



## Effects of Inbreeding on Reproductive Losses in Kota Tribe

T. A. Sivakumaran<sup>1</sup>, S. Karthikeyan<sup>2</sup>

<sup>1</sup>Department of Human Genetics, Andhra University, Visakhapatnam; <sup>2</sup>Department of Biophysics, All India Institute of Medical Sciences, New Delhi, India

**Abstract.** Sanghvi's hypothesis on long term effects of inbreeding was tested in Kotas. Kota is a numerically small tribal population in the Nilgiri district, Tamil Nadu State, India. Consanguineous marriages are common in this tribe. A total of 95 couples were taken for this study and necessary data were collected on a set proforma. Of the 95 couples, 28 (29.5%) were consanguineously related. The inbreeding coefficient for autosomal genes is 0.022 and for sex-linked genes is 0.03. Inbreeding effects on reproductive losses were examined through an exponential regression model. Although the regression coefficient B values are positive, they are insignificant, suggesting no consistent relationship between degree of consanguinity and the reproductive losses. The estimates of genetic load is 1.8 lethal equivalents per gamete and the average B/A ratio is 5. These findings empirically support the Sanghvi's contention.

**Key words:** Kotas, Inbreeding, Inbreeding co-efficient, Genetic load, Prenatal mortality, Infant mortality, Prereproductive deaths

### INTRODUCTION

Inbreeding in a population increases the frequency of deleterious homozygotes in the progeny of consanguineous matings thereby reducing its average fitness. Genetic load is a quantity designed to measure this loss of fitness resulting from selection against the deleterious homozygotes [5]. Morton et al.[17] proposed a method of estimating genetic load in human populations from the relationship of inbreeding coefficient with mortality or morbidity due to deleterious genes.

A number of studies conducted on effects of inbreeding in different populations revealed elevated levels [29, 10, 11, 16, 27, 28, 14, 1, 23] of prereproductive mortality among the offspring of consanguineous marriages. But, most of the studies conducted in India [18, 20, 21, 13, 9, 2, 3, 32, 22] did not reveal any significant effect of inbreeding

on mortality. Lack of inbreeding effects in these populations support the Sanghvi's [25, 26] contention that in areas where the current levels of inbreeding are high and where inbreeding has been the custom for over two millennia or perhaps longer, the effects of inbreeding may not be perceptible. Using alternative hypothesis of selection and mutation, Sanghvi theoretically demonstrated that this effect is due to the gradual elimination of deleterious recessive genes.

In the present study, an attempt was made to test the Sanghvi's hypothesis. To fulfill this aim, effects of inbreeding on prenatal mortality, infant mortality, prereproductive deaths and total mortality were examined and the genetic load was estimated among Kotas.

## MATERIALS AND METHODS

Kota is a hill tribe of the Nilgiris district, Tamil Nadu state, India. It is numerically a small tribe. The actual origin of the Kotas is not known. Several views have been expressed about their origin and migration to the Nilgiri hills. Rev. F. Legrand, [15] says that the Kotas must have come to the Nilgiris along with the Todas about the same time. The Kotas know that they have been living in the Nilgiri hills along with other tribes (Toda, Kurumba and Badaga) since time immemorial. They have developed an economic symbiotic relationship with other tribes of the Nilgiri hills but have almost no social relationship with other communities such as the Hindu and Muslims etc. Consanguineous marriages are highly favoured among the Kotas.

The data on consanguinity, pregnancy history, mortality differentials were collected on a set proforma in 1991. A total of 95 households were covered for this study in four villages, viz. New Kotagiri, Trichigadi, Kollimalai and Sholur Kokkal.

Inbreeding effects on reproductive wastage were examined through an exponential regression model:

$$P_i = 1 - \exp[-(A + BF_i)] \dots\dots\dots (1)$$

where  $P_i$  is the expected proportion of survivors and  $F_i$  is Wright's coefficient of inbreeding for each of the three inbred classes considered. The estimates of A and B were obtained through the weighed least-squares technique of Smith [30, 31] as modified by Chakraborty and Chakravarthi (6). Briefly, if  $Z_i$  denotes  $-\ln(1 - p_i) = A + BF_i$ , where  $p_i = m_i/n_i$  ( $n_i$  is the number of pregnancies or live births in inbreeding class  $F_i$  and  $m_i$  is the number of prenatal losses / infant deaths / prereproductive deaths / total deaths), then A and B were estimated through a procedure to be

$$B = \Delta Fz / \Delta FF \dots\dots\dots (2)$$

$$A = \bar{z} - B\bar{F} \dots\dots\dots (3)$$

where

$$w_i = n_i(1 - p_i) / p_i \dots\dots\dots (4)$$

$$W = \sum w_i \dots\dots\dots (5)$$

$$\bar{z} = \sum w_i z_i / W \dots\dots\dots (6)$$

$$\bar{F} = \sum w_i F_i / W \dots\dots\dots (7)$$

$$\Delta FF = \sum w_i F_i^2 - W\bar{F}^2 \quad \dots\dots\dots (8)$$

$$\Delta Fz = \sum w_i F_i z_i - W\bar{F}\bar{z} \quad \dots\dots\dots (9)$$

A is an estimate of load in a randomly mating population and B is the estimated load due to rare recessive genes that resulted in homozygotes through inbreeding.

A test of the goodness of fit was performed using a Chi-square statistic.

$$\chi^2 = \sum w_i (z_i - A - BF_i)^2 \quad \dots\dots\dots (10)$$

A computer program was developed to calculate A, B and Chi-square values using FORTRAN 77.

**RESULTS**

Twenty eight (29.5%) of the 95 couples studied were consanguineously related. Uncle-niece (5.3%) and first cousin marriages (24.2%) were practiced. The inbreeding coefficient for autosomal genes is 0.022 and for sex-linked genes 0.03.

The data on prenatal mortality, infant mortality, prereproductive deaths and total mortality are given in Table 1. The regression coefficient B (Table 2) for prenatal mortality, infant mortality, prereproductive deaths and total mortality (0.3765±0.3963, 0.445±0.4835, 1.176±0.80 and 1.530±0.896 respectively) were positive and not significant suggesting no consistent relationship between the degree of consanguinity and reproductive losses.

The parameters A and B can be used to estimate (1) the number of lethal equivalents (A+B) and (2) the B/A ratio, which is useful for delineating the relative importance of the mutational and segregational load in maintaining hereditary burden of a population. A high B/A ratio indicates the mutational load while low ratio indicates the segregational load. The number of lethal equivalents per gamete is about 1.8. The B/A ratio for prenatal mortality, infant mortality and prereproductive deaths is (5.412, 4.614 and 5.01 respectively) and the average is about 5.

**Table 1 - Number of marriages, pregnancies, live births and prereproductive deaths according to marriage types**

Relationship	F	No. of marriages	No. of pregnancies	No. of prenatal deaths	Live births	No. of infant deaths	Prereproductive deaths	Total mortality
Uncle Niece	0.1250	5	28	3	25	4	10	13
First Cousin	0.6250	23	111	10	101	11	23	33
Unrelated	0.0000	67	343	23	323*	30	69	92
Consanguineous		28	139	13	126	15	33	46
Total		95	482	36	449	45	102	138

\* three twin births.

**Table 2 - Regression analysis of inbreeding effects**

Effects	A $\pm$ SE	B $\pm$ SE	B/A	Chi-Square
Prenatal mortality	0.0696 $\pm$ 0.014	0.3765 $\pm$ 0.3963	5.412	0.0045
Infant mortality	0.0964 $\pm$ 0.0175	0.445 $\pm$ 0.4835	4.614	0.140
Prereproductive deaths	0.2346 $\pm$ 0.0283	1.176 $\pm$ 0.80	5.01	1.630
Total mortality	0.3065 $\pm$ 0.032	1.530 $\pm$ 0.896	4.981	1.272

## DISCUSSION

The present study on Kota tribe showed no clear cut effect of inbreeding on prenatal mortality, infant mortality, prereproductive deaths and total mortality. This may be due to the long time practice of inbreeding among the Kota tribe and fate of the deleterious genes in this population is largely on random phenomenon [13]. This supports the Sanghvi's [26] contention that inbreeding has little effect in population that have been practicing it for a long period.

Consanguineous marriages should decrease the chances of blood group incompatibilities and hence reduce early fetal losses [19]. This was empirically supported among whites, in which it was shown that fetal losses increased proportionately with outcrossing [4], but much larger inter-racial sample has not supported this hypothesis [12]. In the present study, no significant effect of inbreeding on prenatal mortality was observed. This could be due to adaptation to inbreeding [24]. Any deleterious genes producing abortions might have been bred out, if inbreeding has been practiced for a long time [7, 8]. Some investigators have shown an increase in still birth rates with consanguinity [14, 6] and other investigators [20, 21, 13, 22] support this hypothesis.

Any hidden deleterious genes can be exposed only if individuals, whose ancestors had mated at random for many generations, undertake consanguineous marriage. A history of inbreeding for many generations would cleanse the gene pool very early. Hence a relatively small value of B and therefore of the B/A ratio is expected in highly inbred populations [22]. The number of lethal equivalents observed in the present study is slightly higher than the one reported previously among the Kotas [13]. This is within the range (-0.76 to 2.67) of the values computed for other south Indian populations in the literature [22]. The B/A ratio is low suggesting that the genetic load is predominantly segregational. The B/A ratio is higher than the average B/A ratio (2.1) and within the range (-6.5 to 14.3) found in South Indian populations [22]. The findings of the present study support Sanghvi's [25] hypothesis that continued practice of inbreeding for several generations has resulted in the gradual elimination of deleterious genes by segregation.

**Acknowledgments:** Our thanks are due to Professor G. Golla Reddy and Ms. P. Padmavathi for their help during the period of study. We also thank Professor P. Veerajju, Professor T. Venkateswara Rao and Professor K. Kucheria for critical reading of the manuscript and invaluable comments. One of the authors (SK) thanks CSIR for financial assistance.

## REFERENCES

1. Basu SK (1975): Effects of consanguinity among North Indian Muslims. *Journal of Population Research* 2: 57-68.
2. Bittles AH, Devi ARR, Savithri HS, Sridhar R, Appaji Rao N (1985): Inbreeding and post-natal mortality in South India: Effects on the gene pool. *J Genet* 64: 135-142.
3. Bittles AH, Devi ARR, Savithri HS, Sridhar R, Appaji Rao N (1987): Consanguineous marriages and post-natal mortality in Karnataka, South India. *Man (ns)* 22: 736-745.
4. Bressler JB (1970): Outcrossing in Caucasians and fetal loss. *Soc Biol* 17: 17-25.
5. Cavalli-Sforza LL, Bodmer WF (1971): "The Genetics of Human Populations." San Francisco: W. H. Freeman.
6. Chakraborty R, Chakravarti A (1977): On consanguineous marriages and the genetic load. *Hum Genet* 36: 47-54.
7. Darlington CD (1960): Cousin marriages and the evolution of the breeding system in man. *Heredity* 14: 297-331.
8. Darlington CD (1961): Cousin marriage and population structure. *Eugen Rev* 53: 139-144.
9. Devi ARR, Appaji Rao N, Bittles AH, (1981): Consanguinity, fecundity and post-natal mortality in Karnataka, South India. *Ann Hum Biol* 8: 469-472.
10. Freire-Maia N (1963): The load of lethal mutations in Whites and Negro Brazilian populations. II. Second survey. *Acta Genet Basel* 13: 199-225.
11. Freire-Maia N, Krieger H (1963): A Jewish isolate in Southern Brazil, effective population, intermarriage, fertility, inbreeding, mortality, twinning, sex ratio, genetic load and total mutation rate. *Am J Hum Genet* 27: 31-39.
12. Freire-Maia A, Stevenson C, Morton NE (1974): Hybridity effect on mortality. *Soc Biol* 21: 232-234.
13. Ghosh AK, Majumder PP (1979): Genetic load in an isolated tribal population of South India. *Hum Genet* 51: 203-208.
14. Kumar S, Pai RA, Swaminathan MS (1967): Consanguineous marriages and genetic load due to lethal genes in Kerala. *Ann Hum Genet* 31: 141-147.
15. Legrand Rev F (1955): Tribes of the Nilgiris – The Kotas Madras. "In Tamil Culture." Vol 14: 321-322.
16. Marcallo FA, Freire-Maia N, Azevedo JBC, Simoes IA (1964): Inbreeding effects on mortality and morbidity in South Brazilian populations. *Ann Hum Genet* 27: 203-218.
17. Morton NE, Crow JF, Muller HJ (1956): An estimate of mutational damage in man from data on consanguineous marriages. *Proc Natl Acad Sci USA* 42: 855-863.
18. Murthy JS, Jamil T (1972): Inbreeding load in the newborns of Hyderabad. *Acta Genet Med Gemellol* 21: 327-331.
19. Peritz Z (1971): A statistical study of the intra-urine selection factors related to the ABO system. II. The analysis of fetal mortality data. *Ann Hum Genet* 34: 389-394.
20. Rao PSS, Inbaraj SG (1977): Inbreeding effects on human reproduction in Tamil Nadu of South India. *Ann Hum Genet* 41: 87-98.
21. Rao PSS, Inbaraj SG (1979): Trends in human reproductive wastage in relation to long-term practice of inbreeding. *Ann Hum Genet* 42: 281-288.
22. Reddy BM (1992): Inbreeding effects on reproductive outcome: A study based on a large sample from the endogamous Vadde of Kolleru Lake, Andhra Pradesh, India. *Hum Biol* 64: 659-682.
23. Reddy VR, Naidu GP (1978): Effects of consanguinity on fertility and mortality in the Gampasati Kammars of Andhra Pradesh. "In Verma IC (eds) Medical Genetics in India." Vol 2. Pondicherry: Auroma Enterprises.
24. Roberts DF, Bonne B (1973): Reproduction and inbreeding among the Samaritans. *Soc Biol* 20: 64-70.

25. Sanghvi LD (1966): Inbreeding in India. *Eugen Q* 13: 291-301.
26. Sanghvi LD (1974): The genetic consequences of inbreeding and outbreeding. "In The Role of Natural Selection in Human Evolution. Burg wartenstein Symposium Series. 63."
27. Schull WJ, Neel JV (1965): "The effects of inbreeding on Japanese Children." New York: Harper and Row.
28. Schull WJ, Neel JV (1966): Some further observation on the effects of inbreeding on mortality in Kure, Japan. *Am J Hum Genet* 18: 144-152.
29. Slatis HM, Reis RM, Hoene RE (1958): Consanguineous marriages in Chicago region. *Am J Hum Genet* 10: 446-464.
30. Smith CAB (1967): Note on the paper" Consanguineous marriages and genetic load due to lethal genes in Kerala." *Ann Hum Genet* 31: 146-147.
31. Smith CAB (1969): Corrigenda. *Ann Hum Genet* 32: 419.
32. Srikumari CR, Rajani Kumari J, Rao TV (1985) Variability of genetic load with changing sociocultural environment. *Hum Hered* 35: 388-393.

**Correspondence:** T.A. Sivakumaran, Division of Genetics, Department of Anatomy, All India Institute of Medical Sciences, New Delhi – 110 029, India.