***Original Research Article***

**Consanguinity and Its Health Impacts on Human Populations: Insights from Animal Inbreeding**

**Abstract**

Inbreeding is a customary practice in South India, often involving consanguineous marriages that increase genetic homozygosity and the risk of recessive disorders. This population-based cross-sectional study assessed the prevalence, degrees, and genetic consequences of consanguinity among 6,518 families using stratified random sampling. The results showed a consanguinity rate significant over generations (P < 0.0001). While first-cousin and maternal-uncle marriages persist, their prevalence has over time. The study highlights trend in consanguineous marriages across generations in the Sivagangai district, likely due to increased awareness of genetic risks and evolving societal norms. However, consanguinity remains prevalent, particularly among older generations, reflecting historical endogamous practices. The findings also reveal a higher prevalence of adult diseases, including diabetes (63.2%), heart disease (88.5%), and hearing deficits (88.2%), among individuals from consanguineous unions, reinforcing the genetic risks associated with close-kin marriages. Increasing awareness through genetic counseling, health education, school programs, medical screening, and policy interventions is crucial to mitigating the adverse effects of consanguinity while respecting cultural traditions.

**Keywords:** Consanguinity, inbreeding, genetic risks, Sivagangai population, endogamous marriage, hereditary disorders

**Introduction:**

Inbreeding is one of the intra-familial customary and cultural practices among the populations of South India. It involves the marriage between closely structured related individuals [6] and studied the consequences of biological and social systems and highlighted their significant impact on child health, reproductive outcomes, mortality, morbidity, and mental health. One of its key benefits is the promotion of homozygosity in offspring, which helps preserve advantageous genetic traits in human population [1,2]. Inbreeding leads to an increased probability of offspring inheriting identical alleles from both parents. This increased homozygosity is particularly relevant in selective breeding, where desirable traits are maintained over generations. Studies have consistently shown that each successive increase in inbreeding leads to a proportional decrease in offspring performance, survival, and fertility [3,4,5]. Since the mating partners share a close genetic relationships, the resulting offspring has higher levels of identity-by-descent (IBD) sharing and identical genetic segments from both maternal and paternal lineages. The relatively recent nature of the shared ancestry limits recombination, preserving large genomic segments in an unaltered form [7]. Such genetic continuity may be beneficial in stabilizing inherited traits, it also amplifies recessive genetic disorders, making inbred populations more vulnerable to disease susceptibility and reduced genetic diversity. The effects of inbreeding extend beyond human populations and have been extensively documented in animals. For instance, studies on wood frog (Rana sylvatica) larvae demonstrated that inbreeding significantly reduces survival in the wild, whereas it had no impact on growth or development under controlled laboratory conditions [8]. This suggests that inbreeding depression the reduction in biological fitness. Both field and laboratory research confirm that in small and isolated populations, inbreeding negatively affects fitness, fertility, growth rates, and overall survival, ultimately leading to population decline and increased extinction risk [9,10,11,12,13]. Many species have evolved mechanisms to avoid inbreeding, particularly those that frequently encounter close kin such as olfactory signals aid in kin recognition among Belding’s ground squirrels (Spermophilus beldingi) and ring-tailed lemurs (Lemur catta) [14,15,16]. House mice (Mus musculus) that live in dense, family-based social groups are more likely to encounter and recognize kin, while Macedonia mice (Mus macedonicus) living in low-density populations have fewer kin interactions. House mice exhibit high variability in urinary proteins, aiding kin recognition, whereas Macedonia mice lack such variability [17,18,19].

 The Westermarck effect [22] suggests that children raised together, regardless of biological relation, develop an aversion to sexual relationships with each other [20]. found that early childhood co-residence, particularly from birth to six years of age, was a key factor in sexual aversion during adolescence and adulthood, a finding later supported by Luo [21]. However, the mechanisms preventing incestuous relationships between parents and offspring or between uncles/aunts and their nieces/nephews are less well understood. It is likely that social learning and societal norms play a crucial role in reinforcing incest taboos beyond the biological mechanisms observed in sibling relationships.

In South India, such marriages constitute a significant proportion of all unions, with rates differing across communities. Further cross-cultural studies are necessary to evaluate how different societies regulate incest avoidance and how social learning influences these prohibitions across cultures. In the present study was aimed to evaluate the impact of endogamous marriage on the genetic continuity, and potential hereditary risks of decent offspring.

**Methodolgy**

The current study was a population-based cross-sectional study on the prevalence, degrees and genetic consequences of endogamy using standard methods established by Abdulbari Bener et al., [26]. A total of 6,518 families were selected using a stratified random sampling method to determine the degree of consanguinity. Data were collected through face-to-face interviews conducted in the local language, following standard research protocols. The relationship between spouses was recorded, including whether their parents were consanguineous. Marriages between relatives were classified into six groups, double first cousins, first cousins, first cousins once removed, second cousins, third cousins (less than second cousins), and non-consanguineous marriages [27]. A structured questionnaire was used to gather details on marriage patterns, health history, and socio-cultural perceptions of consanguineous marriage. Additionally, survey data were collected to assess the prevalence of inherited disorders. Statistical analysis included descriptive methods to determine the prevalence of consanguinity and its associated health conditions. Ethical considerations were strictly followed, with informed consent obtained from all participants to ensure confidentiality and compliance with institutional ethical guidelines. The study was approved by the Institutional Ethical Committee of Raja Doraisingam Government Arts College, Sivagangai.

**Result**

Among the selected population (6518), 1567 were found to be a consanguineous couple and 4951 non-consanguineous couple in the parental generation. In the total population, 30.18 % couples were recorded as consanguineous and 69.86 % non-consanguineous.

**Figure 1: Prevalence of Consanguinity and Non-Consanguinity Across Parental Lineages.**

The Figure 1 illustrates the rate of consanguinity by categorizing individuals into Consanguineous and Non-consanguineous groups based on three parental categories. P (Parents) represents direct parental relationships, with 1567 individuals in the consanguineous group and 4951 in the non-consanguineous group. MGP (Maternal Grandparents) reflects the influence of the maternal lineage, showing 1968 consanguineous cases and 4556 non-consanguineous cases. PGP (Paternal Grandparents) represents the paternal lineage contribution, with 2371 individuals in the consanguineous group and 4147 in the non-consanguineous group.

The analysis of marriage patterns across two generations, Parents (P), Maternal Grandparents (MGP), and Paternal Grandparents (PGP) reveals a significant decline in consanguineous marriages over time (P < 0.0001). The parental generation shows the lowest consanguinity rate (8.01%), reflecting increased awareness of genetic risks and shifting societal norms. In contrast, the MGP and PGP generations had higher consanguinity rates (10.03% and 12.13%, respectively), indicating a historical preference for endogamous unions. Concurrently, non-consanguineous marriages have increased, with 25.32% in the parental generation, compared to 23.30% in MGP and 21.21% in PGP (Table 1).

**Table 1: Prevalence of consanguinity among current generation and parental generation.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | *P* | *MGP* | *PGP* |
| *Consanguineous* | **1567****(8.01%)** | **1962****(10.03%)** | **2371****(12.13%)** |
| *Non-consanguineous* | **4951****(25.32%)** | **4556****(23.30%)** | **4147****(21.21%)** |
| *Percentage of consanguinity* | **8.01%** | **22.16%** |

The degree of consanguinity across two generations the current generation, husbands' parents, and wives' parents, categorized into non-consanguineous marriages, first cousin, maternal uncle, second cousin, and first cousin once removed. (Figure 2). The data highlights a clear preference for non-consanguineous marriages across all three generations non-consanguineous marriages are the most common, with 4951 in the current generation, 4556 in the husband's parents, and 4147 in the wife's parents, showing a decline over time. First cousin marriages are less frequent, with 657 in the current generation, 256 in the husband's parents, and 371 in the wife's parents.

**Figure 2:The degree of consanguinity across three generations**.

Maternal uncle marriages were more common in the wife's parents (1162) but have declined in the husband's parents (924) and the current generation (322). Second cousin marriages remain low, recorded at 305 in the current generation, 403 in the husband's parents, and 456 in the wife's parents. Similarly, first cousin once removed marriages show a slight decline, with 283 in the current generation, 379 in the husband's parents, and 382 in the wife's parents.

**Figure 3: Percentage of adult diseases among the Non-consanguineous and consanguineous individuals.**

The (figure 3) pie chart compares the percentage of adult diseases in non-consanguineous and consanguineous population. It highlights that 58.3% of adult diseases were found among individuals of consanguineous, while 41.7% of non-consanguineous unions. This suggests a higher prevalence of adult diseases in consanguineous populations, which could be attributed to the increased genetic risks associated with consanguinity.

Diabetes Mellitus and Heart Diseases showed a higher percentage of prevalence in consanguineous (C) groups across all generations, suggesting a strong hereditary component (Table 2).

|  |  |  |  |
| --- | --- | --- | --- |
| Adult Diseases | Parent | Maternal Grand Parent | Paternal Grand Parent |
| **C** | **NC** | **C** | **NC** | **C** | **NC** |
| Diabetes Mellitus | 65 | 69 | 82 | 63 | 98 | 57 |
| Hypertension | 33 | 73 | 41 | 67 | 49 | 61 |
| Asthma | 11 | 19 | 14 | 17 | 17 | 16 |
| Heart Diseases | 87 | 20 | 109 | 19 | 131 | 17 |
| Mental Disorders | 9 | 24 | 11 | 22 | 14 | 20 |
| Blood Disorders | 2 | 1 | 1 | 0 | 2 | 1 |
| Cancer | 5 | 7 | 6 | 6 | 7 | 6 |
| Hearing Deficit | 10 | 3 | 13 | 2 | 15 | 2 |
| GI Disorders | 2 | 3 | 1 | 3 | 2 | 2 |

Diabetes Mellitus in paternal grandparents is significantly higher in consanguineous cases (63.2%) compared to non-consanguineous (36.8%), while Heart Diseases also exhibit a similar pattern (C: 88.5%, NC: 11.5%). In contrast, Hypertension follows a reverse trend, with non-consanguineous cases being more common, particularly among parents (C: 31.1%, NC: 68.9%), indicating potential environmental or lifestyle influences. Asthma, Mental Disorders, and Cancer show minimal differences between C and NC groups, suggesting a complex interaction between genetic and environmental factors. Blood complaints and Hearing Shortfalls are more frequent in consanguineous cases, with a markedly high prevalence of Hearing Deficit among paternal grandparents (C: 88.2%, NC: 11.8%), reinforcing the association between consanguinity and recessive disorders. Meanwhile, GI Disorders display no major difference between the groups, indicating a weaker genetic correlation.

Discussion:

Consanguineous marriages have been practiced for hundreds of years in many communities throughout the world Jaber et al., (1998). This intra-familial unions is collectively account for 20 – 50% of all marriages (Bittles 2011), Hamamy et al., (2011) and Tadmouri et al., (2009). The rate of consanguinity differs in different countries. Consanguineous marriage is one of the traditional practices in most of the communities of North Africa, Middle East and West Asia. The study by Santosh Kumar Sharma et al.,[32] based on NFHS-4 data (2015–16), highlights that approximately 10% of all marriages in India were consanguineous, with 45,057 such marriages reported among 456,646 ever-married women. Regional variations were significant, with the highest prevalence in South India, particularly in Andhra Pradesh and Tamil Nadu (29.5% each), followed by Karnataka (23.8%) and Telangana (22.0%). In contrast, consanguinity was least common in the North-East, with Tripura recording the lowest rate at 0.2%. The South exhibited the highest overall consanguinity rate at 23.6%, with first-cousin marriages being the most common (20.5%), while uncle-niece marriages were notably high in Pondicherry (54.9%). Kerala stood out for its strict avoidance of consanguineous marriages. Northern and eastern states had lower prevalence, except Jammu and Kashmir, which recorded 16%. Tamil Nadu and Lakshadweep reported the highest inbreeding levels, reaching 33%, with the Arcot district of Tamil Nadu showing the highest frequency of cognate marriages. Sahoo et al., [33] studied consanguineous marriage prevalence in South India, revealing significant regional variations. In Tamil Nadu, Sivagangai district reported a consanguinity rate of 36.9%, ranking among the higher-prevalence areas. It was slightly lower than Pudukkottai (37.2%) but higher than neighboring districts like Tiruchirappalli (36.2%) and Dindigul (32.2%). This indicates a strong cultural preference for endogamous marriages in Sivagangai, aligning with trends observed in many inland districts of Tamil Nadu. The data highlight how consanguinity remains prevalent in certain regions, particularly in rural and semi-urban areas, while coastal and urban districts show lower rates. The current study focuses on Sivagangai district, analyzing a randomly selected population of 6,518 families. The parental generation exhibits the lowest consanguinity rate (8.01%), suggesting a shift towards non-consanguineous marriages due to increased awareness of genetic risks and changing societal norms. In contrast, the MGP (10.03%) and PGP (12.13%) generations had higher consanguinity rates, reflecting a historical preference for endogamous unions. Worldwide, more than 130 million infants are born annually, with approximately 13.5 million born to inbred parents [34]. Consanguineous marriage (CM) is strongly associated with autosomal recessive disorders and birth defects in offspring [35,36,37]. In the previous cross-sectional study conducted in Sivagangai Taluk, which has a diverse native population, several significant associations were observed between various health conditions and the outcomes of interest. For diabetes mellitus, the odds ratio (OR) was 8.75 with a 95% confidence interval (CI) of 6.34–12.09 and a p-value of 0.02, indicating a notable relationship. Similarly, hearing impairment showed a strong association with an OR of 22.53 (95% CI: 15.17–33.47, p = 0.0006), while epilepsy exhibited an OR of 26.48 (95% CI: 18.63–37.63, p = 0.001). Limb defects also demonstrated a significant association (OR = 18.24, 95% CI: 10.99–30.26, p = 0.0108), whereas eye defects showed no significant relationship with the outcome (p = 0.319, OR = 14.44, 95% CI: 9.53–21.87). In this study, non-consanguineous marriages have increased, accounting for 25.32% in the parental generation, compared to 23.30% in MGP and 21.21% in PGP, indicating a gradual decline in consanguineous practices across generations. However, the study also highlights the impact of consanguinity on adult disease prevalence in Sivagangai. Among individuals from consanguineous unions, 58.3% were affected by adult diseases, compared to 41.7% among those from non-consanguineous unions. This suggests a higher prevalence of adult diseases in consanguineous populations, likely due to the increased genetic risks associated with close-kin marriages. Raising awareness through genetic counseling, health education, school initiatives, medical screening, and policy interventions is essential for reducing the health risks associated with consanguinity while preserving cultural sensitivities.

Conclusion:

The study highlights a declining trend in consanguineous marriages across generations in Sivagangai district, likely due to increased awareness of genetic risks and evolving societal norms. However, consanguinity remains prevalent, particularly in older generations, reflecting historical endogamous practices. The findings also reveal a higher prevalence of adult diseases, such as diabetes mellitus and heart diseases, among individuals from consanguineous unions, reinforcing the genetic risks associated with close-kin marriages.

**COMPETING INTERESTS DISCLAIMER:**

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

**Reference**

1. Bittles, A. H., Mason, W. M., Greene, J., & Rao, N. A. (1991). Reproductive behavior and health in consanguineous marriages. Science, 252(5007), 789–794.
2. Munir Ahmad Bhinder, Haleema Sadia, Nasir Mahmood, Muhammad Qasim, Zawar Hussain, Muhammad Mudassar Rashid, Muhammad Yasir Zahoor, Rashid Bhatti, Wasim Shehzad, Ali Muhammad Waryah, Shah Jahan, Consanguinity: A blessing or menace at population level, Annals of Human Genetics, 2019 https://doi.org/10.1111/ahg.12308.
3. Gurnani, M. et al. (1971). Indian Journal of Dairy Science 24: 217-221.
4. Khanna, A. S. et al. (1980). Indian Journal. Animal Science 50: 667-680.
5. Patel, A. N. et al. (2001). Indian Journal of Dairy Science 54: 91-95.
6. Dweep C Sing, Divyani Khurana and Ravinder Sing, Inbreeding to Consanguineous: Is it a beneficial trajactory?, International Journal of Research in Socialogy and Social Anthropology, 2013, 1(3) : 59-74.
7. Alissa L Severson , Shai Carmi , Noah A Rosenberg, The Effect of Consanguinity on Between-Individual Identity-by-Descent Sharing, Genetics. 2019, 212(1):305–316. doi: 10.1534/genetics.119.302136.
8. Halverson, M. A., Skelly, D. K., & Caccone, A. (2006). Inbreeding Linked to Amphibian Survival in the Wild but Not in the Laboratory, Journal of Heredity 97(5): 499–507.
9. Saccheri, I., Kuussaari, M., Kankare, M., Vikman, P., Fortelius, W., & Hanski, I. (1998). Inbreeding and extinction in a butterfly metapopulation. Nature 392: 491–494.
10. Keller, L. F. & Waller, D. M. (2002). Inbreeding effects in wild populations. Trends in Ecology & Evolution 17: 230–241.
11. Rowe, G., & Beebee, T.J.C. (2003). Population on the verge of a mutational meltdown? Fitness cost of genetic load for an amphibian in the wild. Evolution 57: 177–18.
12. Frankham, R. (2005). Stress and adaptation in conservation genetics. Journal of Evolutionary Biology 18: 750–755.
13. Wright, L. I., Tregenza, T., & Hosken, D.J. (2008). Inbreeding, inbreeding depression and extinction. Conservation Genetics 9: 833–843.
14. Mateo, J. M. (2002). Kin-recognition abilities and nepotism as a function of sociality. Proceedings of the Royal Society of London 269: 721–727.
15. Charpentier, M. J. E., Boulet, M., & Drea, C. M. (2008). Smelling right: the scent of male lemurs advertises genetic quality and relatedness. Molecular Ecology 17: 3225–3233.
16. Charpentier, M. J. E., Crawford, J. C., Boulet, M., &Drea, C. M. (2010). Message 'scent': lemurs detect the genetic relatedness and quality of conspecifics via olfactory cues. Animal Behaviour 80: 101-108.
17. Barnard, C. J., Hurst, J. L., & Aldhous, P. (1991). Of mice and kin—the functional significance of kin bias in social behaviour. Biological Reviews of the Cambridge Philosophical Society, 66: 379–430.
18. Sherborne, A. L., Thom, M. D., Paterson, S. et al. (2007). The genetic basis of inbreeding avoidance in house mice. Current Biology 17: 2061–2066.
19. Beynon, R. J., Turton, M. J., Robertson, D. H. L. et al. (2007). Urinary lipocalins in Rodenta: is there a generic model? In Chemical Signals in Vertebrates (eds) Hurst, J. L., Beynon, R. J., Roberts, S. C. & Wyatt, T., 11, 37–50, Springer, New York.
20. Shepher, J. (1971). Mate selection among second generation kibbutz adolescents and adults: Incest avoidance and negative imprinting. Archives of Sexual Behaviour 1: 293-307.
21. Luo, L. (2011). Is there a sensitive period in human incest avoidance? Evolutionary Psychology 9(2): 285-295.
22. Westermarck, E. (1891). The History of Human Marriage. London: Macmillan and Co.
23. Rothwell, Norman V. (1978). Human Genetics. New Delhi: PHI Private Limited.
24. Gipson, T.A. (2002). Preliminary Observations: Inbreeding in Dairy Goats and Its Effects on Milk Production. Pages 51-56 in Proc. 17th Ann. Goat Field Day. Langston, OK: Langston University.
25. Subalakshmi , Jepa Chandra Mohan, Impact of Kinship on the Chosen Autosomal Anomalies in Sivagangai, Tamil Nadu, India.Indian Journal of Public Health Research & Development, January 2020, Vol. 11, No. 01.h & Development, January 2020, Vol. 11, No. 01. 10.37506/v11/i1/2020/ijphrd/193894.
26. Bener, A., & Alali, K. A. (2006). Consanguineous marriage in a newly developed country: the Qatari population. Journal of Biosocial Science, 38(2), 239-246 DOI: 10.1017/S0021932004007060.
27. Bener, A., Hussain, R., Teebi, A. S., & Consanguineous Marriages and Their Effects on Common Adult Diseases: Studies from an Endogamous Population. Medical Principles and Practice, 16(4), 262-267 Doi: <https://doi.org/10.1159/000102147>.
28. Jaber, L., Halpern, G. J., & Shohat, T. (1998). The impact of consanguinity worldwide. Community Genetics, 1(1), 12-17. This study explores the global practice of consanguineous marriages and their implications for genetic disorders.
29. Bittles, A. H. (2011). Consanguinity: global perspectives and implications for genetic disease risk. Nature Reviews Genetics, 12(3), 175-178. Bittles provides a comprehensive overview of the prevalence of consanguineous marriages and discusses the associated risks of genetic diseases.
30. Hamamy, H., Antonarakis, S. E., Cavalli-Sforza, L. L., Temtamy, S., Romeo, G., Kate, L. P., Bennett, R. L., Shaw, A., Megarbane, A., van Duijn, C., & Bittles, A. H. (2011). Consanguineous marriages, pearls and perils: Geneva International Consanguinity Workshop Report. Genetics in Medicine, 13(9), 841-847.
31. Tadmouri, G. O., Nair, P., Obeid, T., Al Ali, M. T., Al Khaja, N., & Hamamy, H. A. (2009). Consanguinity and reproductive health among Arabs. Reproductive Health, 6, 17.
32. Santosh Kumar Sharma, Mir Azad Kalam, Saswata Ghosh and Subho Roy. Prevalence and determinants of consanguineous marriage and its types in India: evidence from the National Family Health Survey, 2015–2016.Journal of Biosocial Science (2020), page 1 - 11.doi:10.1017/S0021932020000383.
33. Harihar Sahoo, Paramita Debnath, Chaitali Mandal, R. Nagarajan ,Sathiyasusuman Appunni. Changing Trends of Consanguineous Marriages in South India, Journal of Asian and African Studies.1–17 (2021) DOI: 10.1177/00219096211012017.
34. Teeuw, ME, Henneman, L, Bochdanovits, Z, Heutink, P, Kuik, DJ, Cornel, MC and Kate, LPT (2010) Do consanguineous parents of a child affected by an autosomal recessive disease have more DNA identical-by-descent than similarly-related parents with healthy offspring? Design of a case–control study. BMC Med Genet 11, 113.10.1186/1471-2350-11-113.
35. Fareed, M and Afzal, M (2017) Genetics of consanguinity and inbreeding in health and disease. Annals of Human Biology 44, 99–107.10.1080/03014460.2016.1265148.
36. Anwar, S, Mourosi, JT, Arafat, Y and Hosen, MJ (2020) Genetic and reproductive consequences of consanguineous marriage in Bangladesh. PLOS ONE 15, e0241610.10.1371/journal.pone.0241610.
37. Sharma, SK, Kalam, MA, Ghosh, S and Roy, S (2021) Prevalence and determinants of consanguineous marriage and its types in India: evidence from the National Family Health Survey, 2015–2016. Journal of Biosocial Science 53, 566–576.10.1017/S0021932020000383.