

Genetic Impact of Consanguineous Marriages on Morbidity Among the Muslims of Alappuzha, Kerala

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ABSTRACT The genetic impact of consanguineous marriages on morbidity is assessed through genetic load estimates in terms of detrimental equivalents among the Sunni sect of Muslims of Alappuzha by using a random sample of 515 marriages. Using weighted regression model, genetic burden manifested in total prereproductive morbidity was estimated between 1.5337 and 1.55119 detrimental equivalents per gamete, suggest that an average person carries in heterozygous condition 4 detrimental equivalent genes, if made homozygous they would cause on the average one genetic defect or disease. The consistently high consanguinity ratio (B/A) obtained in all four parameters of morbidity suggest that genetic load in the Muslim genealogy is predominantly mutational. Consanguinity-associated prereproductive morbidity was found to be 5.23 to 14.4 times higher than controls (Relative risk (RR) = 5.23 to 14.4). The Attributable risk (AR) for the whole sample is about 41%. It could be shown that inbreeding accounts for about 41% of all morbidity in the present population.

INTRODUCTION

The study of population genetics concern the genetic structure and evolution of populations. Mating structure can influence genetic structure of the population directly by preferential or proscribed mating with relatives of various kinds (Leslie et al., 1978). Since consanguineous marriage is the result of some system of mating (probably because of finite population size, spatial proximity or systematic choice of relatives as potential mates), that system itself takes an evolutionary significance. Allelic or genetic combination conveyed by inbreeding dampens population genetic variability by reducing offspring viability and fecundity. This is mainly because consanguineous marriages allow rare deleterious genes present in heterozygote to become homozygote and thus exposed to selection. The concealed hereditary burden revealed by inbreeding in a

given population can be estimated by extrapolation from the data on the progeny of consanguineous parents of a specified degree of relationship, which are homozygous for a known fraction of otherwise heterozygous loci. Estimation of population genetic load has been primarily based on congenital abnormalities and associated diseases. A precise estimation of such genetic damage in a population should weigh genes by their detrimental effectiveness (Morton, 1960; Kaku and Freire-Maia, 1992; Freire-Maia and Elisbao, 1984; Sudhakaran, 1996; Sudhakaran and Vijayavalli, 1997a, c).

The present paper deals with the results of consanguinity studies carried out in a Mendelian population, the Sunni sect of Muslim from Alappuzha district of Kerala, with a view to assess the comparative incidence of some selected defects and diseases between consanguineous and control population and to estimate genetic impact of consanguinity in terms of detrimental equivalents in the group.

MATERIALS AND METHODS

The Muslims of Kerala forms the third largest population group, constituting more than 19.5% of the total population of the state. The representative sample of Muslims of the present study is from Sunni sect. They are a socio-economically backward community, among whom the related marriages has long been favoured and encouraged. For the present study data were collected from door to door survey. The effects of inbreeding on morbidity was computed from the data on total number of surviving children (of age 0 to 20 years) / couple (during the survey period 1993-1996), with a sample of 515 marriages drawn randomly from the urban (139), sub-urban (121), and rural (255) regions of the

district through intensive interviewing of the spouses by using an elaborate questionnaire. Nonconsanguineous families from the same socioeconomic status of the community was taken as control. Morbidity data have been collected and analysed under four broad categories namely physical defects (Craniofacial abnormalities, Polydactyly, Dwarfism, Club foot, Cleft lip, Cleft palate) mental defect (Mental retardation) sensory defect (Blindness, Deafness, Stuttering/Stammering, Squint eyes) and a few systemic diseases (Diabetes, Epilepsy, Heart and Kidney diseases). Estimation of detrimental load in terms of detrimental equivalent was made through an analysis of regression of morbidity on the coefficient of inbreeding using the weighted least square regression equation of Morton (1960).

$$LD = -\log(1-PD) = A + BF$$

Relative risks (RR) and proportional attributable risks (AR) were calculated by using Grant et al.'s formula (cf. Bittles, 1994).

$$RR = 1 + BF/A, AR = BF/A + BF$$

RESULTS

A cross sectional sample of 515 marriages among the Sunni sect of Muslims were studied, out of which 10.68% were consanguineous, resulting an average coefficient of inbreeding $F=0.00596$. The effects of consanguinity at various stages of morbidity are presented in table 1. The computed frequency distribution of physical (3.91%) mental (1.12%), and sensory

However, consanguinity in relation to morbidity was found to be non significant ($0.50 > p > 0.30$). Estimate of detrimental load and equivalent by type of defect and their B/A ratios are also presented in table 1. A and B were computed separately for each type of defect and collectively for total morbidity. In all cases B values were found higher than A values. Of these highest B value obtained for physical defects intermediate for diseases and lowest for sensory defects. Estimates of A and B, obtained for the total morbidity was 0.17496 and 1.5337 respectively with a B/A ratio of 87.66.

The proportional attributable risks (AR) calculated for different levels of relative risks (RR) are presented in table 2. A break down by type of defect showed that offspring of consanguineous marriages have a higher risk of morbidity than controls ($RR=5.23$ to 14.4), corresponding differences were observed in their AR values also ($AR = 80.87$ to 93.05). The AR value for total morbidity was estimated to be 87.26.

DISCUSSION

To isolate and quantify the specific detrimental effects of inbreeding on morbidity in the study sample, the concept of detrimental equivalents advanced by Morton (1960) was employed. Data on morbidity type and their respective detrimental equivalents are given in table 1. The genetic burden manifested in total morbidity in the group is estimated between 1.5337 to 1.55119 detrimental equivalents per

Table 1 : Estimate of detrimental load in terms of detrimental equivalent by type of defect among the Muslims of Alappuzha

Type of defect	No. of cases studies	NC		FC		SC		Total		A	B	B/A
		n	%	n	%	n	%	n	%			
Physical	14	7	0.41	5	3.45	2	5.88	7	3.91	0.00471±.002	0.8077±.30	171.40
Menatal	6	4	0.23	1	0.69	1	2.94	2	1.12	0.00295±.001	0.3063±.19	103.99
Sensory	10	8	0.47	2	1.38	-	-	2	1.12	0.00529±.002	0.2864±.20	54.13
Diseases	14	9	0.52	5	3.45	-	-	5	2.79	0.00586±.002	0.6084±.28	103.77
Total	44	28	1.63	13	8.97	3	8.82	16	8.94	0.01749±.003	1.5337±.45	87.66

Note : NC = Nonconsanguineous, FC = First cousin, SC = Second Cousin, A = Random load, B = Inbred load, B/A = Consanguinity ratio.

defects (1.12%) and diseases (2.79%) among the offspring of consanguineous parents have been found higher than control (physical 0.41%, mental 0.23%, sensory 0.47% and diseases 0.52%).

gamete. The result of inbreeding effects suggest that an average person carries in heterozygous condition 4 detrimental equivalent genes, that if made homozygous, would produce

Table 2 : Estimates of relative risks (RR) and proportional attributable (AR) risks for consanguinity-associated morbidity by type of consanguinity among the Muslims of Alappuzha

Type of defect	RR	AR
Physical	14.39	93.05
Mental	9.11	89.03
Sensory	5.23	80.87
Diseases	9.11	89.02
Total	7.87	87.26

recognisable defects and diseases. This estimate is of the same order of magnitude as those obtained by general mean of majority of other studies (Marcallo et al., 1964; Cavalli-Sforza and Bodmer, 1971; Sudhakaran and Vijayavalli, 1997a, b). Human data generally satisfy the condition $B > A$, depending on the country, population and class of diseases considered, the number of detrimental equivalents per gamete ranges from 0.35 to 2.3 (Cavalli-Sforza and Bodmer, 1971; Sudhakaran and Vijayavalli, 1997a, c). The consistently high B/A ratios obtained in all four parameters of morbidity, suggest that segregational loci make a relatively small contribution to the hidden load revealed by inbreeding, and confirming earlier reports on many other populations (Morton et al., 1956; Marcallo et al., 1964; Kumar et al., 1967; Sudhakaran and Vijayavalli, 1996a, b, 1997b, d) that an appreciable fraction of the genetic load maintained in human populations are of mutational.

The RR calculated for type of defect (Table 2) shows that among the offspring of consanguineous marriages the frequency of abnormalities are 5.23 to 14.4 times higher than controls, indicating a very strong association between consanguinity and morbidity. Calculation of population proportional attributable risk (Khouri et al., 1987) which estimates the fraction of total morbidity associated with consanguinity in the study sample, indicate that about 41% all of morbidity in Muslims genealogy were associated with consanguinity. It could be shown that inbreeding accounts for about 41% of all morbidity in the present population.

The practice of consanguineous marriage is complex, its prevalence, severity and social rationale vary from population to population. The increasing incidence of congenital defects and diseases in the offspring of consanguineous

marriage is of great concern to the society as well as those directly affected. We understood very little of the forces that maintain genes predisposing to these events in the population, which is a major handicap in medical intervention programmes for the treatment of genetically deficient people. People by an large are not aware of the biological and genetic implications of consanguineous marriages. Some people, preoccupied by false prestige and motivated by economic benefits contracting consanguineous marriages and often encourage and persuade their posterity to marry a consanguineal spouse in the guise of doing this consistent with their local custom and tradition. They seemed to be indifferent and complacent about the empirical risks of consanguineous marriages. In this situation, legal decrees and policy statements alone are not likely to abolish this curious custom of preferred marriages. Grass roots community educations and changes in social norms are necessary for long-lasting effects. If not checked through corrective social sanction, it prone to be a social malady, which will have a far reaching destabilising impact on the society.

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