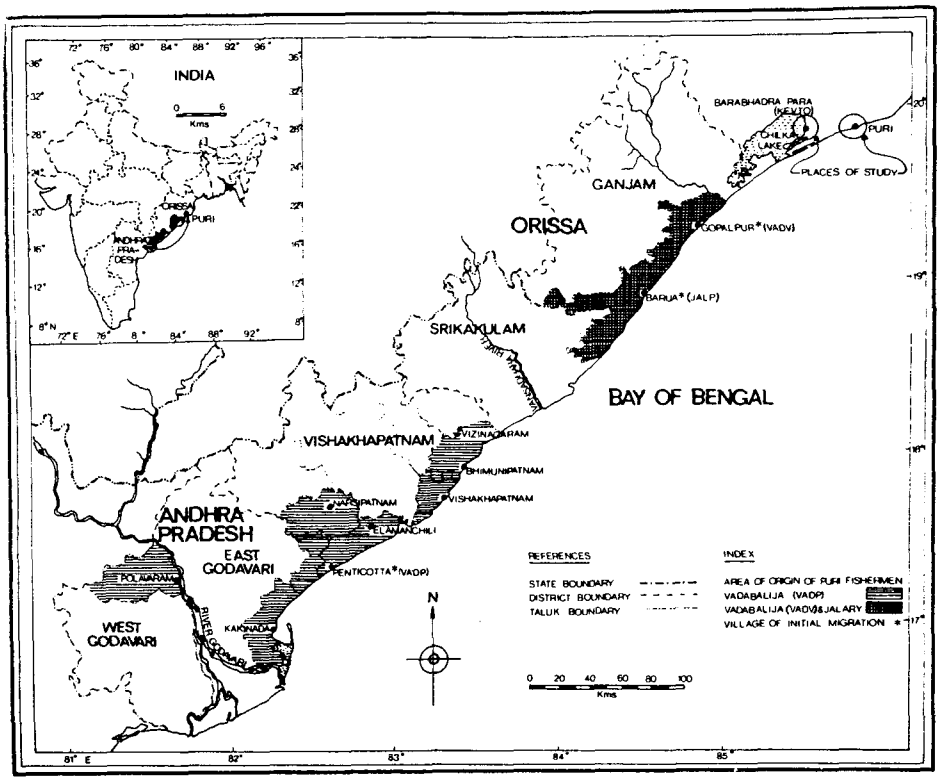


Figure 1. Map showing the studied areas and the geographical backgrounds of the migrant groups of fishermen.

100 years ago from 42 and 17 villages, respectively, of the Srikakulam district of Andhra Pradesh and contiguous Ganjam district of Orissa. However, it may be mentioned here that the probable route of migration of these groups was by land. Demographic investigations suggest that while VADV and JALP have almost formed local breeding units (Reddy 1984) isolated from parental groups, the VADP still has marital contacts with the parental population. The rate of intermarriages between the VADP and VADV amounts to only about 1%. These two grups have no marriage contacts with the JALP who belong to a different caste. At Puri, population sizes of these groups are 8000, 4000, and 800, respectively. More details on the population backgrounds are given in Reddy (1984).

The fourth group is called Kevto (KEVT). They live on the bank of Chilka Lake, about 60 km inland from Puri town. As in most of the Oriya populations, consanguineous marriages are strictly prohibited among them, while such marriages are greatly preferred in the three Puri groups. The three groups of marine fishermen and the Kevto have not had any cultural or biological contacts. All four groups have a similar social status that is relative low in the caste hierachy.

## 2. Materials and methods

During May–June 1985, blood samples were taken from 409 subjects. Subjects belonged to both sexes and ranged in age from 8–60 years. Efforts were made to select subjects from all parts of the settlements, and care was taken to exclude related individuals.

Blood samples were collected in 1 ml vials by pricking the subject's finger. EDTA was used as anticoagulent. The blood specimens were stored in an ice-filled thermacol box and brought to the Biochemical Laboratory of the Indian Statistical Institute, Calcutta. Typing for ABO, MN, and Rh(D) blood groups were done at the same lab, following standard methods. The serum extracts and erythrocyte lysates were deep frozen and later brought by BMR to the Institut für Humanbiologie of the Hamburg University, where screening for red cell enzymes and serum proteins was performed. Typing for enzyme systems was performed on erythrocyte lysates obtained from washed cells. The red cell enzymes AK, ADA, AcP, PGM, ESD, and 6PGD, and the sera of the subjects for Group component (Gc) were screened by cellulose acetate foil gel (CAFG) electophoresis (Biotest), following the method of Sonnerborn (1976). For Hp, the samples were typed by horizontal starch gel electrophoresis (SGE), following the procedure of Prokop and Smithies (As given in Prokop and Göhler 1976). Hp was stained with benzidine, and Gc with nigrosine after immunofixation. The adapted nomenclature was that proposed by Spielmann and Kühnl (1982). The gene frequencies were calculated following Mourant, Kopec and Domaniewska-Sobzak (1976). Both intra- and intergroup analysis was performed using the gene diversity measure of Nei (1973) and distance statistics of Edwards and Cavalli-Sforza (1972).

## 3. Results

The phenotype frequencies for the three blood groups, six red cell enzymes, and the two serum proteins are presented in table 1 for each group, and the gene frequencies are given in table 2.

Table 1. Phenotypic frequencies of the 11 loci in the four fisherman groups.

| Phenotypes | VADP | | VADV | | JALP | | KEVTO | |
|---|---|---|---|---|---|---|---|---|
| | No. | % | No. | % | No. | % | No. | % |
| Blood Groups | | | | | | | | |
| $A_1$ $A_2$ BO | | | | | | | | |
| $A_1$ | 11 | 9·1 | 16 | 16·5 | 17 | 22·1 | 7 | 7·1 |
| $A_2$ | 3 | 2·5 | 4 | 4·1 | 0 | 0·0 | 0 | 0·0 |
| B | 45 | 37·2 | 21 | 21·7 | 19 | 24·7 | 51 | 52·0 |
| O | 50 | 41·3 | 48 | 49·5 | 37 | 48·1 | 36 | 36·7 |
| $A_1B$ | 12 | 9·9 | 4 | 4·1 | 4 | 5·2 | 4 | 4·1 |
| $A_2B$ | 0 | 0·0 | 4 | 4·1 | 0 | 0·0 | 0 | 0·0 |
| Total | 121 | | 97 | | 77 | | 98 | |
| MN | | | | | | | | |
| M | 48 | 40·3 | 23 | 24·2 | 23 | 29·9 | 30 | 30·9 |
| MN | 60 | 50·4 | 57 | 60·0 | 45 | 58·4 | 46 | 47·4 |
| N | 11 | 9·2 | 15 | 15·8 | 9 | 11·7 | 21 | 21·7 |
| Total | 119 | | 95 | | 77 | | 97 | |
| Rh(D) | | | | | | | | |
| D | 85 | 94·4 | 91 | 95·8 | 70 | 90·9 | 94 | 96·9 |
| d | 5 | 5·6 | 4 | 4·2 | 7 | 9·1 | 3 | 3·1 |
| Total | 90 | | 95 | | 77 | | 97 | |
| Red cell enzymes | | | | | | | | |
| ADA | | | | | | | | |
| 1-1 | 80 | 72·7 | 72 | 74·2 | 53 | 77·9 | 64 | 73·6 |
| 2-1 | 28 | 25·5 | 23 | 23·7 | 13 | 19·1 | 18 | 20·7 |
| 2-2 | 2 | 1·8 | 1 | 1·0 | 2 | 2·9 | 5 | 5·8 |
| 6-1 | 0 | 0·0 | 1 | 1·0 | 0 | 0·0 | 0 | 0·0 |
| Total | 110 | | 97 | | 68 | | 87 | |

Table 1. *Cont'd.*

| Phenotypes | VADP | | VADV | | JALP | | KEVTO | |
|---|---|---|---|---|---|---|---|---|
| | No. | % | No. | % | No. | % | No. | % |
| AK | | | | | | | | |
| 1-1 | 78 | 97·5 | 72 | 86·8 | 39 | 90·7 | 68 | 88·3 |
| 2-1 | 1 | 1·3 | 11 | 13·3 | 3 | 7·0 | 8 | 10·4 |
| 2-2 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 |
| 3-1 | 1 | 1·3 | 0 | 0·0 | 1 | 2·3 | 1 | 1·3 |
| Total | 80 | | 83 | | 43 | | 77 | |
| ESD | | | | | | | | |
| 1-1 | 84 | 73·0 | 74 | 74·0 | 63 | 88·7 | 83 | 89·3 |
| 2-1 | 27 | 23·5 | 26 | 26·0 | 8 | 11·3 | 10 | 10·8 |
| 2-2 | 4 | 3·5 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 |
| Total | 115 | | 100 | | 71 | | 93 | |
| 6PGD | | | | | | | | |
| A | 91 | 92·9 | 86 | 97·7 | 54 | 98·2 | 80 | 98·8 |
| AB | 7 | 7·1 | 2 | 2·3 | 0 | 0·0 | 1 | 1·2 |
| B | 0 | 0·0 | 0 | 0·0 | 1 | 1·8 | 0 | 0·0 |
| Total | 98 | | 88 | | 55 | | 81 | |
| PGM1 | | | | | | | | |
| 1-1 | 57 | 50·0 | 45 | 45·9 | 36 | 52·2 | 45 | 50·6 |
| 2-1 | 41 | 36·0 | 44 | 44·9 | 28 | 40·6 | 36 | 40·5 |
| 2-2 | 16 | 14·0 | 9 | 9·2 | 5 | 7·3 | 8 | 9·0 |
| Total | 114 | | 98 | | 69 | | 89 | |
| AcP | | | | | | | | |
| A | 5 | 4·4 | 5 | 5·0 | 1 | 1·4 | 6 | 6·5 |
| AB | 21 | 18·3 | 21 | 20·8 | 15 | 21·1 | 20 | 21·5 |
| AC | 4 | 3·5 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 |
| B | 78 | 67·8 | 66 | 65·4 | 47 | 66·2 | 60 | 64·5 |
| BC | 7 | 6·1 | 9 | 8·9 | 8 | 11·3 | 7 | 7·5 |
| C | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 |
| Total | 115 | | 101 | | 71 | | 93 | |
| Serum proteins | | | | | | | | |
| Hp | | | | | | | | |
| 1-1 | 9 | 12·0 | 1 | 2·1 | 2 | 6·1 | 2 | 2·6 |
| 2-1 | 40 | 53·3 | 17 | 35·4 | 17 | 51·5 | 25 | 32·5 |
| 2-2 | 26 | 34·7 | 30 | 62·5 | 14 | 42·4 | 50 | 64·9 |
| Total | 75 | | 48 | | 33 | | 77 | |
| Gc | | | | | | | | |
| 1-1 | 46 | 58·2 | 19 | 32·8 | 12 | 60·0 | 45 | 64·3 |
| 2-1 | 27 | 34·2 | 28 | 48·3 | 7 | 35·0 | 17 | 24·3 |
| 2-2 | 6 | 7·6 | 11 | 19·0 | 1 | 5·0 | 5 | 7·1 |
| Z-1 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 | 1 | 1·4 |
| B-1 | 0 | 0·0 | 0 | 0·0 | 0 | 0·0 | 2 | 2·9 |
| Total | 79 | | 58 | | 20 | | 70 | |

Except for a marginally significant departure from the ABO system in the VADP, in which the frequency of the AB genotype is found to be in excess, no other locus showed any deviation from Hardy-Weinberg equilibrium. The fishing populations show polymorphic frequencies for all the studied systems, except the 6PGD, for which the Kevto show only 0·6% of the rarer variant $PGD^B$. The frequency of $PGD^B$ allele in Kevto is similar to the values observed in some of the populations of Orissa (Papiha, Roberts and Mishra 1988). In VADP, VADV and JALP, the frequencies of this allele are 3·6,

1·1 and 1·8% respectively. These values are within the range reported for populations from Andhra Pradesh, the region of their origin (Roberts, Papiha, Rao, Habeebullah, Kumar and Murthy 1980).

The Jalari of Puri and the Kevto fail to show the $A_2$ allele, while the Jalari of Waltair (Naidu, Mohrenweiser and Neel 1985), who belong to the same caste as that of JALP, show a rather high frequencey (7·7%). Among the four, the Kevto show the highest frequency of B allele (34%). The frequency of A allele is relatively low in the fishermen (ranging from 5·6–14·5%) and is closely comparable with that of the castes from Andhra Pradesh; tribes of Andhra show a relatively high frequency of this allele (7–29%).

A comparison with the neighbouring caste and tribal populations reveal the following characteristic features. For example, in VADV, one of the 97 persons screened for ADA exhibits the rare $ADA^6$ variant which is absent in the other Telugu speaking populations studied so far (Rao, Blake and Veeraju 1978, Roberts *et al.* 1980, Naidu *et al.*

Table 2. Gene frequencies and the contingency $\chi^2$ for intergroup heterogeneity. Values in the parentheses are the $\chi^2$s for the three marine groups.

| Gene | VADP | VADV | JALP | KEVTO | $\bar{P}$ | $\sigma_p^2$ | $\chi^2$ | d.f. |
|---|---|---|---|---|---|---|---|---|
| p1 | 0·067 | 0·108 | 0·145 | 0·056 | 0·090 | 0·002 | | |
| p2 | 0·020 | 0·030 | 0·000 | 0·000 | 0·013 | 0·000 | 40·8** | 9 |
| q | 0·251 | 0·143 | 0·160 | 0·337 | 0·228 | 0·004 | (18·1** | 6) |
| r | 0·662 | 0·720 | 0·695 | 0·607 | 0·669 | 0·004 | | |
| M | 0·655 | 0·542 | 0·591 | 0·546 | 0·587 | 0·002 | 7·5 | 3 |
| N | 0·344 | 0·458 | 0·409 | 0·454 | 0·412 | 0·002 | (5·8 | 2) |
| D | 0·764 | 0·795 | 0·698 | 0·824 | 0·774 | 0·002 | 8·4* | 3 |
| d | 0·236 | 0·205 | 0·301 | 0·176 | 0·226 | 0·002 | (4·9 | 2) |
| $ADA^1$ | 0·855 | 0·866 | 0·875 | 0·839 | 0·858 | 0·000 | 1·0 | 3 |
| $ADA^2$ | 0·145 | 0·129 | 0·125 | 0·161 | 0·142 | 0·000 | (0·3 | 2) |
| $ADA^6$ | 0·000 | 0·005 | 0·000 | 0·000 | | | | |
| $AK^1$ | 0·987 | 0·934 | 0·954 | 0·942 | 0·954 | 0·000 | 7·5 | 3 |
| $AK^2$ | 0·006 | 0·066 | 0·035 | 0·052 | 0·046 | 0·000 | (6·0* | 2) |
| $AK^3$ | 0·006 | 0·000 | 0·012 | 0·006 | | | | |
| $ESD^1$ | 0·848 | 0·870 | 0·944 | 0·946 | 0·896 | 0·002 | 16·5** | 3 |
| $ESD^2$ | 0·152 | 0·130 | 0·056 | 0·054 | 0·104 | 0·002 | (7·8* | 2) |
| $PGD^A$ | 0·964 | 0·989 | 0·982 | 0·994 | 0·981 | 0·000 | 5·0 | 3 |
| $PGD^B$ | 0·036 | 0·011 | 0·018 | 0·006 | 0·019 | 0·000 | (2·6 | 2) |
| $PGM^1$ | 0·680 | 0·674 | 0·725 | 0·708 | 0·693 | 0·000 | 1·4 | 3 |
| $PGM^2$ | 0·320 | 0·326 | 0·275 | 0·292 | 0·307 | 0·000 | (1·1 | 2) |
| $AcP^A$ | 0·152 | 0·153 | 0·120 | 0·172 | 0·151 | 0·000 | 2·2 | 6 |
| $AcP^B$ | 0·800 | 0·802 | 0·824 | 0·790 | 0·803 | 0·000 | (1·1 | 4) |
| $AcP^C$ | 0·048 | 0·044 | 0·056 | 0·038 | 0·046 | 0·000 | | |
| $Hp^1$ | 0·387 | 0·198 | 0·318 | 0·188 | 0·273 | 0·008 | 18·8** | 3 |
| $Hp^2$ | 0·613 | 0·802 | 0·682 | 0·812 | 0·727 | 0·008 | (9·7** | 2) |
| $Gc^1$ | 0·753 | 0·569 | 0·775 | 0·786 | 0·718 | 0·008 | 17·5** | 3 |
| $Gc^2$ | 0·247 | 0·431 | 0·225 | 0·193 | 0·282 | 0·008 | (12·2** | 2) |
| $Gc^Z$ | 0·000 | 0·000 | 0·000 | 0·007 | | | | |
| $Gc^B$ | 0·000 | 0·000 | 0·000 | 0·014 | | | | |
| Total | | | | | | | 126·6** | 42 |
| | | | | | | | 69·9** | 28 |

* $P<0·05$
** $P<0·01$

1985). In Orissa also, this allele is not observed (Papiha *et al.* 1988). Similarly, $AK^3$ variant is represented by one individual each in three of the four populations. Except in VADP the frequencies of the $AK^2$ allele are similar to the ones observed in the tribal populations of Andhra Pradesh and Orissa (Roberts *et al.* 1980, Papiha *et al.* 1988). The caste groups have relatively higher values. An extremely low value of the $AK^2$ allele in VADP ($< 1\%$) is difficult to explain at present. It may be due to chance only.

At the acid phosphate locus, the C allele is found with rather high frequency (3·8–5·6%), comparable only to the four Gujarati tribes (Bhasin, Singh, Sudhakar, Bharadwaj, Chahal, Walter and Dannewitz 1985). Hindus and Muslims (Roberts *et al.* 1980) and a scheduled tribe, Kondareddy from Andhra Pradesh (Blake, Ramesh, Vijayakumar, Murthy and Bhatia 1981), show this allele in relatively low frequency ($< 1\%$). Also, most other Indian populations studied either lack this allele or show rather a low frequency (Bhasin, Walter, Singh, Hilling and Bharadwaj 1981). The average is only about 0·3%. In the Gc system, the two rare variants, similar to $Gc^{Z-1}$ and $Gc^{B-1}$, are observed among the local Kevto, but are not known from other populations studied.

We have examined the extent of heterogeneity in gene frequency with the help of contingency chi-square, defined as

$$\chi^2 = 2N \sum_{j=1}^{k} \frac{\sigma^2_{Pj}}{\bar{P}_j} \tag{1}$$

where $k$ is the number of alleles at a locus, and $N = \sum_{i=1}^{r} N_i$.

$N_i$ is the sample size of the $i$th population, and r is the number of samples. $\overline{P_j}$ and $\sigma^2_{\bar{P}j}$ are the weighted mean and variance of the $j$th allele, respectively. The results are given in table 2, along with the gene frequencies. ABO, Rh (D), ESD, Hp, and Gc show significant population heterogeneity.

The total $X^2$, pooled over all the loci, is highly significant ($X^2 = 126{\cdot}6$; 42 d.f.; $p < 0{\cdot}01$). Since the three groups of marine fishermen are subpopulations of a larger group (different from the local Kevto), a chi-square test was also performed for them seperately. There is a marked reduction in the $X^2$ value ($X^2 = 69{\cdot}9$; 28 d.f.; $p < 0{\cdot}05$) suggesting an important contribution of Kevto to the total heterogeneity. The comparison of the two $X^2$ values shows that this difference is statistically significant ($F = 126{\cdot}6/69{\cdot}9 = 1{,}81$; 42 and 28 d.f.) at 5% level.

*Gene diversity analysis*

Nei (1973) devised a method to measure the variation within a population which is for a locus $H = 1 - \Sigma x_i^2$, where $x_i$ is the frequency of $i$th allele at locus, and the average gene diversity within a population ($\overline{H}$) is obtained by averaging H-values over all loci. This is otherwise called the average heterozygosity index. These values are given separately for each of the four populations and loci in table 3. The average heterozygosity index is largest for the VADP (0·32) and smallest for the KEVTO (0·291). Among the three Puri groups, the largest population (VADP) with the most heterogeneous background (geographically) shows the highest value of heterozygosity and the smallest population, JALP, which is most settled, shows the lowest value, suggesting also a positive relationship with population size.

According to Nei (1973), the gene diversity of the total population ($H_T$) can be par-

Table 3. Heterozygosity according to locus and population, and the average heterozygosity index.

| Locus | VADP | VADV | JALP | KEVTO |
|---|---|---|---|---|
| $A_1A_2BO$ | 0·493 | 0·449 | 0·470 | 0·515 |
| MN | 0·452 | 0·496 | 0·483 | 0·496 |
| Rh(D) | 0·360 | 0·326 | 0·421 | 0·290 |
| ADA | 0·248 | 0·233 | 0·219 | 0·270 |
| AK | 0·025 | 0·124 | 0·089 | 0·111 |
| ESD | 0·258 | 0·226 | 0·106 | 0·102 |
| 6PGD | 0·069 | 0·022 | 0·036 | 0·012 |
| PGM1 | 0·435 | 0·440 | 0·399 | 0·414 |
| AcP | 0·335 | 0·331 | 0·303 | 0·344 |
| Hp | 0·474 | 0·317 | 0·434 | 0·305 |
| Gc | 0·372 | 0·490 | 0·349 | 0·345 |
| Average (H) | 0·320 | 0·314 | 0·301 | 0·291 |

titioned into the gene diversity within subpopulations ($H_S$) and between subpopulations ($D_{ST}$). Thus, we have

$$H_T = H_S + D_{ST}. \tag{2}$$

By taking average gene frequencies of all the subpopulations as the representative frequency of the entire population, the gene diversity of the total population can be determined. The average gene diversity of all subpopulations will give the value of $H_S$. The value $D_{ST}$ is obtained by subtraction. The ratio $G_{ST} = D_{St}/H_T$ is called the coefficient of gene differentiation. The variance of $G_{ST}$ is calculated as suggested by Chakraborty (1974).

The values of $H_S$, $D_{ST}$, and $G_{ST}$ for each locus and average diversity over all loci among the three marine groups is given in table 4. The average gene diversity over all the loci is observed to be 0·013. There is also a great range of variation among the loci in the degree of diversity, i.e., from zero in ADA to 0·04 in the Gc system. It is also of interest to note that when Kevto is considered for diversity analysis, along with the three marine groups, the $G_{ST}$ values increase consistently in eight of the loci (table 4). On an average, an increase of about 18% in diversity is found due to the inclusion of Kevto.

Table 4. Gene diversity among the fishermen populations. Number 1 refers to that between the three Puri groups and 2 for the four groups including the Kevto.

| Locus | $H_{T1}$ | $H_{T2}$ | $H_{S1}$ | $H_{S2}$ | $D_{ST1}$ | $D_{ST2}$ | $G_{ST1}$ | $G_{ST2}$ |
|---|---|---|---|---|---|---|---|---|
| $A_1A_2BO$ | 0·475 | 0·491 | 0·471 | 0·482 | 0·004 | 0·009 | 0·008 | 0·019 |
| MN | 0·481 | 0·486 | 0·477 | 0·482 | 0·004 | 0·004 | 0·009 | 0·008 |
| Rh(D) | 0·372 | 0·354 | 0·369 | 0·349 | 0·003 | 0·004 | 0·009 | 0·012 |
| ADA | 0·224 | 0·243 | 0·234 | 0·243 | 0·000 | 0·000 | 0·000 | 0·002 |
| AK | 0·080 | 0·088 | 0·079 | 0·087 | 0·001 | 0·001 | 0·014 | 0·010 |
| ESD | 0·200 | 0·177 | 0·197 | 0·173 | 0·003 | 0·004 | 0·017 | 0·021 |
| 6PGD | 0·043 | 0·035 | 0·042 | 0·035 | 0·000 | 0·000 | 0·005 | 0·009 |
| PGM1 | 0·426 | 0·423 | 0·425 | 0·422 | 0·001 | 0·001 | 0·002 | 0·002 |
| AcP | 0·323 | 0·329 | 0·323 | 0·328 | 0·000 | 0·000 | 0·001 | 0·001 |
| Hp | 0·421 | 0·397 | 0·409 | 0·383 | 0·012 | 0·014 | 0·029 | 0·035 |
| Gc | 0·421 | 0·405 | 0·404 | 0·389 | 0·017 | 0·016 | 0·040 | 0·041 |
| Average | 0·316 | 0·312 | 0·312 | 0·307 | 0·004 | 0·005 | 0·013 | 0·016 |
| SE | | | | | | | ±0·004 | ±0·004 |

*Genetic distances*

One of our objectives is to examine the nature of inter-population affinities of the fisherman. There are several measures available to compute genetic distances. Nei's method (1972) is said to have several theoretical advantages over the of Cavalli-Sforza and Edwards and others. To see if this is reflected in the pattern of genetic distances, we computed the distance matrix by both methods. Since the two methods showed a similar pattern of interrelationships, we present only the results based on Edwards and Cavalli-Sforza's (1972) E distance.

The distance matrix based on the 11 loci are given in table 5. The observed pattern of distances, however, does not support either ethnic or geographical affiliations of the groups. The largest distance is obtained between the VADP and VADV, the two reproductive isolates of the same caste, and the smallest distance is between the VADP and JALP, who belong to neither same caste nor geographical region originally. The three Puri groups, however, show similar distances from the Kevto with whom they did not have any contact, either cultural or biological.

Table 5. Distance matrices based on Edwards and Cavalli-Sforza's method including 9 (above diagonal) and 11 (below diagonal) loci.

| Population | VADP | VADV | JALP | KEVTO |
|---|---|---|---|---|
| VADP | | 0·0524 | 0·0547 | 0·0607 |
| VADV | 0·0704 | | 0·0404 | 0·0592 |
| JALP | 0·0521 | 0·0597 | | 0·0609 |
| KEVTO | 0·0688 | 0·0686 | 0·0621 | |

Sample size for the two serum protein loci (Hp and Gc) is rather small, leaving scope for large amounts of random fluctuations. Therefore, we have also computed the distances excluding these two loci (table 5). Now the VADV and JALP, the two sympatric populations, show the smallest distance followed by that between VADP and VADV. Each of the three marine groups exhibit relatively large distances from the Kevto, compared to that between them at Puri. The population relationships can be seen from the dendrograms (figure 2).

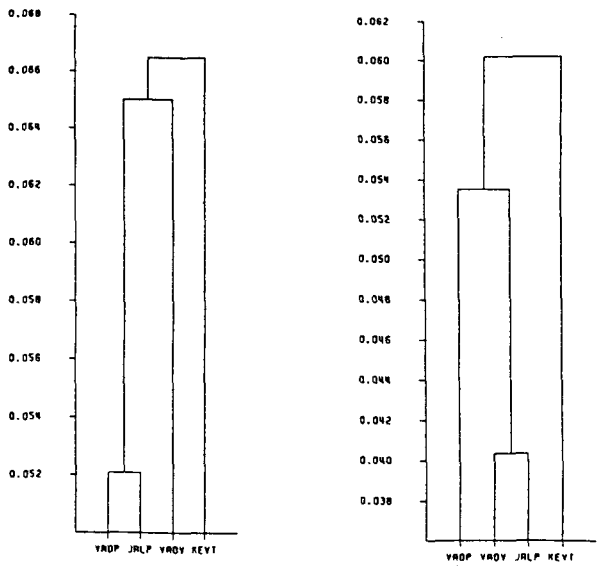


Figure 2. Dendrograms of the four fishing groups based on 11 loci (left) and 9 loci (right).

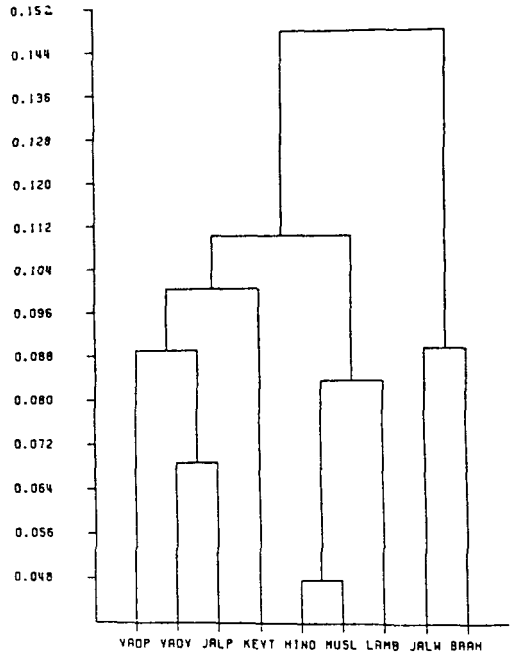


Figure 3. Dendrogram of the nine Telugu speaking groups, based on 8 loci.

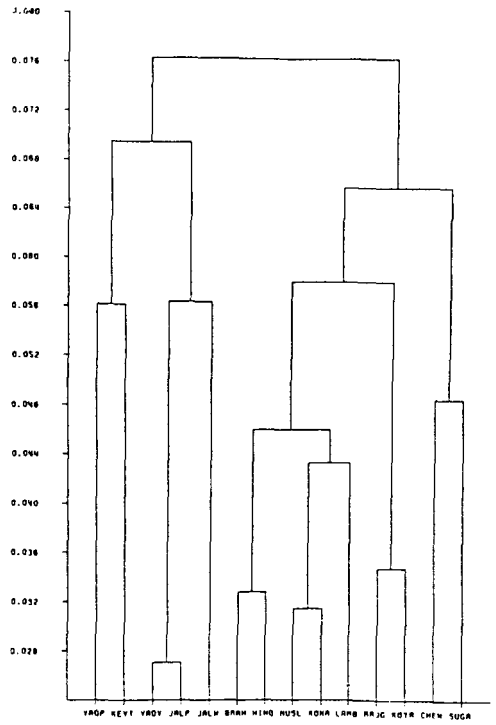

Figure 4. Dendrogram of the 14 Telugu populations, based on 5 loci. Source: HIND, MUSL, and LAMB (Roberts *et al.* 1980), BRAH and JALW (Naidu *et al.* 1985), RAJG, KOYA, KONR, and SUGA (Blake *et al.* 1981), CHEN (Ramesh *et al.* 1980), VADP, VADV, JALP, and KEVTO (present study).

Since the three migrant groups speak Telugu, their affinities with the neighbouring Telugu speaking populations from the state of Andhra Pradesh are also examined. We could collect comparable data from the literature on eight of the 11 loci (the three blood groups, AK, ADA, ESD, PGM, and AcP) for five groups, and on 5 loci (ABO, MN, AK, PGM, and AcP) for ten groups. For the 8 and 5 loci, we computed the genetic distance E matrix for 9 and 14 groups, respectively. For easier understanding of the population relationships, the distances were subjected to cluster analysis and reduced to dendrograms (figure 3 and 4). The first dendrogram based on 8 loci (figure 3) contains three subclusters of which one is formed by the fishing groups of Puri, the second by the Muslims (MUSL), Hindus (HIND) and Lambadis (LAMB) of Hyderabad, and the third by the Jalaries (JALW) and Brahmins (BRAH) of Waltair, conforming strictly to the geographical backgrounds. In the other dendrogram (figure 4), the 14 populations are grouped into two main clusters of which one is formed by the five fishing groups (VADP, VADV, JAPL, KEVT, and JALW). The second major cluster includes the remaining nine populations. Within this, Brahmins and Hindus, Muslims and Kondareddies (KONR), Raj Gond (RAJG) and Koya (KOYA), and Chenchu (CHEN) and Sugali (SUGA) form four subclusters. Although the ethnic and geographical backgrounds are not portrayed in minor details, with rather small number of loci, the observed clustering is in general interpretable. For example, the tribal groups are found closer to each other, as is the case with fishermen. Also, the clustering of Hindus with Brahmins, and the closeness of Muslims to Hindus rather than to tribals is expected considering the history and social backgrounds of the respective groups. It is also interesting to note that the Lambadies, a caucasoid tribe who migrated relatively recently from the northern parts of India, form a single point cluster but lie close to the geographically sympatric Muslims and Kondareddies.

## 4. Discussion

From the distance matrix (table 5), computed using nine of the eleven loci, a distance configuration conformating to geographical backgrounds is obtained, in that the sympatric VADV and JALP show the smallest distance. This is also generally the case with the clustering of other Telugu speaking populations in figures 3 and 4, and with several earlier investigations from India (Gaud and Rao 1979, Blake *et al.* 1981, Papiha *et al.* 1982, Pingle 1984) and other parts of the world (Ward 1972, Blanco and Chakroborty 1975, Roychoudhury 1975). However, the fact that the second smallest distance is between the two reproductive isolates of the same caste, the VADP and VADV, and that the fishing groups are closer to each other, as are Hindus to Brahmins and tribals between them than to non-tribals etc., would suggest that the geographical clustering is subtly intertwined with ethnohistorical backgrounds as well.

In general, the pattern of genetic distances is in congruence with that of anthropometric and dermatoglyphic distances (Reddy *et al.* 1987, 1988) between the three Puri groups. But, while in anthropometry the differentiation is quite marked, in dermatoglyphics it was observed that the relative differences in the interpopulation distances are rather small and these populations were considered to have been placed at equidistance. This is the case with genetic distances too. In this connection, it may be mentioned that Rao (1980) and Reddy (1982), analyzing sociocultural backgrounds, observed that both Jalari and Vadabalija are subcastes of a main caste, Vada, and therefore belong to the same ancestral group. For this reason, it may be said that they are in the initial stage of differentiation and thus the genetic differences are too small to show a marked pattern of variation reflecting their present ethnic situation. The gene diversity analysis

supports this contention. For example, only 1·3% of the total diversity among the marine fishermen ($G_{ST} = 0{\cdot}013$) is due to differences between them. If sampling variance is any indication of the significance of differentiation, as suggested by Chakraborty (1974), the differentiation would be statistically significant, for the magnitude of $G_{ST}$ value is three times its standard error.

The history of separation of Puri groups is relatively short. To see if this is reflected in the $G_{ST}$ values, a comparison with other Indian populations would be of interest. Though strictly not comparable, due to the different set of loci used in the computations, the $G_{ST}$ values reported for various populations with different backgrounds are rather similar. The values range between 0·01 and 0·03 (Das, Mukherjee, Malhotra and Majumder 1978, Malhotra *et al.* 1978, Bhasin *et al.* 1985, Roychoudhury 1974, 1977). None of the differences reach statistical significance as the standard errors are large, due to the small number of loci used. On the basis of this evidence, we may conclude tentatively that the coefficient of gene differentiation is small among the Indian populations and the Puri groups follow this pattern. Similarly, the average heterozygosity index observed (29–32%) is similar to most other populations studied in India (e.g. Roychoudhury 1984).

In conclusion, it may be said that the three groups of Puri are recent migrants to this place from about 100 villages along the 400 km coast, south of Puri, and are in different stages of settlement. Any argument on the relationship between the ethnic affinity and the genetic pattern would remain inconclusive unless one justifies the assumption that the populations at Puri represent their parental groups. For ascertaining this, we are in the process of analyzing the data collected from their parental groups. At present, we can only say that the fishing groups, as they are at Puri, genetically stand at equidistance from each other, and the differentiation is relatively small.

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**Résumé.** On a étudié les groupes sanguins, les enzymes érythrocytaires et les protéines sériques (11 loci) de quatre groupes endogames de pêcheurs vivant aux alentours de la ville de Puri (située sur la côte est de l'Inde). 1.3% seulement de la diversité totale des groupes étudiés proviennent des différences qu'ils présentent entre eux estimées par la méthode d'Edwards et Cavalli-Sforza. La structure des distances génétiques reflète la distribution géographique de ces groupes. En général, ces observations concordent avec les modèles de variation fondés sur des variables anthropométriques et dermatoglyphiques.

**Zusammenfassung.** Die vier endogamen Gruppen von Fischern, die um die Stadt Puri leben (an der Ostküste von Indien), werden auf Blutgruppen, Erythrozytenenzyme und Seroproteine untersucht (11 Loci). Nur 1.3% der gesamten Unterschiedlichkeit bei den untersuchten Gruppen ist durch Unterschiede zwischen ihnen bedingt ($G_{ST} = 0.013$). Die genetischen Abstände zwischen den Bevölkerungen wurden mit der Methode von Edwards und Cavalli-Sforza geschätzt. Die Struktur des genetischen Abstands reflektiert die geographische Verteilung dieser Gruppen. Im allgemeinen unterstützen diese Beobachtungen die Struktur der Variabilität nach anthropometrischen und dermatoglyphischen Variablen.