Consanguinity, inbreeding and genetic load in salis: A sub divided population of Andhra Pradesh, South India

P. Mohan Rao[1*], M. Ramesh[2], K. Geetha Kumari[2], G. Sudhakar[2]

[1]Associate Professor, Community Medicine, GEMS Hospital, Ragolu, Srikakulam Dist, Andhra Pradesh, India
[2]Department of Human Genetics, Andhra University, Visakhapatnam, Andhra Pradesh, India

ABSTRACT

Aims and Objectives: The objective of the present study is to assess the genetic composition of the two subgroups of Salis and the extent of genetic differentiation among them with the help of various demographic and genetic variables. **Materials and Methods:** A total of 520 couples belonging to two sub-groups namely, Padmasalis and Pattusalis residing in and around Visakhapatnam and Vizianagaram of Andhra Pradesh were included in this study. Demographic data pertaining to consanguinity and reproductive histories were obtained. Statistical analysis was done using SPSS v 19 software. **Results:** Out of 520 married couples, 180 women had practiced consanguineous marriages (34.62%) and 340 women had adapted to non-consanguineous (65.38%) marriages. The overall consanguinity is more among the Padmasalis (36.98%) than among the Pattusalis (32.16%). However, the difference between the two groups is not statistically significant. The coefficient values for autosomal genes is higher in Padmasalis (0.0354) than the Pattusalis (0.0279). Likewise, the coefficient values for sex-linked genes is higher in Padmasalis (0.0340) than the Pattusalis (0.0319). In the present study population the inbreeding load (B) obtained for Pattusalis was positive (0.8850) but in Padmasalis it was negative (-2.5714) indicating an increase in survival of individuals with increased homozygosity. The random load (A) in Pattusalis was 1.5944 and in Padmasalis it was 1.9290. The pooled data of Salis recorded a negative B value indicating an increase of fitness of offspring in comparison to the fitness of their parental generations. **Conclusion:** The frequency of consanguinity was found to be high in Salis. The findings are in concurrence with the earlier reports of high prevalence of consanguineous marriages in South India. Female education, socio-economic status and parental decisions in marriages may be the reasons.

Keywords: Consanguinity, Inbreeding, Genetic Load, Salis

Introduction

The terms inbreeding and consanguinity are used interchangeably to describe union between couples who share at least one common ancestor. Inbreeding in population genetic terms refers to a departure from nonrandom ''mating'' in which individuals ''mate'' with those more similar (genetically) to them than if they ''mated at random'' in the population. In clinical genetics, it is called the relationship by marriage between first and second cousins [1]. Rate of

consanguineous marriage in different countries are dependent on different factors like education level, religion, local tradition, and socio-economic status [2,3]. One of the most interesting aspects of the practice is its decline in some areas specifically, Europe and North America, and its prevalence in other areas specifically Western and Central Asia. Numerous studies have investigated consanguineous marriage as a 'legal union of male and female of a common ancestor or between a man and woman related by blood' [4-6]. The most common prevailing form of consanguineous marriage is between first cousins [7]. The populations in the southern states of India (Andhra, Kerala, Tamilnadu and Maharashtra) are unique in the occurrence of a fair frequency of consanguineous marriages within the sub castes, and they thus provide an excellent opportunity for studying the detrimental effects of low levels of inbreeding and for estimating

*Correspondence

P.Mohan Rao
Associate Professor, Community Medicine, GEMS Hospital, Ragolu, Srikakulam Dist, Andhra Pradesh, India
E Mail: ramesh_mandarapu@rediffmail.com

the genetic load. Morton [8] developed formulae for the estimation of genetic load in terms of A and B statistics which could be used for discrimination between the mutational and segregational components of loads.The genetic variability present in any gene pool in the form of recessive mutations imposes a hereditary burden in population in the form of mortality and morbidity suffered by the homozygotes. This hereditary burden is referred as the genetic load, which has been defined in a number of ways by Muller, Crow, Wallace and by Dobzhansky [9, 10, 11]. One approach currently used to estimate the load is from the data provided consanguineous matings. The assumption in this approach is that deleterious mutations are recessive genes and their presence in the gene pool of a population should be revealed in the reproductive performance of consanguineous matings. As the closely related individuals have a greater chance of carrying identical alleles, the children of consanguineous matings have a greater chance of being homozygous for rare recessive alleles than the children from non-consanguineous matings. The caste system in India provides a variety of important and rare material for specific enquiries from the field of population genetics, when combined with genetical demographic studies. Salis is a 'Telugu Weavers' caste or social group found largely in the state of Andhra Pradesh in India. Salis are divided into two main endogamous groups, Padma or lotus (Padmasali), and Pattu or silk (Pattusali). The Salis follow weaving (Padmasalis – cotton weavers and Pattusalis – silk weavers) as their traditional profession. Other occupations include agriculture, farm labours, personal servants, shop-keepers and masons. The Padmasalis occupy a better socio-economic condition than the Pattusalis in general. They are identified by different names in various regions throughout India. The present genetic study is carried out on two endogamous subgroups of the Salis caste population of Andhra Pradesh, South India. Both the subgroups are distributed throughout Andhra Pradesh. The main objective of the present study is to assess the genetic composition of these two subgroups and the extent of genetic differentiation among them with the help of various demographic and genetic variables.

Material and methods

A total of 520 couples belonging to two sub-groups of Sali populations, namely, Padmasalis and Pattusalis residing in and around Visakhapatnam and Vizianagaram of Andhra Pradesh have participated in this study. These families were selected randomly from rural and urban areas. A pre-tested, pre-designed and semi-structured proforma was used for the data collection. The women were explained the objectives of our study and were assured that their identities won't be disclosed. Consent was obtained from all the participants of the study. Demographic data pertaining to consanguinity and reproductive histories were obtained.   Based on pedigrees, consanguineous marriages are classified as uncle-niece and first cousin marriages. First cousin marriages are further classified as marriage with father's sister's daughter (FSD) and mother's brother's daughter (MBD). Our data has been compared with available other caste populations of Andhra Pradesh.

Statistical analysis: The data were analysed by SPSS v 19.0 software. Standard procedures of chi-square test and regression analysis were employed to analyze the data. The values of co-efficient of inbreeding for various kinds of consanguineous marriages for autosomal (Fa) and sex linked (Fs) genes are different. In the present investigation the following Wright's formula as illustrated by Rao [12] was used. $Fa = \Sigma\ Ci.\ Fai$; $Fs = \Sigma\ Ci.\ Fsi$, where Ci is the proportion of marriage type and Fai is the inbreeding coefficient for autosomal genes (Fsi) for sex linked genes.

The genetic loads were estimated from the data of consanguinity-related risk effects on mortality in units of lethal equivalents based on the A and B statistics obtained by the weighted regression analysis following the MCM formula, $-\log_e S = A + BF$ [8], where S is the proportion of survivors, F the coefficient of inbreeding, A the estimates of deaths that occur in the non-inbred offspring and B the measure of the hidden genetic damage expressed by inbreeding. The measure of total genetic damage is the quantity equal to the sum of B and A, and hence the number of lethal equivalents per gamete lies between B and B + A. The B/A value provide critical information about the relative importance of mutational and segregational loads such that if the ratio is more than 10, the load element is mutational, and less than 10 indicating segregational.

Results

Table 1: Distribution of Consanguineous and Inbreeding Coefficients among Salis

Population	Total Marriages	Affinal	Consanguineous Marriages				Inbreeding Coefficient	
			UN	MBD	FSD	Total	Fa	Fs
Padmasalis	265	167 (63.02)	52 (19.77)	20 (7.60)	26 (9.88)	98 (36.98)	0.0354	0.0340
Pattusalis	255	173 (67.84)	32 (12.65)	33 (13.04)	17 (6.71)	82 (32.16)	0.0279	0.0319
Salis (Pooled)	520	340 (65.38)	84 (16.28)	53 (10.27)	43 (8.34)	180 (34.62)	0.0647	0.0672

UN = Uncle-Niece; MBD = Mother's Brother's Daughter; FSD = Father's Sister's Daughter
Fa = Inbreeding Co-efficient for Autosomal genes; Fs= Inbreeding Co-efficient for Sex-linked genes
^{2} =0.1401, 0.80>p>0.70

The distribution of consanguineous marriages and inbreeding coefficients are given in Table 1.

Out of 520 married couples, 180 women had practiced consanguineous marriages (34.62%) and 340 women had adapted to non-consanguineous (65.38%) marriages. Among the Padmasalis uncle-niece marriages (19.77%) are the most frequent followed by first cousins (FSD-9.88% and MBD-7.60%). Among the Pattusalis first cousin marriages (MBD - 13.04% and FSD – 6.71%) are the most frequent followed by Uncle-niece (12.65%).   The overall consanguinity is more among the Padmasalis (36.98%) than among the Pattusalis (32.16%). However, the difference between the two groups is not statistically significant. The coefficient values for autosomal genes are higher in Padmasalis (0.0354) than the Pattusalis (0.0279). The pooled data shows a value of 0.0647. Likewise, the coefficient values for sex-linked genes is higher in Padmasalis (0.0340) than the Pattusalis (0.0319). The pooled data shows a value of 0.0672.Table 2 represents the consanguinity and inbreeding coefficient for autosomal & sex linked genes among salis in comparison to different castes of Andhra Pradesh. The frequency of consanguineous marriages is highest among Jalaris (47.06%) [13] and lowest among Brahmins (13.91) [14]. The average coefficient of inbreeding for autosomal genes (F_{ai}) is highest among Yadavas (0.077) [15] and lowest among Brahmin II (0.011) [16]. The average coefficient of inbreeding for sex-linked genes (F_{si}) is highest among Vadabalijas (0.055) [15] and lowest among Kshatriyas (0.011) [17].

Table 2: Consanguinity and Inbreeding Coefficient (Autosomal & Sex Linked) in different castes of Andhra Pradesh

Population	Total no. of	Consanguine Marriages		F_{ai}	F_{Si}	Source
		Number	Percent			
Padmasali	265	98	36.98	0.035	0.034	Present Study
Pattusali	255	82	32.16	0.028	0.032	Present Study
Kalinga	205	65	31.71	0.024	0.028	Sridevi, 2014 [18]
Brahmin -III	631	-	14.90	0.012	0.016	Seethalakshmi,2002 [19]
Rajaka	227	76	33.48	0.024	0.028	Parvatheesam,1995 [20]
Aryavysya	301	-	20.60	0.018	0.025	Lakshmi,1994 [21]
Kalinga Vysya	287	-	26.13	0.023	0.029	Lakshmi,1994 [21]
Trivarnika	258	-	31.40	0.025	0.029	Lakshmi,1994 [21]
Dawoodi Bahras	105	27	25.71	0.015	0.015	Khaja,1993 [22]
Pooled Muslims	443	138	31.16	0.019	0.015	Khaja,1993 [22]
Shias Muslims	114	43	37.72	0.023	0.02	Khaja,1993 [22]

Sunni Muslims	224	68	30.36	0.014	0.014	Khaja,1993 [22]
Reli-I	208	83	39.90	0.033	0.035	Ramesh,1992 [23]
Relli-II	220	93	42.27	0.030	0.023	Ramesh,1992 [23]
Relli(pooled)	428	176	41.12	0.031	0.029	Ramesh,1992 [23]
Vadde	2078	-	32.40	0.022	-	Reddy,1992 [24]
Chakali	104	33	31.73	-	-	Babu & Naidu,1989 [25]
Kummari	63	10	15.87	-	-	Babu & Naidu,1989 [25]
Madiga-I	92	30	32.61	-	-	Babu & Naidu,1989 [25]
Mangali	112	43	38.39	-	-	Babu & Naidu,1989 [25]
Yadava	260	87	33.46	0.077	0.052	Raja Rajeswari,1988 [15]
Vadabaliji	196	70	35.71	0.071	0.055	Raja Rajeswari,1988 [15]
Madiga-II	168	-	-	0..025	0.036	Rao & Murthy,1986 [26]
Mala	88	-	-	0.026	0.055	Rao & Murthy,1986 [26]
Reddy-II	321	-	-	0.014	0.029	Rao & Murthy,1986 [26]
Vysya-II	244	-	-	0.016	0.028	Rao & Murthy,1986 [26]
Reddy-I	179	75	41.90	0.033	-	Govindareddy,1986 [27]
Brahmin -II	623	86	13.91	0.011	0.016	Srikumari,1986 [16]
Jalari – I	102	48	47.06	0.038	0.054	Veerraju,1978 [28]
Kammas	60	26	43.33	0.042	0.046	Veerraju,1978 [28]
Salis	82	22	26.83	0.020	0.031	Veerraju,1973 [13]
Kshatriya	100	40	40.00	0.035	0.011	Reid,1973 [17]
Kapu-II	610	169	27.70	0.017	0.024	Reid,1971 [30]
Muslim	356	124	36.24	0.025	0.042	Sanghvi,1966 [31]
Brahmin -I	83	21	25.30	0.019	0.032	Sanghvi,1966 [31]
Harijans	1185	-	39.32	0.029	0.046	Sanghvi,1966 [31]
Vysya-I	229	70	30.57	0.022	0.036	Sanghvi,1966 [31]

Table 3: Estimates of genetic load among Sali population of Coastal Andhra Pradesh

Population	A	B	B/A	Chi-Square df = 1	Regression df = 3	Deviation df =4
Padmasalis	1.9290	-2.5714	-1.3330	0.5317	3.1935	**3.7253**
Pattusalis	1.5944	0.8854	0.5551	0.0524	0.2922	**0.3446**
Pooled	1.7506	-0.8908	-0.5088	0.1219	0.6859	0.8078

Table 3 depicts the estimations of genetic load among Sali population of Coastal Andhra Pradesh. In the present study population the inbreeding load (B) obtained for Pattusalis was positive (0.8850) but in Padmasalis it was negative (-2.5714) indicating an increase in survival of individuals with increased homozygosity. The random load (A) in Pattusalis was 1.5944 and in Padmasalis it was 1.9290. The pooled data of Salis recorded a negative B value indicating an increase of fitness of offspring in comparison to the fitness of their parental generations. The chi-square values of regression are not significant in the pooled data. Also the deviation from fitted regression and the total chi-squares are not significant.

Table 4: Estimates of Genetic load in different castes of Andhra Pradesh

Population	A	B	B/A	Reference
Padmasalis	1.9290	-2.5714	-1.3330	**Present Study**
Pattusalis	1.5944	0.8854	0.5551	**Present Study**
Salis (Pooled)	1.7506	0.8908	0.5088	**Present Study**
Kapu	0.0305	1.4325	46.9700	**Prakash et al., 2010 [32]**
Settibalija	0.0762	-0.0457	-0.6000	**Prakash et al., 2010 [32]**
Paki	0.0210	1.0823	51.5400	**Prakash et al., 2010 [32]**
Chachati Relli	1.4431	0.7064	0.4895	**Ramana et al., 1999 [33]**

Kapu Relli	0.9479	-1.1415	-1.2042	Ramana et al., 1999 [33]
Arya Vysya	0.1074	1.2548	11.6859	Lakshmi,1994 [21]
Kalinga Vysya	0.1214	-0.2912	2.3983	Lakshmi,1994 [21]
Thrivarnika	0.1240	0.1125	0.9069	Lakshmi,1994 [21]
Madiga	0.4439	-0.2263	0.5100	Govindareddy,1986 [27]
Brahmin	0.1497	0.0085	0.0570	Sri kumari, et al.,1985 [14]
Mala	0.3688	0.0231	0.0600	Rao, 1984 [34]
Reddy	0.2251	1.2908	5.7300	Rao, 1984 [34]
Vysya	0.1524	2.1494	14.1000	Rao, 1984 [34]

Estimates of A and B and B/A ratio in different population of Andhra Pradesh are presented in Table 4. Three populations viz., the Padmasalis of the present study, Settibalija, Kapu Relli, Kalinga Vysya and Madiga exhibited negative values of B. A negative value of B means an increase in the fitness value of inbred. This may also be the result of under reporting of mortality in the offspring of consanguineous parents. Because of high rate of illiteracy the people may not realize the importance of reporting ill-fated conceptions or they may not be able to recollect past events despite thorough enquiry by the author. The B/A ratio is found to be more among the Paki and Kapu [32], Vysya [34] and the Arya Vysya [21].

Discussion

Consanguineous marriages are common in Andhra Pradesh and they have a very long history. In such a long history of consanguinity, its effects are naturally greatly reduced due to natural selection. The same is observed in the present study.   The highest rates of consanguineous marriage in South India are usually reported in traditional rural areas and among the poorest and least educated groups. However, close kin marriage is commonplace even in Brahmin communities [35], and it may be strongly favoured among major land-owning families as a means of ensuring the maintenance of their estates. The only communities in which consanguinity appears to be specifically avoided are those with origins in North India, and which continue to follow the traditions of that region [36].Although the most common form of consanguineous marriage in all major societies is between first cousins, the importance of customary influences is apparent from variations in the specific types of first-cousin marriage contracted. While marriage to mother's brother's daughter is the strongly preferred form of consanguineous union among South Indian Hindus [37], all four types of first-cousin union, i.e. to father's brother's daughter, to father's sister's daughter, to mother's brother's daughter, and to mother's sister daughter, are arranged in South Asian Muslim communities.In the present study population the inbreeding load (B) obtained for Pattusalis was positive (0.8850) but in Padmasalis it was negative (-2.5714) indicating an increase in survival of individuals with increased homozygosity. The random load (A) in Pattusalis was 1.5944 and in Padmasalis it was 1.9290.   The pooled data of Salis recorded a negative B value indicating an increase of fitness of

offspring in comparison to the fitness of their parental generations. The subgroups of Salis in the present study belong to low socio-economic conditions; only Padmasalis recorded a negative load value, a characteristic feature of the present study. The negative value, might obviously be due to high mortality in non-inbred group of individuals. The negative regression could also arise due to effect of inbreeding on incompatibility [38]. Another argument, the high levels of inbreeding in the low socio-economic castes would have been eliminating the deleterious genes, and under interaction with living conditions, such high inbreeding might also lead to increased homozygosity of many of the genes, that might have adapted to those conditions. Such an increase in homozygosity of the adapted genes would explain the increased survival of individuals under inbreeding in these caste [26] populations. In the present study the number of lethal equivalents was high in Pattusalis 2.4794.   The Padmasalis recorded a negative value of -0.6424 due to a negative regression coefficient B value. The pooled data of Salis also recorded a negative value of A +B (-0.5088), indication a decrease in prenatal & pre-reproductive deaths or increase in survival capacity due to environmental and genetic factors.The B/A ratio above 10 and upwards indicate that the load is predominantly due to mutation-selection balance.   If low, it is due to herterozygote advantage In the present study the B/A ratio recorded -1.3330 in Padmasalis and -0.5088 in the pooled data indicating that load does not exist either by mutation selection balance or heterozygote advantage.   Instead, the present generations of Salis are more capable of surviving than the parental generation. But in the case

of Pattusalis along the B/A ratio was found to be of a positive value i.e., 0.5551, which is low considered to be due to heterozygote advantage.Inbreeding is observed to be high among the lower strata population, while it is less among the upper strata populations. This is perhaps because the lower strata groups move in an area of small radius and live closely knitted while the people of upper strata are spread over an area of larger radius, and hence come in contact with people of distant areas which dilutes inbreeding and enhances scope of random mating. Inbreeding coefficients also follow the same trend.

Conclusion

The Hindu populations throughout India are organized into castes and sub castes which are largely endogamous. The populations in the southern states of India are unique in the occurrence of a high rate of consanguineous marriages within the endogamous groups. The prevalence of consanguineous marriages is high in our study. There is a lack of awareness and knowledge about the ill effects of consanguinity. Health education and genetic screening were suggested to curb consanguineous marriages in order to prevent adverse outcomes for better health.

Acknowledgements

References

1. Teebi A. Genetic Diversity among the Arabs, Genetic Disorders among Arab Populations. Springer, 2014.
2. Fuster V, Colantonio SE. Socioeconomic, demographic, and geographic variables affecting the diverse degree of consanguineous marriage in Spain. Hum Bio, 2004; 76: 1-14.
3. Jaber L, Shohat M, Halpern GJ. Demographic characteristics of the Israeli Arab community in concentration with consanguinity. Isr J Med Sci, 1996; 32: 1286-1289.
4. Centerwall WR. A preliminary study of consanguinity and congenital anomalies in South India. Paediatr Indones, 1965; 5: 906-914.
5. Jurdi R, Saxena PC. The prevalence and correlates of consanguineous marriages in Yemen: Similarities and contrasts with other arab countries. Journal of Biosocial Science, 2003; 35: 1–13.
6. Yunis KE Rafei R & Mumtaz G. Consanguinity: Perinatal outcomes and prevention—a view from the Middle East. NeoReviews, 2008; 9(2): e59.
7. Al-Salem M & Raishdeh N. Consanguinity in north Jordan: Prevalence and pattern. Journal of Biosocial Science, 1993; 25(4): 553–556.
8. Mortan NE, Crow JF & Muller HJ. An estimate of the mutational damage in man from data on consanguineous marriages. Proc. Natn. Amd. Sci, U.S.A. 1956; 42, 855-63.
9. Muller HJ. Our load of mutations. Am.J.Hum.Genet, 1950; 2: 111-76.
10. Crow JF. Mutation and Selective balance as factors influencing population fitness. In: Molecular Genetics and Human Disease. L.I.Gardner (ed)., Charles C.Thomas, Springfield, Illinois, 1960
11. Wallace B and Dobzhansky T. Radiation, genes and man. Henry Holt, New York, 1959.
12. Rao PSS. Consanguinity and Inbreeding in India. Paper presented at the international symposium on population structure and human variation, Bombay, 1978; Dec 18-21.
13. Veerraju P. Inbreeding coastal Andhra Pradesh. Proceedings of International symposium of Human Genetics, Waltair, 1973; pp. 309 – 318.
14. Srikumari CR. A study of natural slection and genetic adaptation among the four endogamous sub papulations of Andhra Pradesh. Ph.D. Thesis, Andhra University, Visakhapatnam (Unpublished), 1985.
15. Raja Rajeswari. Demographic study of Yadava and Vadabalija communities of Visakhapatnam, Ph.D., Thesis, Andhra University, Visakhapatnam,1988.
16. Srikumari CR, Rajanikumari J. and Rao TV. Gene differentiation in four subcastes of Brahmins from Visakhapatnam, Andhra Pradesh, Hum. Hered, 1986; 36: 373 – 378.
17. Reid RM. Social Structure and Inbreeding in a South Indian Caste in: Genetic Structure of Population (ED) Morton, NE. University, Hawaii, 1973.
18. Sridevi S. A Population Genetic Study of Kalingas. Serials Publictions. New Delhi, 2014.
19. Seetha Lakshmi. Dermatoglyphic study of Brahmins of Andhra Pradesh, Ph.D Dissertation, Andhra University, Visakhapatnam, 2002.
20. Parvatheesam. A population Genetic Treatise of Rajaka Caste from Andhra Pradesh, Ph.D Dissertation, Andhra University, Visakhapatnam, 1995.

21. Lakshmi N. Microevolutionary genetic differentiation in three endogamous populations of Andhra Pradesh. Ph.D. Thesis submitted to Andhra University (Unpblished), 1994.
22. Khaja N. Md. Genetic Variation in Muslims. Ph.D Thesis, Andhra University, Visakhapatnam, 1993.
23. Ramesh M, Khaja Md. N, Veerraju P. and Kali TM. Red cell glyxalase I Polymorphism among Madigas of Andhra Pradesh. J. Hum. Ecol, 1992; 235 – 236.
24. Reddy BM. Inbreeding effects on reproductive outcome: A study based on a large sample from the endogamous Vadde of Kollure lake, Andhra Pradesh, India. Hum. Biol, 1992; 64: 659 – 682.
25. Babu BV and Naidu JM. A demographic profile of four Andhra caste populations. Ind. J. Phys. Anthrop. & Hum. Genet, 1989; 15: 97-102.
26. Rao VV and Murty JS. Mortality load dislosed by Inbreeding in different castes of Andhra Pradesh, Hum. Biol, 1986; 58: 699 – 708.
27. Govinda Reddy P. Effects of Consanguineous Marriages on Fertility and Infant Mortality Among the Reddy and the Mala of Southern Andhra Pradesh, Indian Journal of Physical Anthropology and Human Genetics. 1986; 13:43-49.
28. Veerraju, P. Consanguinity in Tribal communities of Andhra Pradesh. In: Medical Genetics in India. Iswar. C. Verma (ed). Vol 2, Auroma Enterprises, Pondicherry, 1978.
29. Veerraju P. Inbreeding coastal Andhra Pradesh. Proceedings of International symposium of Human Genetics, Waltair, 1973; pp. 309 – 318.
30. Reid RM. Marriage patterns, demography and population genetics in South Indian Caste. A study of inbreeding in human population. Ph.D. thesis, Univ. of Illinoes, Urbana, U.S.A, 1971.
31. Sanghvi LD. Inbreeding in India. Eugen. Quart, 1966; 13: 291 – 301
32. Prakash DSRS. Kiran Deedi M. and Siva Prabodh V. Genetic Load among Four Endogamous Populations of Coastal Andhra Pradesh. Anthropologist, 2010; 12(2): 149-151.
33. Ramana GV, Busi BR, Vishnupriya S and Murty JS. Mortality, Inbreeding, Genetic Load in Rellis: A Subdivided Population of Andhra Pradesh, India. Acta Medica et Biologica, 1999; 47 (3): 103-106
34. Rao VV. Genetic Effect of Inbreeding in Population Groups Under Socio – Cultural Environments. Ph.D. Thesis, Osmania University, Hyderabad, 1984.
35. Srinivasan S. and Mukherjee DP. Inbreeding among some Brahman populations of Tamil Nadu. Hum. Hered, 1976; 26:131–136.
36. Appaji Rao N, Savithri HS, Radha Rama Devi A. and Bittles AH. Consanguinity—a common human heritage? The effects on the health and well-being of Indian populations. In The Indian human heritage (ed. D. Balasubramanian and N. Appaji Rao), 1998; pp. 11–21. Universities Press, Hyderabad.
37. Rao PSS and Inbaraj SG. Inbreeding in Tamil Nadu, South India. Soc. Biol. 1977; 24, 281–288.
38. Crow JF and Kimura M. An introduction to population genetic theory. Harper and Row. New York, 1970