Demography India
Vol. 25, No. 2 (1996), pp. 199-204

M. V. Sudhakaran* and B. Vijayavalli*

Genetic Effects of Inbreeding on Mortality among the Pulayas of Alappuzha, Kerala

Introduction

THE biosocial phenomena of inbreeding is a topic of considerable interest to human geneticists because of its assortative nature of mating deviating from panmixia, and such matings give an opportunity for recessive genes to manifest themselves by becoming homozygous. Since most deleterious traits in man are recessive, inbreeding tends to bring into open such recessive alleles previously hidden by heterozygosity, resulting in increased risk of genetic defects in inbred progeny. A precise estimation of the effects of inbreeding is one of the most powerful tools available to geneticists in the appraisal of relative importance of mutation versus selection in maintaining genetic burden (genetic load) of a population. Crow (1958) has defined genetic load as the relative decrease in the average fitness of a population in comparison to the genotype with maximum or optimal fitness. Many investigators have used the data of inbreeding on mortality to estimate the genetic load in man (Morton *et al.*, 1956; Crow, 1958; Freire-Maia, 1963 and Schull and Neel, 1972).

Despite being a vast conglomerate of various endogamous castes, communities and tribes providing excellent material for consanguinity studies in India, reports on such investigation in India are fragmentary and only a few reports on genetic load are available in literature (Rao and Inbaraj, 1977; Reddy, 1992; and Babu *et al.,* 1994). Only a few such studies were conducted on the population groups of Kerala (Kumar *et al.*, 1967; Pillai and Mathew, 1995; and Sudhakaran and Vijayavalli 1996). The data on the effects of inbreeding on mortality among the Pulayas of Alappuzha district of Kerala is used here for estimating the genetic load in the group.

* Department of Botany, University of Kerala, Kariavattom, Thiruvananthapuram - 695 581.

Materials and Methods

The Pulayas are the major Scheduled Caste community of Kerala, constituting more than 9.92% of the total population of the state. They are almost evenly distributed, mostly in the central and southern districts of the state including Alappuzha and among whom the practice of related marriages has long been favoured and encouraged. For our study, data were collected exclusively from door to door survey. The effects of inbreeding on mortality was computed from the data on the reproductive histories (abortion and still birth were considered as prenatal loss, while death upto 20 years of age—infant (birth to 1 year), child (1-10 year) and juvenile (10-20 year), were recorded as postnatal deaths. Information is collected from 601 couples drawn randomly from the urban (112), sub-urban (126) and rural (363) regions of the district through intensive interviewing of the spouses by using an elaborate questionnaire. Nonconsanguineous families from the same socio-economic status of the community was taken as control. Estimation of genetic load was made through an analysis of regression of mortality on the coefficient of inbreeding using the weighted regression equation (Morton *et al.*, 1956):

$$-\log_e S = (A + BF)$$

where,

S = Fraction of survivors (number of individuals surviving/total number of birth),
A = the amount of expressed damage (genetic and/or environmental) in a random mating population,
B = estimate of the concealed genetic damage revealed by inbreeding,
$-\log_e S$ = number of lethal equivalents per gamete,
F = coefficient of inbreeding (measures the rate of reduction in heterozygosity per generation due to inbreeding, F = 1/16 for children of first cousins, 1/32 for those of one and a half cousins, 1/64 for those of second cousins etc.

Inbreeding was represented by only a few individuals in our sample. Hence, it is likely that the observed variability being zero in certain inbreeding classes, results in an undefined logarithm, and hence a small size correction was necessary before performing the regression. The appropriate correction used for a logarithm regression was as recommended by

$$ln \frac{x+1}{n+2} = -A - BF$$

Where, x = number of individuals surviving, n = total number of births.

Templeton and Read (1983).

Results

A sample of 601 marriages were studied, out of which 9.48% were consanguineous with mean coefficient of inbreeding, $F = 0.00759$. The effects of consanguinity at various stages of mortality are presented in Table 1. The computed frequency distribution of prenatal (6.73%) postnatal (12.5%) and total prereproductive mortality (19.23%) among the offspring of consanguineous parents have been found higher than control (prenatal 1.77%, postnatal 3.71% and total prereproductive mortality 5.48%). Consanguinity was found to be positively correlated with postnatal ($p < 0.01$) and total prereproductive mortality ($p < 0.05$). Estimate of genetic load in terms of A and B statistics obtained are presented in Table 2. A and B were computed separately for prenatal and postnatal mortality and collectively for total prereproductive mortality. In all cases, B values were found higher than A values. Estimates of A and B obtained for the total prereproductive mortality was 0.05682 and 3.1249 respectively with a BIA ratio of 54.99.

TABLE 1: EFFECT OF INBREEDING ON MORTALITY IN THE PULAYAS OF ALAPPUZHA

Parameters	*No. of cases*	*NC*		*1C*		*1.5C*		*2C*		*Total*	
		n	%	*n*	%	*n*	%	*n*	%	*11*	%
Abortion	24	15	0.88	9	5.20	—	—	—	—	9	4.33
Still birth	20	15	0.88	3	1.74	—	—	2	6.25	5	2.40
Prenatal	44	30	1.77	12	6.94	—	—	2	6.25	14	6.73*
Infant	25	11	0.65	14	8.09	—	—	—	—	14	6.73
Child	50	40	2.36	10	5.78	—	—	—	—	10	481
Juvenile	14	12	071	2	1.16	—	—	—	—	2	0.96
Postnatal	89	63	3.71	26	15.03	—	—	—	—	26	12.50**
Total Mortality	133	93	5.48	38	21.97	—	—	2	6.25	40	19.23***
Total Pregnancy	1905	1697	100.00	173	100.00	3	100.00	32	100.00	208	100.00

*0.50 > p > 0.30 **p < 0.01 ***p < 0.05

Note: 1C = First cousin, 1.5C = One and a half cousin, 2C = Second cousin, NC = Non consanguineous.

TABLE 2: ESTIMATES OF GENETIC LOAD IN TERMS OF A AND B STATISTICS FOR PRENATAL, POSTNATAL AND TOTAL MORTALITY IN THE PULAYAS OF ALAPPUZHA

Mortality	*A*	*B*	*A+B*	*B/A*
Prenatal	0.0 1897 ±0.003	1.1058± 0.36	1.12479	58.29
Postnatal	0.03813 ± 0.005	2.0400 ± 0.51	2.07816	53.50
Total	0.05682 ± 0.006	3. 1249 ±0.64	3.18172	54.99

Discussion

Natural populations of almost all diploid and out-breeding organisms carry burden or load of genetic defects which may sometimes be expressed phenotypically or remain hidden in heterozygous condition. These hidden recessive genetic variants are not ordinarily expressed, but may become manifest by inbreeding. Genotypes that confer a fitness distinctively below the mean of the adaptive norms may periodically be eliminated from the gene pool during prenatal and postnatal stages and the components of concealed genetic load become expressed more frequently in the inbred progeny. Many inbreeding studies world over, have highlighted increased rated of prenatal and postnatal deaths in consanguineous progeny compared to control (Marcallo *et al.*, 1964; Kumar *et al.*, 1967; Baki *et al.*, 1992: Pillai and Mathew, 1995 and Sudhakaran and Vijayavaili, 1996). In the present study, consanguinity-associated prenatal and postnatal mortality was found 3.37 to 3.8 times higher than control (Table 1). These findings indicate that a reduction in consanguinity can reduce the frequency of mortality to a considerable extent.

Morton *et al.*, (1956) have developed a convenient index for measuring the fitness of inbred versus noninbreds in a group or population level in terms of lethal equivalents estimated from the values of *A* and *B*. A lethal equivalent may be defined as a group of mutant genes of such numbers that, if dispersed in different individuals, they would cause on the average one death. By performing linear regression of the log proportion of survivors (-log *S)* onto the respective F values, *A* can be determined from the Kintercept at zero inbreeding *(F* - 0), and *B* is given by the slope of the regression. According to the load theory, the measure of total genetic damage per gamete is a quantity which is equal to the sum of *B* and the genetic component of *A* and hence lies between *B* and *B* + *A*. The *B/A* ratio provide critical information on the relative importance of mutational and segregational loci in maintaining the genetic load (Crow, 1958). Usually *B/A* ratio will be high (> 10) if the load is predominantly mutational and if low predominantly segregational.

In the present group of Pulayas, the *A* and *B* parameters, *B/A* ratios and their standard errors have been calculated from the data in Table 1. The genetic burden manifested in total prereproductive mortality in the group is estimated between 3.1249 and 3.1817 lethal equivalents per gamete (Table 2). The result of inbreeding effects suggests that an average person (Keralite) carries 6-7 lethal equivalent genes, finding expression between birth and maturity. This estimate is in good agreement with the earlier reports on the population groups of Kerala (Kumar *et al.*, 1967; Roberts, 1969 and Sudhakaran and Vijayavaili, 1996)..The distribution of the number of lethal equivalents per human beings forms a wide range of estimates (< 1 to 10) in different population groups across the globe (Freire-Maia, 1960 and Schull and Neel, 1972). Bittles and Makov (1985) have pointed out that effects of inbreeding vary markedly between different populations, the number of lethal equivalents per gamete are independent of each other and are characteristic of a particular population at a specific point in its evolution. The high *B/A* ratio (54.99) is suggestive that mortality disclosed by inbreeding in the group is predominantly from mutational load.

The consistently lower values of *A* in all three parameters of mortality may be a reflection of the relatively better public health condition of the outbred population.

The effect of any long term practice of inbreeding may be good or bad depending on many factors, including the frequency and nature of the gene concerned and the magnitude and degree of inbreeding. Both prospective and retrospective studies carried out in the populations of Tamil Nadu by Rao and Inbaraj (1977, 1979) have reported that, there is no significant positive association between consanguinity and prereproductive mortality. They contended that this may possibly be due to the substantial reduction in the frequency of lethal and sublethal genes among them, because of the periodic elimination of such genes from the population as a result of continuous practice of inbreeding over the past several centuries. However, the concept of such narrowing differentials between the consanguineous and nonconsanguineous groups has been questioned by Chakraborty and Chakravarthi (1977) and Khoury *et al.* (1987). The difference in the magnitude of consanguinity effects observed between the present community and those on the other regions of South India may be mainly because of the difference in their genetic constitutions. According to the genetic theory, rarer the disorder higher will be the proportion of affected individuals born from consanguineous marriages. Faster reduction in the frequency of deleterious genes take place in cases where their frequency is relatively high. Whereas, in the case of very rare deleterious recessive genes even with complete elimination of recessive homozygotes in every generation, the net change in gene frequency is too negligible and in such cases, obvious narrowing of differentials through prolonged inbreeding would not happen.

References

Babu, B. V., Kusuma, Y. S. and Naidu, J. M, 1994, Genetic load among four Andhra caste populations. *Social Biology*, 41: 127-129. Baki, A., Karaguzel, A., Beser, E., Cakmakei, T., Ucar, F. and Omeroglu, A., 1992, Consanguineous marriages
in the province of Trabzon, Turkey. *East African Medical Journal*, 69: 94-95. Bittles, A. H. and Makov, U. E., 1985, Linear regressions in the calculation of lethal gene equivalents in man. *Annals of Human Biology*, 12(3): 287-289. Chakraborty, R. and Chakravarthi, A., 1977, On consanguineous marriages and the genetic load. *Human Genetics*,
56: 330-338.
Crow, J. F., 1958, Some possibilities for measuring selection intensities in man. *Human Biology*, 30: 1-13. Freire-Maia, N., 1960, Deleterious mutations in man. *Eugen Quarterly*, 7: 193-203. Freire-Maia,N., 1963, The load of neutral mutations in White and Negro Brazilian populations. II. Second Survey.
Acta Genetica, 13: 199-225.
Haldane, J. B. S., 1937, The effects of variation on fitness. *American Naturalist*, 71: 337-349. Khoury, M. J., Cohen, B. H., Chase, G. A. and Diamond, E. L., 1978, An epidemiological approach to the evaluation
of the effect of inbreeding in prereproductive mortality. *American Journal of Epidemiology*, 125: 251-262.
Kumar, S. R., Pai, A. and Swaminathan, M. S., 1967, Consanguineous marriages and the genetic load due to lethal
genes in Kerala. *Annals of Human Genetics*, 31: 141-147. Marcallo, F. A., Freire-Maia, N., Azevedo, J. B. C. and Simoes, I. A., 1964, Inbreeding eftecton mortality and morbidity
in South Brazilian populations. *Annals of Human Genetics*, 27: 203-21. Morton, N. E., Crow, J. F. and Muller, H. J., 1956, An estimate of the mutational damage in man from data On
consanguineous marriages. *Proceedings of the National Academy of Sciences (USA)*, 42: 856-863.

Muller, H. J., 1950, Our load to mutations. *American Journal of Human Genetics, 2:* 111-176.

Pillai, P. G. and Mathew, P. M., 1995, Frequency and genetic effects of consanguinity in the Nayars of Trivandrum District, South India. *Journal of Cytology and Genetics,* **30:** 157-161.

Rao, P. S. S. and Inbaraj, S. G., 1977, Inbreeding effects on human reproduction in Tamil Nadu of South India. *Annals of Human Genetics,* 41: 87-98.

Rao, P. S. S. and Inbaraj, S. G., 1979, Inbreeding effects on fertility and sterility in South India. *Journal of Medical Genetics,* **16:** 24-31.

Reddy, B. M., 1992, Inbreedingeffects on reproductive outcome: A study based on a large sample from the endogamous Vadde of Kolleru Lake, Andhra Pradesh, India. *Human Biology,* 64: 659-682.

Roberts, D. F., 1969, Consanguineous marriages and calculation of the genetic load. *Annals of Human Genetics,* 32: 407-410.

Schull,W.J.andNeel,J.V., 1972,Theeffectof parental consanguinity and inbreeding in Hirado, Japan. V. Summary and interpretation. *American Journal of Human Genetics,* 24: 425-453.

Sudhakaran, M. V. and Vijayavalli, B., 1996, Effects of inbreeding on mortality in Ezhavas of Alappuzha, South India. *Journal of Cytology and Genetics,* **31:** 179-183.

Templeton, A. R. and Read, B., 1983,The Elimination of Inbreeding Depression in aCaptive Herd of Speke's Gazelle. *In:* C. M. Schonewlad-Cox, S. M. Chambers, B. MacBryde and W. L. Thomas(eds.), *Genetics and Conservation: A Reference for Managing Wild Animal and Plant Populations.* Benjamin/Cummings Publishing Co., USA.