

An Estimate of Genetic Load in The Nayars of Alappuzha, Kerala

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ABSTRACT A sample of 1191 marriages of the Nayars of Alappuzha district of the state of Kerala was studied for estimating the component of genetic load operating in the prenatal and postnatal stages. Consanguinity-associated prenatal and postnatal mortality was found to be 1.88 to 5.6 times higher than control. The genetic burden manifested in total prereproductive mortality was estimated between 2.366 and 2.424 lethal equivalents per gamete, suggests that an average person carries 5 lethal equivalent genes finding expression between birth and maturity. The high B/A ratio (41.53) is suggestive that mortality disclosed by inbreeding in the group is predominantly from mutational load.

INTRODUCTION

The basic ideas of genetic load was first introduced by Haldane (1937) and the concept of genetic load was first used by Muller (1950) to convey the burden of death, illness, sterility and sorrow imposed on humans by mutation. Morton et al. (1956) have found it useful to express the load in terms of lethal equivalents to study the influence of inbreeding on the viability or sterility of progeny. 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. There are several components of genetic load, of which mutational and segregational are more important with reference to inbreeding populations. The nature and magnitude of the load depends on the level of inbreeding in the population as well as on the types of genes involved. 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. 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; Schull and Neel, 1972).

Despite the occurrence of innumerable inbreeding castes, communities, tribes and a variety of racial isolates in India, providing excellent material for consanguinity studies, reports on such investigations in India are fragmentary and only a few reports on genetic load are available (Rao and Inbaraj, 1977; Reddy, 1992; 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; Sudhakaran and Vijayavalli, 1996). The data on the effects of inbreeding on mortality among the Nayars of Alappuzha district of Kerala is used here for estimating the genetic load in the group.

MATERIALS AND METHODS

The Nayars are the major Hindu forward (socio-economically) community of Kerala. Numerically they are the second largest group among Hindus, constituting more than 14% of the total of population of the state. They are almost evenly distributed, mostly in the central and southern districts of the state including Alappuzha, among whom the practice of related marriages has long been favoured and encouraged. Data were collected exclusively from door to door survey. The effects of inbreeding on mortality was computed from the data on the reproductive histories of couples drawn randomly from the urban, sub-urban and rural 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 of Morton et al. (1956), $-\log_e S = (A + BF)$. Inbreeding was represented by only a few individuals on our sample. Hence it is likely that observed viability to be zero in certain inbreeding classes, which results in an undefined logarithm, and hence a small size correction was made before performing the regression. The appropriate correction used for a logarithm regression was:

$$\ln \left(\frac{x_i + 1}{n_i + 2} \right) = -A - BF \text{ (Templeton and Read, 1983)}$$

RESULTS

A sample of 1191 marriages were studied, out of which 12.68% were consanguineous with $F=0.00759$. The effects of consanguinity at various stages of mortality are presented in table 1. The computed frequency distribution

of prenatal (10.92%), postnatal (6.55%) and total prereproductive mortality (17.47%) among the offspring of consanguineous parents have been found higher than control (Prenatal 1.95%, postnatal 3.49% and total prereproductive mortality 5.44%). 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 0.05699 and 2.3664, respectively with a B/A ratio of 41.53.

DISCUSSION

Natural population of almost all diploid and outbreeding 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 be revealed by inbreeding.

Table 1 : Effect of consanguinity on prereproductive mortality in the Nayars of Alappuzha

| Parameters | No. of cases | NC | | IC | | DFC | | 2C | | Total | |
|-----------------|--------------|------|--------|-----|--------|-----|---------|----|--------|-------|--------|
| | | n | % | n | % | n | % | n | % | n | % |
| Abortion | 67 | 41 | 1.34 | 26 | 6.62 | 4 | 36.36 | 6 | 11.11 | 36 | 7.86 |
| Still birth | 33 | 19 | 0.62 | 12 | 3.05 | - | - | 2 | 3.70 | 14 | 3.06 |
| Prenatal | 110 | 60 | 1.95 | 38 | 9.67 | 4 | 36.36 | 8 | 14.81 | 50 | 10.92 |
| Infant | 31 | 27 | 0.88 | 4 | 1.02 | - | - | - | - | 4 | 0.87 |
| Child | 73 | 55 | 1.79 | 16 | 4.07 | 2 | 18.18 | - | - | 18 | 3.93 |
| Juvenile | 33 | 25 | 0.81 | 6 | 1.53 | - | - | 2 | 3.70 | 8 | 1.75 |
| Postnatal | 137 | 107 | 3.49 | 26 | 6.62 | 2 | 18.18 | 2 | 3.70 | 30 | 6.55 |
| Total Mortality | 247 | 167 | 5.44 | 64 | 16.29 | 6 | 54.54 | 10 | 18.51 | 80 | 17.47 |
| Total Pregnancy | 3530 | 3072 | 100.00 | 393 | 100.00 | 11 | 100.000 | 54 | 100.00 | 458 | 100.00 |

Note : IC = First cousin, DFC = Double first 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 prereproductive mortality in the Nayars of Alappuzha

| Mortality | A | B | A+B | B/A |
|-----------|--------------|------------|---------|-------|
| Prenatal | 0.02077±.003 | 1.6731±.28 | 1.69386 | 80.55 |
| Postnatal | 0.03577±.003 | 0.6666±.23 | 0.70237 | 18.64 |
| Total | 0.05699±.004 | 2.3664±.37 | 2.42387 | 41.53 |

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 rates of prenatal and postnatal deaths in consanguineous progeny than control (Marcallo et al., 1964; Kumar et al., 1967; Baki et al., 1992; Pillai and Mathew, 1995; Sudhakaran and Vijayavalli, 1996). In the present study, consanguinity-associated prenatal and postnatal mortality was found to be 1.88 to 5.6 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. According to the load theory, the A value measures the mortality of noninbred fraction ($F=0$), which is supposed to be an index of public health condition, while B reflects the hidden or concealed genetic damage revealed by inbreeding ($F=1$). The measure of total genetic damage per gamete 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).

In the present group of Nayers, 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 2.366 and 2.424 lethal equivalents per gamete (Table 2). The result of inbreeding effects suggests that an average person (Keralite) carries 5 lethal equivalent genes, finding expression between birth and maturity. This estimates is in good agreement with the earlier reports on the population groups of Kerala (Kumar et al., 1967; Roberts,

1969; Sudhakaran and Vijayavalli, 1996). The distribution of the number of lethal equivalents per human beings forms a wide range of estimates (1-10) in different population groups across the globe (Freire-Maia, 1960; 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 (41.53) 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.

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