ISSN 0970-9274 ONLINE: ISSN 2456-6608
J Hum Ecol, 55(1,2): 35-40 (2016)
DOI: 10.31901/24566608.2016/55.1-2.05

Consanguinity and Associated Genetic Effects in Five Backward Class Communities of Palakkad District, Kerala

P. Jyothilekshmi[1] and P.M. Mathew[2]

[1]Department of Botany, N.S.S. College, Nemmara 678508, Palakkad, Kerala, India
E-mail: jyothi.lp.thanal@gmail.com
[2]Department of Botany, University of Kerala, Trivandrum 695581, Kerala, India

KEYWORDS Inbreeding. Mating Pattern. Measure. Morbidity. Mortality

ABSTRACT The consanguinity study was carried out in five backward class communities of the Palakkad district in the state of Kerala for assessing and evaluating the inbreeding-related harmful effects in them. Data was collected through random sampling using a structured questionnaire. The major mating patterns observed were first cousin, second cousin, first cousin once removed and uncle-niece types. The frequency of consanguinity in these communities ranged from 12.6 (Vaduka) to 33.3 (Telugu Chetty) percent. Total mortality rates ranged from 13.3 (Muslim) to 21 (Vaduka), and morbidity rates from 5.7 (Ezhava) to 13.3 (Vaduka), and the differentials were consistently significant in either case. The risk effects were positively correlated with degree of relatedness of spouses. It is contented that the magnitude of risk effects of inbreeding incident in the communities could be due to genetic homozygosis of lethal or sub-lethal recessive genes inherited by the consanguineous spouses from their common ancestor.

INTRODUCTION

Marital union involving spouses who are related to each other by common ancestry is referred to as consanguineous. The chance of two related spouses to be carriers of the same recessive lethal genes concealed in heterozygous state is pretty high, and inbreeding would bring them together resulting in higher frequencies of recessive homozygous offspring in blood-related families. Offspring carrying the lethal or sub-lethal recessive genes in homozygous state are prone to meet with developmental hazards *in utero* or after birth, and become non-viable leading to mortality at various pre-reproductive stages, and also succumbing to diverse diseases and congenital defects with genetic predisposition. It is from this expectation that the genetic effects of inbreeding are primarily interpreted and evaluated. The Indian population has a uniquely heterogeneous composition comprising innumerable endogamous castes and communities and hundreds of tribal groups, which differ greatly in culture, tradition, language and religion. (Bhasin and Nag 2012). The pioneering inbreeding studies in the country are those by Dronamraju and Meerakhan (1963) and Sanghvi (1966). Since the 1980s, there has been a spate of interest in consanguinity studies in the south Indian states including Kerala, and the studies have yielded interesting findings highlighting varying degrees of harmful effects of the phenomenon (Mathew et al. 2006; Jyothilekshmi and Sudhakaran 2013, 2014; Sindu and Mathew 2013; Vasanthakumari and Mathew 2013, 2014; Jyothilekshmi 2015; Jyothilekshmi and Mathew 2015; Mathew and Jyothilekshmi 2016). The present paper concerns the results of a consanguinity study carried out in five backward class communities of the Palakkad district in the state of Kerala.

Address for correspondence:
Dr. P. Jyothilekshmi
Associate Professor and Head,
Department of Botany,
N.S.S. College,
Nemmara 678508, Palakkad,
Kerala, India
Phone: 9446475457,
E-mail: jyothi.lp.thanal@gmail.com

MATERIAL AND METHODS

All the five communities studied such as Ezhava, Muslim, Vadukan, Telugu Chetty and Kaikolan belong to the backward class. The Ezhavas by number constitute the largest backward class community in Kerela, and they are believed to be descendants of early migrants from Sri Lanka (Singh 1998). There are two regional groups in Ezhavas, those with concentration in the erstwhile Travancore-Cochin in the south, and those in the north Malabar region. In the 20th century, the renowned sage Sri Narayana

Guru's philosophy influenced and effected reformation in the community, in their socio-religious outlook, and culture. The Muslims of Kerala were the descendant of the Hindu converts in the 7th century (Singh 1998). The religious council, *'Jamat'* supervises their religious and social functions. Inheritance is after the Islamic law, and endogamy is by and large the marriage norm. The Vadukans, meaning 'northerners', form the immigrant community from Andhra Pradesh. The Telugu Chetty is an immigrant community. They are known as '*Janappan*', since these people were specialized in the manufacture of gunny bags from the Hemp (*Janapa*) fiber in the past. Now many of them are merchants or brokers and also engaged in agriculture and other jobs (Singh 1998). They follow Telugu culture and tradition and speak Telugu at home. Kaikolan, the Tamil immigrant community, have their origin in Kanchipuram of Tamil Nadu (Singh 1998). They are specialists in hand weaving, and their name is derived from the Tamil words, *'Kai'* and *'Kol'* associated with hand weaving.

The consanguinity data was collected by door-to-door visits using comprehensive questionnaires, which include a variety of socio-economic, demographic, reproductive and genetic parameters. Random samples of families ranging from 661 to 1173, that is about ten to thirty percent of the total households of the different communities were subjected to the study. Genetic relatedness of the spouses was quantified in terms of the frequency of consanguinity and mean coefficient of consanguinity (F). The frequency of consanguinity is the rate at which all the different patterns together occur, calculated as the percent of the total sample. The mean F is calculated using the formula $F = \Sigma Fc \times n/N$ (Wright 1922), where 'Fc' is the coefficient of consanguinity of different degrees of spousal relationships including the non-consanguineous, 'n' the frequencies of different categories of marriage and 'N' the total number of marriages. The coefficient of consanguinity (Fc) is the probability that a consanguineous offspring is an identical homozygote, which is 1/8 for U-N and DFC, 1/16 for 1C, 1/32 for 1.5C and 1/64 for 2C patterns.

The effects of consanguinity were assessed in terms of pre-reproductive mortality and morbidity. The risk of mortality due to inbreeding was estimated by comparing the prenatal (abortion and still birth), postnatal (neonatal, post neonatal, infant, child and juvenile) and total mortality rates in the case and control groups. The risk of morbidity due to inbreeding was assessed by categorizing the congenital defects in the case and control groups into sensory, mental, physical and diseases, and were analyzed. Since the data of individual morbid conditions were too small, the pooled data was considered for analysis. The data was hand-coded and the Z-test for proportion was used to find the significance of differentials with respect to various parameters.

RESULTS

The common patterns of consanguinity noticed in the five communities in the order of incidence were first cousin (1C), second cousin (2C), first cousin once removed (1.5C) and uncle-niece (U-N) type. The frequency of different patterns by degree of spousal relationship and the computed mean F values are furnished in Table 1. The frequency of consanguinity in them varied from 12.6 (Vaduka) to 33.3 percent (Telugu Chetty) and the corresponding mean Fs ranged from 0.0064 to 0.021. The effect of consanguinity on pre-reproductive mortality and morbidity were analyzed with respect to the de-

Table 1: Pattern, Frequency and mean F in 5 Backward class communities of Palakkad district

S.No.	*Communities*	*C (%)*	*Different patterns (%)*				*Mean F*
			U-N	*1 C*	*1.5 C*	*2C*	
1	Ezhava	27.7	_	24	1.9	1.8	0.016 ± 0.001
2	Muslim	23.1		18.2	2.6	2.3	0.0126± 0.0007
3	Vaduka	12.6	_	9	1.5	2.1	0.0064± 0.0007
4	Telugu Chetty	33.3	6.2	17.6	4.7	4.8	0.021 ± 0.001
5	Kaikolan	31.3	8.2	14.8	3.3	5	0.021 ± 0.002

C: consanguineous U-N: uncle-niece I C: First cousin
1.5C: first cousin once removed F: coefficient of inbreeding
2C: second cousin

gree of spousal relationship, and the data furnished in Tables 2 and 3. The prenatal mortality rates ranged from 9.8 (Muslim) to 15.9 (Kaikolan), while the postnatal rates ranged from 2.8 (Ezhava) to 10.1 (Vaduka). The total mortality profiles ranged from 13.3 (Muslim) to 21 (Vaduka). The mortality differentials were highly significant in all the communities and at all the levels. The morbidity rates ranged from 5.7 (Ezhava) to 13.3 (Vaduka), and the differentials in all five communities were highly significant. The mortality and morbidity profiles showed consistent positive association with the degree of spousal relationship, the uncle-niece group registering the highest rate of mortality (25.4%) and morbidity (17.9%), and the 2C type of families showing the lowest mortality (6.1%) and morbidity (1.6%) incidences.

DISCUSSION

The result of the study shows that the first cousin type union was the most prevalent pattern in all the five backward class communities, with the matrilateral cross cousin sub-type having an edge over the other first cousin sub-types. The south Indian Hindu communities, including many in Kerala have been found to exhibit higher affinity for matrilateral cross cousin type marriages (Krishnamoorthy and Audinarayana 2001; Banerjee and Roy 2002; Sindu and Mathew 2013;

Table 2: Rate of prenatal, postnatal and total mortality in five communities of Palakkad

S. No.	*Community*	*Type of mortality*	*Percentage of mortality*					
			N C F= 0	*UN F=1/8*	*I C F=1/16*	*1.5 C F=1/32*	*2 C F=1/64*	*C Total*
1	*Ezhava*	Prenatal	4.3	-	12.2	10.9	7.5	11.9 **
		Postnatal	0.6	-	2.8	3.5	2.7	2.8 **
		Total	**4.9**	**-**	**14.7**	**14.1**	**10**	**14.4 ** **
2	*Muslim*	Prenatal	3.3	-	10	12.5	4.5	9.8 **
		Postnatal	0.6	-	4.1	4.3	1.6	3.9 **
		Total	**3.9**	**-**	**13.7**	**16.2**	**6.1**	**13.3 ** **
3	*Vaduka*	Prenatal	3.5	-	12.4	16	8.9	12.1 **
		Postnatal	0.7	-	7.1	33.3	9.8	10.1 **
		Total	**4.1**	**-**	**18.6**	**44**	**17.8**	**21.0 ** **
4	*Chetty*	Prenatal	5.4	20.5	13.5	15.8	8.5	14.5 **
		Postnatal	0.4	6.1	0.3	4.3	1.5	3.5 **
		Total	**5.8**	**25.4**	**16**	**19.4**	**9.9**	**17.5 ** **
5	*Kaikolan*	Prenatal	3.8	22.5	12.5	17.3	14.3	15.9 **
		Postnatal	0.7	3.6	4	4.6	2.6	3.7 **
		Total	**4.5**	**25.3**	**16.1**	**21.1**	**16.5**	**19.1 ** **

NC-Non-consanguineous C-Consanguineous UN-Uncle-niece IC-First cousin 1.5C-First cousin once removed 2C-Second cousin ** Significant p<0.01

Table 3: Rate of morbidity by type in seven communities of Palakkad

S. No.	*Community*	*Type of*	*Types of morbidity*				
		Marriage	*Physical*	*Mental*	*Sensory*	*Diseases*	*Total*
		NC	0.8	1.2	2.1	0.3	4.5
1	*Ezhava*	**C**	**1.3 ** **	**2 ** **	**1.2 (NS)**	**1.2 ** **	**5.7 ** **
		NC	0.4	0.6	0.8	0.2	2
2	*Muslim*	**C**	**2.5 ** **	**3.5 ** **	**5.4 ** **	**1.8 ** **	**13.3 ** **
		NC	0.9	1.7	1.7	0.3	4.6
3	*Vaduka*	**C**	**0 (NS)**	**5.6 ** **	**3.1 ** **	**4.6 ** **	**13.3 ** **
		NC	0.5	0.4	0.5	_	1.4
4	*Chetty*	**C**	**1.3 ***	**2.3 ** **	**3.7 ** **	**0.5 ** **	**7.8 ** **
		NC	0.4	0.5	0.4	0.3	1.6
5	*Kaikolan*	**C**	**2.3 ** **	**2.1 ** **	**3.7 ** **	**0.9 ** **	**8.9 ** **

** significant P<0.001 * Significant (p<0.05) NS Not Significant

Vasanthakumari and Mathew 2013; Mathew and Jyothilekshmi 2016). Among the Muslim community studied here, the parallel cousin type, mostly matrilateral, predominated. This is in tune with the tradition followed by their counterparts in other regions of India and also elsewhere, especially the Middle East (Bittles and Hussain 2000; Banerjee and Roy 2002). Uncle-niece union was observed only in the immigrant communities such as Telugu Chetty and Kaikolan. In most communities of Kerala previously studied the uncle-niece pattern was rare (Krishnamoorthy and Audinarayana 2001; Banerjee and Roy 2002; Mathew and Jyothilekshmi 2016). The higher preference of uncle-niece alliances in Kaikolan and Telugu Chetty communities should be due to their strong adherence to the Dravidian tradition and culture in matters of mate selection and kinship ties.

A perusal of the consanguinity data of world population groups shows a wide range of consanguinity rates with less than one percent in the developed countries like USA, Australia and some European countries (Bittles 1998), and fairly high rates of forty to sixty percent among the population groups of north and sub-Saharan Africa, the Middle East countries and South India (Saha et al. 1990; Bittles 1998), to a highest of over seventy percent in some tribal groups of Kerala (Mathew et al. 2006; Sindu and Mathew 2013). The rate of inbreeding in the present five communities ranged from a lowest of 12.6 in Vaduka to highest of 33.3 in Telugu Chetty and the correspondingly varying mean coefficient of inbreeding values (F), ranged from 0.0064 to 0.021. Mathew et al. (2006) have arbitrarily classified the inbreeding rates in the Kerala communities under five classes such as <10, 10-30, 30-50, 50-70 and >70. In most of the Hindu forward and backward class communities, the inbreeding rates fall under the ten to thirty percent class. The present five backward groups also come under this category. The uneven distribution of consanguinity among various population groups across the world and also in Kerala is found to be strongly associated with a myriad of socioeconomic and demographic factors such as education, occupation, family income, age of spouses, year of marriage of spouses and age at marriage (Mathew et al. 2006; Bittles 2012).

Risk effects of consanguinity are assessed in terms of pregnancy outcomes such as mortality and morbidity. The consanguinity studies carried out among different population groups the world over have revealed varying outcomes in mortality profiles, some indicating harmful effects, while others no effect and still others even beneficial effects (Stoltenberg 2009; Tadmouri et al. 2009; Bittles 2012). The present result reveals a positive association of consanguinity with mortality, both in prenatal and postnatal levels, in all the five communities. Significantly higher rates of prenatal mortality occurring in the inbred communities of different world population groups have been variously explained such as, increase in homozygosity of recessive lethals that cause growth retardation and growth defects in the fetus (Stoltenberg 2009; Bittles 2012), the effect of additive poly genes that induce elevated fetal loss (Stoltenberg 2009), the sharing of common human leukocyte antigen (HLA) by related spouses in turn negatively influencing development of fetus causing recurrent abortions, and the gynecological immaturity associated with the consanguineous mothers of very young ages causing elevated fetal loss (Bittles 2012). Among the present communities the differentials of postnatal mortality rates were also highly significant. A comparison of incidence of pre- and postnatal mortality shows an excess risk for the latter. Such a situation was reported in studies previously in Kerala and elsewhere. The reasons proposed for the increased risk for postnatal mortality are genes responsible for prenatal mortality are less in the populations (Kaku and Freira-Maia 1992), the developing fetus is protected against genes causing fetal impairment (Schull and Neel 1972), less prenatal operation of lethal genes, and the level of homozygosity in the mother rather than that in the fetus is responsible for fetal death (Bittles 2012). The total mortality, which is the sum of both pre- and postnatal mortality, is significantly higher in the consanguineous spouses, and the differentials were consistently higher in all the five communities. The risk of total mortality is more than four times higher in consanguineous unions compared to the non-consanguineous. The mortality rates are found to be higher in closer degree unions in the Telugu Chetty (25.4%) and Kaikolan communities (25.3%), while lowest rates in the second cousin unions (6.1%). Similar results were reported in other population groups, for which the explanation given is the perfect correlation between the relative increase in the risk of mortality with the degree of spou-

sal relationship due to the monogenic lethal recessive genes that are culpable for mortality (Harlep et al. 2008; Stoltenberg 2009; Bittles 2012). This could be apparently applicable to the present group of communities also.

The practice of consanguinity is known to trigger various monogenic autosomal recessive disorders, and this being attributed to the susceptibility to various diseases (Kaku and Freire-Maia 1992; Stoltenberg 2009; Bittles 2012). The morbidity profiles noticed in all the present communities are by and large significantly higher in the inbred groups. Many studies have pointed out increased incidence of different rare recessive autosomal disorders in consanguineous societies (Harlap et al. 2008; Tadmouri et al. 2009). There was also a positive association of morbidity incidence with degree of spousal relatedness. Great bulk of the previous studies in the Indian subcontinent as well as from other parts of world has documented the same trend (Harlep et al. 2008; Stoltenberg 2009; Tadmouri et al. 2009; Mathew and Jyothilekshmi 2016).

CONCLUSION

The degree and magnitude of harmful effects incident in the present inbred group of communities observed in terms of pre-reproductive mortality and morbidity are primarily genetic in nature brought out by consanguineous unions, which led to genetic homozygosis of lethal and sub-lethal recessive genes inherited by the related spouses. The study revealed that several factors both genetic and non-genetic are involved in the increased incidence of detrimental conditions. Non-genetic factors include socioeconomic backwardness and illiteracy, which was singularly evident in the socioeconomically backward communities.

RECOMMENDATIONS

Necessary genetic counseling programs and literacy promotions are to be planned and implemented among the socioeconomically poor and illiterate backward communities in a bid to disseminate proper awareness of the risk effects of inbreeding.

ACKNOWLEDGEMENTS

The researcher is grateful to the University Grants Commission for financial assistance under the Faculty Improvement Program.

REFERENCES

Banarjee SK, Roy TK 2002. Parental consanguinity and offspring mortality: The search for possible linkage in the Indian context. *Asia-Pacific Population J*, 17: 17-38.

Bhasin MK, Nag S 2012. Consanguinity and its effects on fertility, mortality and morbidity in the Indian region: A review. *Int J Hum Genet*, 12: 197-301.

Bittles AH 1998. Empirical Estimates of the Global Prevalence of Consanguineous Marriage in Contemporary Societies. Morrison Institute for Population and Resource Studies, *Working Paper* 0074, Stanford University, Stanford.

Bittles AH 2012. *Consanguinity in Context*. Cambridge: Cambridge University Press.

Bittles AH, Hussain R 2000. An analysis of consanguineous marriage in the Muslim population of India at regional and state levels. *Ann Hum Biol*, 27: 163-171.

Dronamraju KR, Meerakhan P 1963. The frequency and effects of consanguineous marriages in Andhra Pradesh people. *J Genet*, 58: 387.

Harlap S, Kleinhaus K, Perrin MC, Calderon-Margalit R, Paltiel O, Deutsch L, Manor O, Tiram E, Yanetz R, Friedlander Y 2008. Consanguinity and birth Defects in the Jerusalem Perinatal Study Cohort. *Hum Hered*, 66: 180-189.

Jyothilekshmi P 2015. Consanguinity study in the immigrant Tamil Brahmins of Palakkad district, Kerala. *J Cytol Genet*, 16: 31-37.

Jyothilekshmi P, Mathew PM 2015. Impact of consanguinity on the fertility profiles of some inbreeding communities of Palakkad district, Kerala. *J Cytol Genet*, 16: 55-60.

Jyothilekshmi P, Sudhakaran MV 2013. Genetic effects of consanguinity in Eravallan tribal community of Palakkad district of Kerala. *J Cytol Genet*, 14: 83-89.

Jyothilekshmi P, Sudhakaran MV 2014. Does Inbreeding Lead to Increased Fertility, Mortality and Morbidity Among the Tribes of Attappady of Palakkad district? *26th Kerala Science Congress*, January 28-31, Wayanad, Kerala.

Kaku M, Freire-Maia N 1992. Inbreeding effect on mortality: IV. Further data in Brazilian populations. *Am J Med Genet*, 42: 420-423.

Krishnamoorthy S, Audinarayana N 2001. Trends in consanguinity in South India. *J Biosoc Sci*, 33: 185-197.

Mathew PM, Jyothilekshmi P 2016. *Fundamentals of Population Genetics with Emphasis on Human Inbreeding*. Trivandrum: Southern Book Stall.

Mathew PM, Vijayavalli B, Devipriya V 2006. Consanguinity and its effects with special reference to inbreeding communities of Kerala. *J Cytol Genet*, 7: 185-195.

Saha N, Hamad RE, Mohamed S 1990. Inbreeding effects on reproductive outcome in a Sudanese population. *Hum Hered*, 40: 208-212.

Sanghvi LD 1966. Inbreeding in India. *Eugen Quart*, 13: 291-301.

Schull WJ, Neel JV 1972. The effects of parental consanguinity and inbreeding in Hirado, Japan. V. Summary and interpretation. *Am J Hum Genet*, 24: 425-453.

Sindu N, Mathew PM 2013. Genetic Implication of Excessive Incidence of Infant/ Child Mortality Among the Tribals of Kerala. *16th All Kerala Congress of Cytol Genet Nat Symp, Dept of Botany,* Kerala University, 15 December.

Singh KS 1998. *People of India: Kerala, Vol XXVII. Part I, II and III*. Delhi: Oxford University Press.

Stoltenberg C 2009. Commentary: Of the same blood. *In J Epidemiol*, 38: 1442-1447.

Tadmouri GO, Nair P, Obeid T, Al-Ali MT, Al-Khaja N, Hamamy HA 2009. Consanguinity and reproductive health among Arabs. *Reprod Health*, 6: 1-9.

Vasanthakumari B, Mathew PM 2013. Time and temporal trends and risk effects of inbreeding in 15 communities of Kanyakumari District, Tamil Nadu. *J Cytol Genet*, 14: 53-61.

Vasanthakumari B, Mathew PM 2014. Public health impact of inbreeding in 15 communities of Kanyakumari District, Tamil Nadu. *J Cytol Genet*, 15: 39-43.

Wright S 1922. Coefficients of inbreeding and relationship. *Am Nat*, 56: 330-338.

Paper received for publication on January 2016
Paper accepted for publication on July 2016