© Kamla-Raj 1999
PRINT: ISSN 0970-9274 ONLINE: 2456-6608

J. Hum. Ecol., 10(2): 87-91 (1999)
DOI: 10.31901/24566608.1999/10.02.02

# Consanguinity and Its Effects on Differential Fertility and Mortality in Two Caste Populations of Andhra Pradesh, India

**B.V. Babu*, G. Sudhakar[1], C. Parvatheesam[1] and V. Padma[1]**

*Department of Anthropology, Andhra University, Visakhapatnam 530 003, Andhra Pradesh, India*
*1. Department of Human Genetics, Andhra University, Visakhapatnam 530 003 Andhra Pradesh, India*

**KEY WORDS** Genetic Demography. Inbreeding. Fertility. Mortality. Genetic Load. Andhra Castes.

**ABSTRACT** Date on marriage type, fertility and mortality among Rajaka and Koppala Velama caste populations of Andhra Pradesh, India are utilized to report the degree of consanguinity and its effect on reproductive outcome. About one third of the total marriages are consanguineous in these populations. The present study confirms the hypothesis that fertility would be greater in consanguineous couples to compensate for the high mortality that will be experienced due to inbreeding. The prenatal wastage is significantly higher among consanguineous group. The genetic load analysis also reveals the strong positive association of inbreeding with prenatal and overall total mortality. The association between inbreeding and postnatal mortality is not significant. The values of A, supposed to be an index of public health conditions, are relatively higher. In general, the load is mainly due to mutation-selection balance. The results are discussed in the light of various hypothesis on inbreeding effects.

## INTRODUCTION

India is one of the few countries where consanguinity is practised. In South Indian populations, traditionally, the most desirable mate for a man has been his sisters daughter, or mother's brother's daughter or father's sister's daughter. However these marriages are tabooed among majority of the North Indian populations. The state of Andhra Pradesh in India harbours about 200 Hindu caste groups, thirty three tribes and a few religious minority groups (Babu et al., 1996). All these groups are endogamous in nature and practice consanguineous marriages. The magnitude of consanguinity in contemporary populations is dependent on various socio-economic changes. As Srinivas (1978) mentioned, confirmity as well as departure from tradition is contexual. The marriage practices are not exceptional. Hence there is need to study the impact of consanguinity on populations' biology at different time frames. The consanguinity or inbreeding increases homozygosity in the population resulting in increased average fitness, and ultimately have the effect on vital events like fertility and mortality. The magnitude of these effects depends on frequency of deleterious genes in the population, changes in the practice of consanguinity, socio-economic development, etc. In this context it is our aim to record the magnitude and effect of inbreeding in two caste populations of Andhra Pradesh State of India, namely Rajaka and Koppala Velama castes.

## MATERIALS AND METHODS

The present study caste populations, Rajaka and Koppala Velama are service and peasant castes respectively and belong to *Sudra varna* of Hindu caste system. Rajaka are washermen by profession and the majority are engaged in washing clothes of other communities, while Koppala Velama are engaged in agriculture and agriculture labouring. Both the groups belong to low socio-economic strata. The demographic data pertaining to marriage type and reproductive histories of 377 women belonging to Rajaka and Koppala Velama caste populations of Andhra Pradesh, India, were obtained. The Rajaka was sampled from a slum in Visakhapatnam city and Koppala Velama was sampled from rural and semi-urban areas of West Godavari district. Marriages between maternal uncle and niece, and between first cross cousins (marriages with father's sister's daughter and mother's brother's daughter)

---

* *Present Address for Correspondence:*
Dr. B.V. Babu, Division of Epidemiology, Regional Medical Research Centre, Indian Council of Medical Research, C.S. Pur, Bhubaneswar 751 016, India, *E-mail*: icmrrcbh@ren.nic.in

were considered as consanguineous marriages and all other marriages were considered as non-consanguineous type. Inbreeding coefficients for autosomal and sex linked genes were estimated by Wright's path coefficient method. Fertility is measured in terms of mean number of conceptions, live births and surviving children per woman. Regarding mortality, abortions and still births were considered as prenatal mortality while deaths up to the age of 15 years were recorded as postnatal mortality.

The inbreeding effects on foetal loss (prenatal mortality), postnatal mortality and total mortality were estimated in terms of genetic load using the following exponential regression model as illustrated by Rao (1988).

$$P_i = 1\text{-}e^{-(A+BF_i)}$$

where, $P_i$ is the expected proportion of survivors, and $F_i$ is the Wright's coefficient of inbreeding of the i th subgroup based on the type of marriage.

The weighted regression coefficient A and B were obtained by iterative computational method and these values of genetic load were interpreted as mentioned below.

The intercept A and slope B from the above formula are utilized to estimate two important quantities namely, (i) the number of lethal equivalents and (ii) the B/A ratio. According to Morton et al. (1956) weighted regression coefficient B represents an estimate of the average of lethal equivalent per gamete. The value of B is an underestimate of the mean number of lethal equivalents and lies between B and B+A. Thus the upper limit of the value of lethal equivalents is B+A while B itself is the lower limit. Morton et al. (1956) also introduced the ratio B/A, where intercept A represents the non-inbred fraction, which is supposed to be an index of public health condition and B shows the inbred fraction of mortality, which results from the homozygous recessive lethals. The B/A ratio is expected to be high ≥10 for a predominantly mutational load and nearer to 2 for a predominantly segregational load.

## RESULTS AND DISCUSSION

### *Consanguinity*

The distribution of different types of marriages and inbreeding coefficient values for autosomal and sex linked genes are given in table 1. Among these caste groups, about one third of the total marriages are consanguineous. The Koppala Velama recorded relatively higher frequency of uncle-niece marriages. Among cross cousin marriages, marriages with mother's brother's daughter (MBD) type are more. The mean inbreeding coefficient for autosomal and sex-lined genes are 0.0242±0.0002 and 0.0275±0.0003, and 0.0279±0.0010 and 0.0341±0.0004 among Rajaka and Koppala Velama respectively. Reviews of earlier studies on castes (Parvatheesam, 1995) and tribal populations (Babu, 1993) indicate that the frequency of consanguineous marriages is higher among tribal populations than among caste groups. Among tribes, the frequency of consanguineous marriages vary from 22.30 per cent among Andh (Pingle, 1983) to 73.43 per cent among Valmiki (Naidu and Babu, 1997). Among caste populations, it ranges between 13.61 per cent among Brahmin (Srikumari, 1985) and 47.06 per cent among Jalari (Veerraju, 1973). Marriage between uncle (mother's brother) and niece (sister's daughter) is prohibited in many tribal populations, however it is approved practice in Hindu castes. Hence, the values of inbreeding coefficient for sex-linked genes are higher in caste

**Table 1: Distribution of consanguineous and nonconsanguineous marriages and inbreeding coefficients among Rajaka and Koppala Velama castes**

| *Castes* | *Sample* | *Consanguineous Marriages*[1] | | | | *Nonconsanguinesous marriages* | *Mean inbreeding coeffieients ± SE* | |
|---|---|---|---|---|---|---|---|---|
| | | *UN* | *FSD* | *MBD* | *TC* | | *Sex Linked* | *Autosomal* |
| *Rajaka* | 227 | 12<br>5.29% | 26<br>11.45% | 38<br>16.74% | 76<br>33.48% | 151<br>66.52% | 0.0242<br>±0.0002 | 0.0275<br>±0.0003 |
| *Koppala Velama* | 150 | 22<br>14.67% | 4<br>2.67% | 19<br>12.67% | 45<br>30.00% | 105<br>70.00% | 0.0279<br>±0.0010 | 0.0341<br>±0.0004 |

1. UN, uncle-niece; FSD, father's sister's daughter; MBD, mother's brother's daughter; TC, total consanguineous marriages

groups than in tribes due to presence of uncle-niece marriages in castes.

### *Inbreeding Effect on Fertility and Mortality*

Table 2 illustrates the fertility, measured in terms of mean conception, live births and surviving children per woman. It is assumed that fertility would be greater in consanguineous couples, to compensate for the high mortality expected due to inbreeding. The present study castes confirm the above hypothesis by recording relatively higher mean number of conceptions for consanguineous couples than for non-consanguineous couples. However the mean number of live births and surviving children are higher in non-consanguineous couples, indicating higher survival of non-inbreds during the prenatal stage. Nevertheless, the differences are marginal and statistically not significant except for mean number of conceptions in Koppala Velama. A quick glance at the table reveals that one out of three or four conceptions is being wasted, leaving only two or three surviving children. Though the present results are not consistent, the fertility rates are relatively higher in consanguineous couples. Schull and Neel (1972) reported that parental consanguinity had significantly increased the total conceptions and live births in Japanese population. In Indian populations too, Basu (1978), Puri et al. (1978) and Naidu et al. (1995) have confirmed the effect of inbreeding resulting in higher fertility. On the other hand, the results are not consistent in several other Indian populations reported by Rao (1978), Saheb et al. (1978), Rao and Imbaraj (1979), etc.

The information on mortality at both prenatal and post-natal stages as well as total mortality among consanguineous and non-consanguineous couples (Table 3) reveals relatively higher rates of mortality among consanguineous couples than non-consanguineous unions in both the caste populations. These differences are highly significant for prenatal wastage and total mortality. The mean values of mortality (0.63 among Rajaka and 0.71 among Koppala Velama per woman) indicate that on average at least one conception per woman is being ended up in death either at prenatal or post-natal stages. The present result suggests that the reproductive loss is positively associated with inbreeding in these caste populations.

### *Genetic Load*

The inbreeding effects on the reproductive wastage, estimated in terms of genetic load for prenatal, prereproductive postnatal deaths and total mortality are presented in table 4. The present study castes show a positive and significant regression values for prenatal loss and total mortality indicating an increase of mortality with increasing inbreeding coefficient. The B values for post-natal mortality is not significant, in both the populations, and Koppala Velama records inverse association. The B/A values which categorize the load into mutational and segregational indicate that the load is mainly mutational for prenatal and total mortality in both the populations which might have resulted from higher B values and lower A values. The lower values of B/A for post-natal mortality indicate that the load is

**Table 2: Details of fertility in consanguineous and nonconsanguineous couples among Rajaka and Koppala Velama castes**

| *Marriage type*[1] | *Rajaka* | | | *Koppala Velama* | | |
|---|---|---|---|---|---|---|
| | *Conceptions* | *Live births* | *Surviving children* | *Conceptions* | *Live births* | *Surviving children* |
| UN | 3.75±0.45 | 3.58±0.46 | 2.92±0.39 | 3.45±0.26 | 2.54±0.27 | 2.36±0.32 |
| FSD | 3.58±0.43 | 3.27±0.42 | 2.54±0.25 | 3.75±0.96 | 2.75±0.75 | 2.58±0.64 |
| MBD | 3.21±0.29 | 3.05±0.31 | 2.25±0.21 | 3.95±0.50 | 2.84±0.41 | 2.63±0.37 |
| TC | 3.24±0.22 | 3.21±0.22 | 2.61±0.16 | 3.68±0.26 | 2.68±0.22 | 2.48±0.22 |
| NC | 3.40±0.50 | 3.33±0.15 | 2.85±0.13 | 3.08±0.16 | 2.81±0.14 | 2.59±0.15 |
| Total | 3.41±0.07 | 3.29±0.07 | 2.77±0.06 | 3.26±0.13 | 2.78±0.12 | 2.56±0.12 |
| t-value[2] | 0.0751 | 0.4507 | 1.1642 | 1.9654[3] | 0.4985 | 0.4131 |

1. UN, uncle-niece; FSD, father's sister's daughter; MBD, mother's brother's daughter; TC, total consanguineous marriages; NC, nonconsanguineous marriages; Total, total marriages
2. t-value for difference between consanguineous and nonconsanguineous couples
3. $p<0.05$

**Table 3: Details of mortality in consanguineous and nonconsanguineous couples among Rajaka and Koppala Velama castes**

| *Marriage type*[1] | *Rajaka* | | | *Koppala Velama* | | |
|---|---|---|---|---|---|---|
| | *Prenatal mortality* | *Post natal mortality* | *Total mortality* | *Prenatal mortality* | *Post natal mortality* | *Total mortality* |
| UN | 0.17±0.06 | 0.67±0.14 | 0.83±0.11 | 0.95±0.21 | 0.18±0.18 | 1.14±0.19 |
| FSD | 0.31±0.08 | 0.73±0.09 | 1.04±0.04 | 1.00±0.41 | 0.25±0.25 | 1.25±0.21 |
| MBD | 0.16±0.06 | 0.50±0.08 | 0.66±0.08 | 1.10±0.27 | 0.21±0.21 | 1.32±0.18 |
| TC | 0.21±0.05 | 0.61±0.06 | 0.82±0.04 | 1.02±0.16 | 0.20±0.19 | 1.22±0.17 |
| NC | 0.07±0.03 | 0.48±0.04 | 0.54±0.04 | 0.25±0.06 | 0.23±0.22 | 0.49±0.11 |
| Total | 0.11±0.02 | 0.52±0.03 | 0.63±0.01 | 0.48±0.07 | 0.22±0.21 | 0.71±0.12 |
| t-value[2] | 2.4010[3] | 1.8028 | 4.9497[4] | 4.5061[4] | 0.1032 | 3.6052[4] |

1. UN, uncle-niece; FSD, father's sister's daughter; MBD, mother's brother's daughter; TC, total consanguineous marriages; NC, nonconsanguineous marriages; Total, total marriages
2. t-value for difference between consanguineous and nonconsanguineous couples
3. P<0.05 4. p<0.001

segregational. In general the results indicate that the load is mainly due to mutation-selection balance. It is worth mentioning that the values of regression coefficient B are positive and significant for prenatal mortality indicating a general trend of manifestation of inbreeding effectively during the foetal stage. The lethal equivalents per gamete, which lie between B and B+A, vary considerably. The intercept A measures the mortality of the non-inbred fraction, supposed to be an index of public health condition. The values of intercept A are relatively more particularly for total mortality which are consistent with low socio-economic condition and poor public health facilities of these caste groups.

Thus the effects of inbreeding on mortality are obvious and the load in mainly by mutation-selection balance. However, Crow (1958) observed that segregational load is larger than mutational load. An overview of earlier studies on genetic load among some Andhra populations (Srikumari et al., 1985; Reddy, 1992; Babu et al., 1994 and Naidu et al., 1995) reveals that generally field based population studies record segregational load rather than mutational load. Few of the Andhra populations such as Vadabalija, Vadde and Mangali castes, and Jatapu and Manzai Mali tribes reported negative and non-significant regression coefficient B for prenatal wastage. For post-natal loss also majority of populations reported negative or non-significant values of regression coefficient B, which infer weak association between inbreeding and post-natal mortality. The non-significant mortality differences between inbreds and non-inbreds can be expalined by Sanghvi's (1966) hypothesis that the effect of inbreeding will be minimized due to elimination of lethal and deleterious genes from gene pool through a long history of consanguinity, particularly in Andhra populations. In this context the observations of Reddy (1992) are worth mentioning. He compiled the data on

**Table 4: Regression coefficients for genetic load among Rajaka and Koppala Velama castes**

| *Castes mortality* | *Estimates of genetic load* | | | *$\chi^2$ for goodness of fit* | | |
|---|---|---|---|---|---|---|
| | *A* | *B* | *B/A* | *$\chi^2_1$ regression* | *$\chi^2_2$ residual* | *$\chi^2_3$ total* |
| *Rajaka* | | | | | | |
| Prenatal | 0.0208 | 0.4397 | 21.15 | 0.2350 | 9.0174[1] | 0.2624 |
| Post natal | 0.1569 | 0.6386 | 4.07 | 0.2912 | 2.1968 | 2.4880 |
| Total | 0.1767 | 1.0998 | 6.22 | 0.8348 | 6.1045[1] | 6.9393 |
| *Koppala Velama* | | | | | | |
| Prenatal | 0.0937 | 2.1126 | 22.55 | 3.7280 | 37.6298[2] | 41.3578[2] |
| Post natal | 0.0895 | -0.1157 | -1.29 | 0.0094 | 0.1498 | 0.1592 |
| Total | 0.1787 | 2.0888 | 11.69 | 2.7228 | 15.8159[2] | 18.5387[2] |

1. p<0.05; 2. p<0.001

inbreeding effects on reproductive wastage and computed genetic load for about 30 South Indian populations. Nearly half of the populations reported negative B values indicating inverse relation between inbreeding and foetal loss, while one fourth of the populations showed the same relation for post-natal mortality also. The average of regression coefficient A and B are 0.223 and 0.383 respectively. It is to be noted that the average value of B and number of lethal equivalents of South Indian populations computed by Reddy (1972) are significantly lower than the average values of the Japanese (Vogel and Motulsky, 1986; Schull and Neel, 1972) and Western Whites (Cavalli-Sforza and Bodmer, 1971; Vogel and Motulsky, 1986) even though the degree as well as the history of consanguinity in South Indian populations are much higher than that of Japanese and Whites. Sanghvi's hypothesis cannot explain the inverse relation between inbreeding and foetal wastage. According to the hypothesis of Peritz (1971), consanguinity decreases the chance of blood group incompatibility and hence reduces foetal loss. However all these hypotheses may be verified in contemporary populations by extensive studies with both genetic and epidemiological perspectives by considering all confounding factors such as socio-economic differentials, demographic factors, etc.

## REFERENCES

Babu, B.V.: *A Population Genetic Study of Sub Tribes of Mali from Andhra Pradesh*. Ph. D. Thesis. Andhra University, Visakhapatnam (1993).

Babu, B.V., Kusuma, Y.S. and Naidu, J.M.: Genetic load among four Andhra caste populations. *Soc. Biol.*, **41**: 127-129 (1994).

Babu, B.V., Kusuma, Y.S. and Naidu, J.M.: Genetic diversity of PTC taste sensitivity among tribal and caste populations of Andhra Pradesh, India. *Z. Morph. Anthrop.*, **81**: 217-221 (1996).

Basu, S.K.: Effect of consanguinity among Muslim groups of India. pp. 178-187. In: *Medical Genetics in India*. I.C. Verma (Ed.). Auroma Enterprises, Pondicherry (1978).

Cavalli-Sforza, L.L. and Bodmer, W.F.: *The Genetics of Human Populations*. W.H. Freeman and Company, San Francisco (1971).

Crow, J.F.: Index to total selection, some possibilities for measuring selection intensities in man. *Hum. Biol.*, **30**: 1-13 (1958).

Morton, N.E., Crow, J.F. and Muller, H.J.: An estimation of the mutational damage in man from data on consanguineous marriages. *Proc. Acad. Sci. USA*, **42**: 855-863 (1956).

Naidu, J.M. and Babu, B.V.: Inbreeding, fertility and mortality among tribal populations of north coastal Andhra Pradesh. In: *J.B.S. Haldane Birth Centenary Volume*. P.K. Das (Ed.). (in press) (1997).

Naidu, J.M., Babu, B.V., Kusuma, Y.S., Yasmin and Sachi Devi, S.: Inbreeding effects on reproductive outcome among seven tribes of Andhra Pradesh, India. *Am. J. Hum. Biol.*, **7**: 589-595 (1994).

Parvatheesam, C.: *A Population Genetic Treatise of Rajaka Caste from Andhra Pradesh*. Ph. D. Thesis. Andhra University, Visakhapatnam (1995).

Peritz, E.: A statistical study of the intra-uterine selection factors related to the ABO system-II. The analysis of fetal mortality data. *Ann. Hum. Genet.*, **34**: 389-394 (1971).

Pingle, U.: Comparative analysis of mating systems and marriage distance patterns in five tribal groups of Andhra Pradesh, India. *Soc. Biol.*, **30**: 67-74 (1983).

Puri, R.K., Verma, I.C. and Bhargava, I.: Effect of consanguinity in a community in Pondicherry, pp. 129-139. In: *Medical Genetics in India*. I.C. Verma (Ed.). Auroma Enterprises, Pondicherry (1978).

Rao, P.S.S.: Inbreeding in Tamil Nadu and its effects on human reproduction. pp. 121-128. In: *Medical Genetics in India*. I.C. Verma (Ed.). Auroma Enterprises, Pondicherry (1978).

Rao, P.S.S.: The measurements of inbreeding and its effects. pp. 208-241. In: *Statistical Methods in Human Population Genetics*. K.C. Malhotra (Ed.). IBRAD, ISI and ISHG, Calcutta (1988).

Rao, P.S.S. and Inbaraj, S.G.: Trends in human reproductive wastage in relation to long-term practice of inbreeding. *Ann. Hum. Genet.*, **42**: 281-288 (1979).

Reddy, B.M.: 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 (1992).

Saheb, S.Y., Sirajuddin, S.M., Raju, C.M., Sastry, D.B. and Gulati, R.K.: Consanguinity and its effects on fertility and mortality in Kodava and Ammakodava populations of Kodagu district. *Proc. V Ann. Conf. Ind. Soc. Hum. Genet.*, Bombay (1978).

Sanghvi, L.D.: Inbreeding in India. *Eug. Q.*, **13**: 291-301 (1966).

Schull, W.J. and Neel, J.V.: The effect of parental consanguinity and inbreeding in Hirado, Japan, V. Summary and interpretation. *Am. J. Hum. Genet.*, **24**: 425-453 (1972).

Srikumari, C.R.: *A study of Natural Selection and Genetic Adaptation among Four Endogamous Sub populations of Andhra Pradesh*. Ph. D. Thesis, Andhra University, Visakhapatnam (1985).

Srikumari, C.R., Rajani Kumari, J. and Rao, T.V.: Variability of genetic load with changing socio-cultural environment. *Hum. Hered.*, **35**: 388-393 (1985).

Srinivas, M.N.: *The Changing Position of Indian Women*. Oxford University Press, Delhi (1978).

Veerraju, P.: Inbreeding in coastal Andhra Pradesh. pp. 309-318. In: *Proc. Int. Symp. Hum. Genet.* M.R. Chakravartti (Ed.). Andhra University, Visakhapatnam (1973).

Vogel, F. and Motulsky, A.G.: *Human Genetics: Problems and Approaches*. Springer-Verlag, Berlin (1986).