Impact of consanguinity on spontaneous pregnancy loss and descendants' health in north Morocco

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Abstract

Purpose – The present study aims to bring out the impact of consanguinity on spontaneous pregnancy loss (SPL) and on descendants' health, among the population of north Morocco.

Design/methodology/approach – Convenience sampling was used for collecting data. A questionnaire was randomly administered to 385 couples represented by either the husband, the wife or both. The study lasted for three months, from January to March 2015.

Findings – In total, 238 valid questionnaires were analysed. The results showed that the consanguinity rate was 45.23% and that most consanguineous unions were between first cousins (91%). Data analysis revealed that SPL risk was similar in consanguineous and non-consanguineous couples (OR = 1.6; IC95% = 0.9–2.9). Also, no significant difference was observed in terms of SPL type (OR = 1.6; IC95% = 0.7–3.9) and frequency ($p = 0.81$). However, late SPL frequency was significantly lower in consanguineous couples ($p < 0.001$), whereas no significant difference was registered in terms of early SPL frequency ($p = 0.73$). On the other hand, consanguineous couples displayed a significantly higher risk of descendants' health disorders in comparison with non-consanguineous ones. Moreover, the consanguineous couples had a significantly higher number of children with health disorders ($p < 0.001$). The risk analysis also showed that consanguineous couples displayed a significantly higher risk of congenital malformations (OR = 7.23; IC95% = 3.52–14.84) and multifactorial diseases (OR = 3.72; IC95% = 1.46–9.49), but no significant difference was observed in terms of behavioural disorders risk.

Originality/value – The population awareness regarding the negative effects of consanguinity should be raised through education programmes and premarital, prenatal and genetic counselling services.

Keywords Consanguinity, Risk, Spontaneous pregnancy loss, Health disorders, North Morocco

Paper type Research paper

Introduction

Consanguinity consists in non-random marriages that result from the union between blood-related individuals, having at least one common ancestor. Consanguineous marriages are still very common in certain areas of the world. In fact, about 20% of the population live in consanguineous communities (Tadmouri *et al.*, 2009). In Morocco, several studies have shown that consanguinity remains a common, social and privileged practice justified by emotional

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and financial security (Hami, Soulaymani, & Mokhtari, 2006; Latifi, Sbii, & Hami, 2010; Talbi, Khadmaoui, Soulaymani, & Chafik, 2008).

This type of non-random marriage can be seen all over the different ethnic and religious groups and is due to socio-economic, religious, demographic and cultural factors (El Goundali *et al.*, 2022; Talbi *et al.*, 2008; Bittles, 2008; Bittles, 2001; Hamamy and Bittles, 2009; Jabeen and Malik, 2014; Hussain and Bittles, 2000).

Certain research revealed some consanguinity-positive effects, such as homozygosity of alleles in offspring which preserves the advantageous genetic traits in human as well as animal populations (Bhinder *et al.*, 2019) and increases gross fertility (Bittles, Mason, Greene, & Rao, 1991). Moreover, consanguinity has been reported to protect against breast cancer, multiple sclerosis and malaria (Medimegh *et al.*, 2015; Maghzi, Shaygannejad, Minagar, Hassanzadeh, & Maghzi, 2016; Denic and Nicholls, 2007; Bener, Ayoubi, Ali, Al-Kubaisi, & Al-Sulaiti, 2010).

Nevertheless, the negative effects of consanguinity seem to be more important. Indeed, it reduces inter and intra-population genetic variability, which increases the abnormalities caused by the appearance of deleterious genes in these groups (Mohamed *et al.*, 2022; Solignac, Periquet, Anxolabehere, & Petit, 1995). As a result, such marriages have a significant implication in recessive diseases and can increase polygenic or multifactorial diseases, sterility, spontaneous pregnancy loss (SPL), stillbirths, child deaths, infant mortality, as well as congenital malformations (Romdhane *et al.*, 2019; Temaj, Nuhii, & Sayer, 2022; Lal *et al.*, 2016; Alharbi *et al.*, 2020; Emery, 1976; Motulsky and Vogel, 1982; Zlotogora, 1991).

In this context, the present work aims to bring out the impact of consanguinity on SPL, which refers to pregnancy loss at less than 20 weeks' gestation in the absence of elective medical or surgical measures to terminate the pregnancy (Scroggins, Smucker, & Krishen, 2000), as well as on descendants' health, among the population of Tanger-Tetouan-Al Hoceima region.

What makes investigating consanguinity interesting in this region of Morocco is the limited number of previous similar research.

Materials and methods

The region of Tanger-Tetouan-Al Hoceima is located in the extreme northwest of Morocco over an area of 17,262 km^2. It is limited to the north by the Strait of Gibraltar and the Mediterranean, to the west by the Atlantic Ocean, to the south-west by the Rabat-Salé-Kenitra region, to the south-east by the Fes-Meknes region and to the east by the Oriental region.

In 2014, the regional urban environment was home to 2,131,725 inhabitants, compared to 1,425,004 in rural areas. Thus, 93.9% of the increase in the regional population during the period 2004–2014 is due to the increase in the urban population. Indeed, the annual urban population growth rate is 2.45% against only 0.21% in rural areas [1].

We used convenience sampling for collecting data. This is a non-probabilistic technique frequently used in quantitative studies. In convenience samples, the fact that the opportunity to participate is not equal for all individuals in the target population makes the study results not necessarily generalizable to this population (Suen, Huang, & Lee, 2014). The research tool was a randomly administered questionnaire containing questions about personal and sociodemographic information of both husbands and wives, relationship between them, pregnancy loss and health problems in children. The questionnaire was administered in public places. Respondents, who were either husbands, wives or both, all expressed their will to participate in the study through a written consent. The ethical approval was obtained, on January 2 2015, at the level of the department in which the present work was done.

The study lasted for three months, from January to March 2015.

Inclusion criteria:

(1) Couples living in Tanger-Tetouan-Al Hoceima region and during the survey period,

(2) Couples married for over one year.

Exclusion criteria:

(1) Undefined or unclearly defined relationship between spouses,

(2) Couples not living in Tanger-Tetouan-Al Hoceima region during the survey period.

Dependent variable:

(1) Consanguinity: a consanguineous union is a union in which the husband and the wife are relatives. The consanguinity was not determined through the pedigree construction but through self-reported relationships between spouses.

After the examination of 385 completed questionnaires, we eliminated 147 ones in which consanguinity was not provided. Thus, only 238 questionnaires were analysed.

Explanatory variables:

(1) SPL: occurrence (present/absent) and type (early if happened within 12 week of gestation/late if happened after the 12th completed week of gestation), frequency per couple.

(2) Health disorders in descendants: they were self-reported by the participants. According to the responses, we considered:

- As congenital malformations (present/absent): Down syndrome, cerebral paralysis, paraplegia, deafness-dumbness...
- As multifactorial diseases (present/absent): diabetes, autism, tuberculosis, cancer...
- Behavioural disorders (present/absent): without defined cause.

The statistical analysis, which was performed using SPSS 25.0., was organised into two parts. In the first part, we described the characteristics of consanguineous couples (107 cases) according to each of the independent variables. In the second part, an analytical study was conducted on all 238 studies couples (consanguineous and non-consanguineous) to evaluate the relationship between consanguinity and each of the independent variables. For this purpose, the Chi-squared test was used to determine the association significance, the Cramer V test to measure the association intensity, Student *t*-test to compare consanguineous and non-consanguineous couples in terms of SPL frequency and health disorders' frequency. All these tests are considered significant when p-value is lower than 0.05.

Odds Ratio test (OR) was performed to evaluate the risk of:

(1) SPL occurrence (present/absent) according to consanguinity (present/absent);

(2) SPL type (early/late) according to consanguinity (present/absent);

(3) Health disorders' occurrence (present/absent) according to consanguinity (present/absent);

(4) Occurrence of each disorder's type (present/absent) according to consanguinity (present/absent);

The OR is considered significant when the confidence interval (CI) does not include the value 1.

Results

Among the 238 studied couples, a consanguinity rate of 45.4% was recorded, with 107 consanguineous couples. Consanguineous unions between first cousins represented 91%, whereas first cousins once removed and second cousins represented 7% and 2%, respectively.

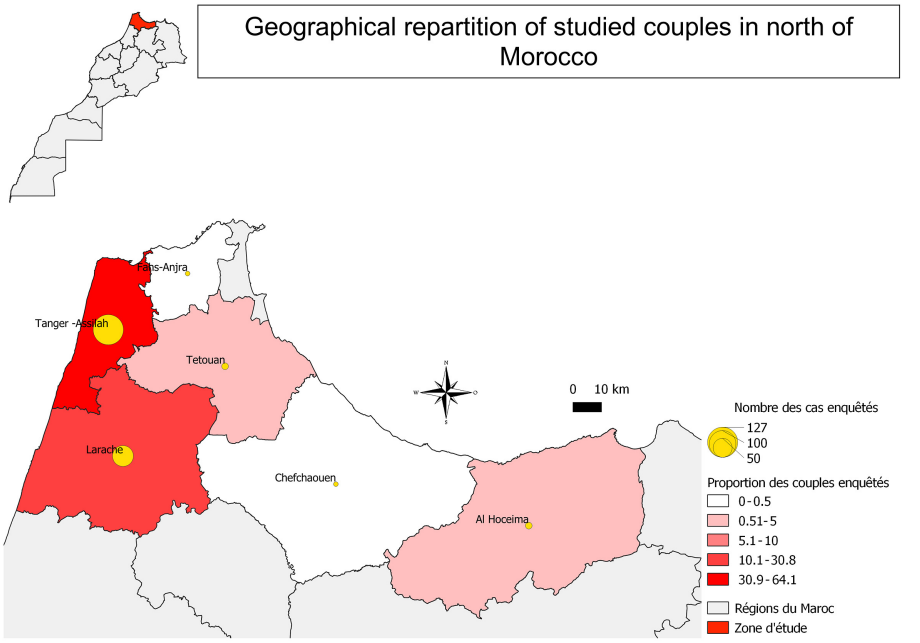
Concerning the geographical repartition of participants, most studied couples are of urban origin with 83.5%. Indeed, the province of Tanger-Asilah was the most represented with 64%, followed by Larache with 30.8% (Figure 1).

Descriptive characteristics of SPL: 48.5% of studied couples experienced SPL. Moreover, 51.2% of couples who experienced SPL were consanguineous. The mean number of SPL per couple was higher in consanguineous unions (Table 1).

Concerning SPL type, 57.5% of couples who experienced early SPL were consanguineous, whereas only 45.2% of couples who had late SPL were consanguineous. In terms of frequency, the mean number was lower in consanguineous couples for both early and late SPL (Table 1).

Descriptive characteristics of health disorders: 31.9 % of studied couples had children with health disorders. Among these couples, 75% were consanguineous. Indeed, consanguineous couples represented 76.7% of couples with congenital malformations descendants, 72% of couples with multifactorial diseases and 75% of couples with behavioural disorders (Table 2).

In terms of descendants' number, among 822 children with health disorders, 41.9% belonged to consanguineous couples (Table 2).



Source(s): Figure by the authors

Figure 1.
Geographical repartition of studied couples

Relationship between consanguinity and SPL:

SPL occurrence: The analysis of the association between consanguinity and SPL occurrence displayed a statistically non-significant association ($p = 0.15$). Also, we found no statistical difference in SPL risk between consanguineous and non-consanguineous couples (Table 3).

SPL type: No statistically significant association was registered between consanguinity and SPL type ($p = 0.26$). Also, no significant difference was observed between consanguineous and non-consanguineous couples in terms of early SPL risk (Table 3).

SPL frequency: The comparison of total number of SPL cases between consanguineous and non-consanguineous couples showed no statistical significance ($p = 0.81$). Concerning SPL type, the number of late SPL cases was significantly lower in consanguineous couples ($p < 0.001$), whereas no significant difference was observed in terms of early SPL number ($p = 0.73$).

Relationship between consanguinity and health disorders in descendants:

All health disorders: The association between consanguinity and the occurrence of health disorders was found to be statistically significant ($p < 0.001$), with strong intensity ($V = 0.51$).The risk analysis showed that consanguineous couples present a significantly higher risk of health disorders in comparison with non-consanguineous ones (Table 3).

On the other hand, even if there was no significant difference between the consanguineous and non-consanguineous couples in terms of a total number of children ($p = 0.87$), the consanguineous couples had a significantly higher number of children with health disorders ($p < 0.001$).

Characteristics	Consanguineous Couples	Non-consanguineous couples	Total
SPL occurrence			
Spontaneous SPL in couples	42(51.2%)	40(48.8%)	82(100%)
Mean number of SPL per couple	0.88 ± 1.11	0.84 ± 1.29	0.86 ± 1.21
SPL type			
Early spontaneous SPL in couples	23 (57.5%)	17 (42.5%)	40(100%)
Late spontaneous SPL in couples	19 (45.2%)	23 (54.8%)	42(100%)
Mean number of early SPL per couple	2.13 ± 1.18	2.29 ± 1.8	2.2 ± 1.45
Mean number of late SPL per couple	1.0 ± 0.0	1.65 ± 0.71	1.36 ± 0.62

Source(s): Table by the authors

Table 1. Characteristics of Spontaneous pregnancy loss (SPL) in the studied sample

	Consanguineous Couples	Non-consanguineous couples	Total
Disorders categories		*Number of couples*	
Congenital malformation	46(76.7%)	14(23.3%)	60(100%)
Multifactorial diseases	18(72.0%)	7(28.0%)	25(100%)
Behavioural disorders	3(75%)	1(25%)	4(100%)
Total	57(75%)	19(25%)	76(100%)
Disorders occurrence		*Number of descendants*	
Total number of descendants	480(49.64%)	487(50.36%)	967(100%)
Descendants with health disorders	344(41.85%)	478(58.15%)	822(100%)

Source(s): Table by the authors

Table 2. Repartition of couples and descendants according to health disorders

Congenital malformations: the relation between consanguinity and congenital malformations occurrence was statistically significant ($p < 0.001$), with strong intensity ($V = 0.43$). The risk analysis showed that consanguineous couples present a significantly higher risk of congenital malformations in comparison with non-consanguineous ones (Table 3).

Multifactorial diseases: consanguinity and multifactorial disease occurrence were significantly associated ($p = 0.004$), with a moderated intensity ($V = 0.22$). The risk of multifactorial disease was significantly higher in consanguineous couples (Table 3).

Behavioural disorders: The analysis of the relation between consanguinity and behavioural disorders displayed no significant association ($p = 0.34$). Also, no significant difference was observed between consanguineous and non-consanguineous couples in terms of behavioural disorders risk (Table 3).

Discussion

According to these results, consanguineous unions are still a common practice in Tanger-Tetouan-Al Houceima region, as in many other countries, especially in Africa, the Middle East and West Asia (Al Arrayed and Hamamy, 2012; Hamamy and Antonarakis, 2011; Ben M' rad and Chalbi, 2004; Small, Bittles, Petherick, & Wright, 2017).

The consanguinity rate reported by the present work is higher than that reported by another study conducted in the same region (24.37%) (Habibeddine, Ouardani, El Ossmani, Amzazi, & Talbi, 2018) and in other regions of Morocco, such as the Middle Atlas (30.32%) (Latifi *et al.*, 2010), Doukkala (26.03%) (Talbi *et al.*, 2008), Gharb (24.8%) (Attazagharti *et al.*, 2006), Rabat-Salé-Zemmour-Zaer (20.6%) (Hami, Soulaymani, & Mokhtari, 2009) and Souss Massa Drâa (22.80%) (Sbii, 2013). The highest rates were registered in Azgour (36%) (Baali, 1994).

Furthermore, most consanguineous unions were between first cousins, which is in concordance with other Arabic countries (Kulkarani and Kurian, 1990; Gunaid, Hummad, & Tamim, 2004).

No relationship was found between consanguinity and SPL occurrence, whereas late SPL was less frequent in consanguineous couples. A similar result was reported by other studies which found no effect of relatedness on reproductive wastage (Robertson *et al.*, 2022; Abbas and Yunis, 2014). However, many researchers found a significant impact of consanguinity on SPL, which would be explained by the fact that consanguinity increases the risk of occurrence of both recessive and polygenic conditions in the offspring (Bachir and Aouar, 2019; Hamamy, Al-Bayati, & Al-Kubaisy, 1986). In fact, deleterious recessive genes, creating homozygotes, may interfere with the adaptability of offspring to both intrauterine life and the extra-uterine environment; as a result, prenatal wastage or neonatal deaths or biochemical or/and congenital malformations may occur (Basaran *et al.*, 1989; Al-Awadi *et al.*, 1986). It must be noted that other studies showed lower rates of SPL in families where consanguinity is customary across successive generations, presumably because of the increasing effect of homozygosity on fetal development (Fareed and Afzal, 2017; Hussain and Bittles, 1998; Freire-Maia and Takehara, 1977; Khlat, 1988; Rao and Inbaraj, 1977; Rao and Inbaraj, 1979).

Table 3. Analysis of consanguinity determining factors

Factors		Khi2	*p*-value	V De cramer	OR	IC
Abortion	Occurrence of SPL	2.05	0.15	0.11	1.56	[0.85- 2.87]
	Early/late SPL type	1.23	0.26	0.12	1.64	[0.68- 3.92]
Health disorders	Occurrence of disorders	45.21	<0.001*	0.51	9.5*	[4.75-19.00]
	Congenital malformations	32.34	<0.001*	0.43	7.23*	[3.52- 14.84]
	Multifactorial diseases	8.32	0.004*	0.22	3.72*	[1.46-9.49]
	Mental retardation	1.38	0.34	0.09	3.61	[0.36-35.51]

Source(s): Table by the authors

Regarding SPL type, no significant association with consanguinity was found. This is in concordance with another study carried out in India (Robertson *et al.*, 2022). Nevertheless, in terms of frequency, early pregnancy loss was more frequent in consanguineous couples. This could be explained by different mechanisms. Firstly, the increased frequencies of homozygotes for genes with large phenotypic effects, as in fully penetrant, autosomal recessive disorders. Secondly, under models of additively acting polygenes, increases in early death may be explained by increased proportions of individuals above certain thresholds, since the additive genetic variance increases linearly with the degree of inbreeding (Kempthorne, 1957).

On the other hand, it was found that consanguinity is significantly associated with the occurrence of health disorders, which is consistent with what was reported by many other studies (Aleissa *et al.*, 2022; Alshammary and Khan, 2021; Fareed and Afzal, 2017; Ben-Omran *et al.*, 2020). Indeed, both congenital malformations and multifactorial diseases were found to be significantly associated with consanguinity (Oniya, Neves, Ahmed, & Konje, 2019; AbdulAzeez, Al Qahtani, & Almandil, 2019; Stoll, Alembik, Roth, & Dott, 1999; Diatewa *et al.*, 2021; Romdhane *et al.*, 2019; Singer, Davidovitch, Abu Fraiha, & Abu Freha, 2020). Furthermore, a Norwegian study comparing the offspring of 848 women mated to their first cousins with the offspring of 1,696 control women has shown a high percentage of malformations for cases compared to for controls. These differences may be attributed to the increased homozygosity in the offspring of first cousins (Magnus, Berg, & Bjerkedal, 1985).

Limitations

(1) Some of the limitations of the present study is the authenticity of the information revealed by the respondents according to their descendants' diseases. In fact, there was no clinical evidence of their statements.

(2) 38% of total questionnaires were eliminated from the study for the unknown or undefined relationships between spouses, which reduced significantly the sample size.

Conclusion

The effects of consanguinity on health are being increasingly reported by researchers over the world. In the present work, we showed that consanguinity in north Morocco is associated with a higher risk of congenital malformations and multifactorial diseases in descendants but has no significant effect on spontaneous pregnancy loss.

These results suggest that population awareness regarding the negative effects of consanguinity should be raised through education programmes and premarital, prenatal and genetic counselling services.

In addition, further studies should be conducted to investigate other aspects of consanguinity effects through a multidisciplinary approach.

Note

1. https://www.hcp.ma/region-tanger/attachment/2099765/ (accessed 7 March 2023)

References

Abbas, H. A., & Yunis, K. (2014). The effect of consanguinity on neonatal outcomes and health. *Hum Hered*, *77*(1-4), 87–92.

AbdulAzeez, S., Al Qahtani, N.H., & Almandil, N. B. (2019). Genetic disorder prenatal diagnosis and pregnancy termination practices among high consanguinity population, Saudi Arabia. *Scientific Reports*, *9*, 17–248.

Al Arrayed, S. S., & Hamamy, H. (2012). The changing profile of consanguinity rates in Bahrain, 1990-2009. *J Biosoc Sci*, *44*(3), 313–9.

Al-Awadi, S. A., Naguib, K. K., Moussa, M. A., Farag, T. I., Teebi, A. S., & El-Khalifa, M. Y. (1986). The effect of consanguineous marriages on reproductive wastage. *Clin Genet*, *29*, 384–388.

Aleissa, M., Aloraini, T., Alsubaie, L. F., Hassoun, M., Abdulrahman, G., Swaid, A, … Alfares, A. (2022). Common disease associated gene variants in a Saudi Arabian population. *Ann Saudi Med*, *42*(1), 29–35.

Alharbi, K. K., Al-Sheikh, Y. A., Alsaadi, M. M., Mani, B., Udayaraja, G. K., Kohailan, M., & Ali Khan, I. (2020). Screening for obesity in the offspring of first-cousin consanguineous couples: A phase-I study in Saudi Arabia. *Saudi J Biol Sci*, *27*(1), 242–6.

Alshammary, A. F., & Khan, I. A. (2021). Screening of obese offspring of first-cousin consanguineous subjects for the angiotensin-converting enzyme gene with a 287-bp Alu sequence. *J Obes Metab Syndr*, *30*(1), 63–71.

Attazagharti, N., Hami, H., Soulaymani, A., Benali, D., Khadmaoui, A., & Mokhtari, A. (2006). Consanguinité et isonymie dans la région du Gharb au Maroc. *Biologie et Santé*, *6*(2), 103–110.

Baali, A. (1994). Effet de la consanguinité sur la fertilité, la fécondité et la mortalité des enfants dans une population berbere Guedmiwa (Vallée d'Azgour, cercle d'Amizmiz, Marrakech, Maroc. *Bulletins et Mémoires de la Société d'anthropologie de Paris*, *6*(3), 155–162.

Bachir, S., & Aouar, A. (2019). Study of the impact of consanguinity on abortion and mortality in the population of Beni Abbes (southwestern Algeria). *Egyptian Journal of Medical Human Genetics*, *20*(1), 1–7.

Basaran, N., Hassa, H., Basaran, A., Artan, S., Stevenson, J. D., & Sayli, B. S. (1989). The effect of consanguinity on the reproductive wastage in the Turkish population. *Clin Genet*, *36*, 168–173.

Bener, A., Ayoubi, H. R., Ali, A. I., Al-Kubaisi, A., & Al-Sulaiti, H. (2010). Does consanguinity lead to decreased incidence of breast cancer?. *Cancer Epidemiol*, *34*(4), 413–8.

Ben M'rad, L., & Chalbi, N. (2004). Le choix matrimonial en Tunisie est-il transmissible?. *Antropo*, *7*, 31–37.

Ben-Omran, T., Al Ghanim, K., Yavarna, T., El Akoum, M., Samara, M., Chandra, P., & Al-Dewik, N. (2020). Effects of consanguinity in a cohort of subjects with certain genetic disorders in Qatar. *Mol Genet Genomic Med*, *8*(1), 1–10.

Bhinder, M. A., Sadia, H., Mahmood, N., Qasim, M., Hussain, Z., Rashid, M. M, … Jahan, S. (2019). Consanguinity: A blessing or menace at population level?. *Ann Hum Genet*, *83*(4), 214–219.

Bittles, A. H. (2001). Consanguinity and its relevance to clinical genetics. *Clin Genet*, *60*(2), 89–98.

Bittles, A. H. (2008). A community genetics perspective on consanguineous marriage. *Community Genet*, *11*(6), 324–330.

Bittles, A. H., Mason, W. M., Greene, J., Rao, N. A. (1991). Reproductive behavior and health in consanguineous marriages. *Science*, *252*(5007), 789–794.

Denic, S., & Nicholls, M. G. (2007). Genetic benefits of consanguinity through selection of genotypes protective against malaria. *Human Biology*, *79*(2), 145–158.

Diatewa, B. M., Maneh, N., Domingo, A. S., Wamba, Mewamba, R., Amouzou, D, … Patrice Balo, K. (2021). Association between consanguinity with the ocular congenital abnormalities in Togo. *J Fr Ophtalmol*, *44*(1), 63–66.

El Goundali, K., Chebabe, M., Zahra Laamiri, F., & Hilali, A. (2022). The determinants of consanguineous marriages among the Arab population: A systematic review. *Iran J Public Health*, *51*(2), 253–65.

Emery, A. E. H. (1976). *Methodology in medical genetics*. Edinburgh: Churchill Livinstone Press.

Fareed, M., & Afzal, M. (2017). Genetics of consanguinity and inbreeding in health and disease. *Ann Hum Biol*, *44*(2), 99–107.

Freire-Maia, N., & Takehara, N. (1977). Inbreding effect on precocious mortality in Japanese communities of Brazil. *Ann Hum, Genet*, *41*, 99–102.

Gunaid, A. A., Hummad, N. A., & Tamim, K. A. (2004). Marriage in the capital city Sana'a, Yemen. *Journal of Biosocial Science*, *6*(1), 111–121.

Habibeddine, L., Ouardani, M., El Ossmani, H., Amzazi, S., & Talbi, J. (2018). Study of consanguinity of the population of northern Morocco. *Journal of Forensic Research*, *9*, 1–4.

Hamamy, H., Al-Bayati, N., & Al-Kubaisy, W. (1986). Consanguineous marriages in Iraqi urban population and the effect on pregnancy outcome and infant mortality. *Iraqi Med J*, *34*, 76–80.

Hamamy, H., & Antonarakis, S. E. (2011). Consanguineous marriage, pearls and perils: Geneva international conanguiniy workshop report. *Genet Med*, *13*(9), 841–847.

Hamamy, H., & Bittles, A. H. (2009). Genetic clinics in Arab communities: Meeting individual, family and community needs. *Public Health Genomics*, *12*(1), 30–40.

Hami, H., Soulaymani, A., & Mokhtari, A. (2006). Endogamie, Isonymie et Consanguinité dans la région du Gharb Chrarda Béni Hsen (Maroc). *Antropo*, *11*, 223–233.

Hami, H., Soulaymani, A., & Mokhtari, A. (2009). Les Déterminants des Mariages Consanguins dans la Région de Rabat-Salé-Zemmour-Zaer (Maroc). *Antropo*, *18*, 27–35.

Hussain, R., & Bittles, A. H. (1998). The prevalence and demographic characteristics of consanguineous marriages in Pakistan. *J Biosoc Sci*, *30*(2), 261–275.

Hussain, R., & Bittles, A. H. (2000). Sociodemographic correlates of consanguineous marriage in the Muslim population of India. *J Biosoc Sci*, *32*(4), 433–42.

Jabeen, N., & Malik, S. (2014). Consanguinity and its sociodemographic differentials in bhimber district, Azad Jammu and Kashmir, Pakistan. *J Health Popul Nutr*, *32*(2), 301–313.

Kempthorne, O. (1957). *An introduction to genetic statistics*. New York: John Wiley & Sons.

Khlat, M. (1988). Consanguineous marriage and reproduction in Beirut, Lebanon. *Am J Hum Genet*, *43*, 188–196.

Kulkarani, M., & Kurian, M. (1990). Consanguinity and its effect on fetal growth and development: A south Indian study. *Journal of Medical Genetic*, *27*(6), 348–352.

Lal, D., Neubauer, B. A., Toliat, M. R., Altmüller, J., Thiele, H., Nürnberg, P., and . . . Nothnagel, M. (2016). Increased probability of co-occurrence of two rare diseases in consanguineous families and resolution of a complex phenotype by next generation sequencing. *PLoS One*, *11*(1), 1–8.

Latifi, M., Sbii, L., & Hami, H. (2010). Le Choix du conjoint dans la région de Fritissa (Est du Maroc). *Antropo*, *23*, 99–107.

Maghzi, H., Shaygannejad, V., Minagar, A., Hassanzadeh, A., & Maghzi, A.H. (2016). Consanguinity and multiple sclerosis susceptibility: A case control study. *Multiple Sclerosis and Related Disorders*, *10*, 179–180.

Magnus, P., Berg, K., & Bjerkedal, T. (1985). Association of parental consanguinity with decreased birth weight and increased rate of early death and congenital malformations. *Clin Genet*, *28*, 335–342.

Medimegh, I., Troudi, W., Omrane, I., Ayari, H., Uhrhummer, N., Majoul, H., . . . Elgaaied, A.B. (2015). Consanguinity protecting effect against breast cancer among Tunisian women: Analysis of BRCA1 haplotypes. *Asian Pacific Journal of Cancer Prevention*, *16*(9), 4051–4055.

Mohamed, M., Tellez, J., Bergmann, C., Gale, D. P., Sayer, J. A., & Olinger, E. (2022). Pseudodominant Alport syndrome caused by pathogenic homozygous and compound heterozygous COL4A3 splicing variants. *Ann Hum Genet*, *86*(3), 145–152.

Motulsky, A. G., & Vogel, F. (1982). *Human genetics, problems and approaches*. Berlin: Springer-Verlag.

Oniya, O., Neves, K., Ahmed, B., & Konje, J. C. (2019). A review of the reproductive consequences of consanguinity. *Eur J Obstet Gynecol Reprod Biol*, *232*, 87–96.

Rao, P. S. S., & Inbaraj, S. G. (1977). Inbreeding effects on human reproduction in Tamil Nadu of South India. *Ann Hum Genet*, *41*, 87–98.

Rao, S. S., & Inbaraj, S. G. (1979). Trends in human reproductive wastage in relation to long-term practice of inbreeding. *Ann Hum Genet*, *42*, 401–412.

Robertson, J. M., Basany, K., Farooq, F., Tan, X., Tang, G., Bunker, C. H, … Haggerty, C. L. (2022). Consanguineous marriage and early pregnancy loss in rural to peri-urban India. *J Obstet Gynaecol India*, *72*(4), 314–321.

Romdhane, L., Mezzi, N., Hamdi, Y., El-Kamah, G., Barakat, A., & Abdelhak, S. (2019). Consanguinity and inbreeding in health and disease in north African populations. *Annu Rev Genomics Hum Genet*, *20*, 155–179.

Sbii, L. (2013). *Etude de la Consanguinité, Isonymie et Endogamie dans la région de Souss Massa Drâa* (pp. 149–157). Siences Faculty, Ibn Tofail University, Kénitra, Morocco: Doctoral thesis.

Scroggins, K. M., Smucker, W. D., & Krishen, A. E. (2000). SPL: Evaluation, management, and followup counseling. *Prim Care*, *27*, 153–67.

Singer, S., Davidovitch, N., Abu Fraiha, Y., & Abu Freha, N. (2020). Consanguinity and genetic diseases among the Bedouin population in the Negev. *J Community Genet*, *11*(1), 13–19.

Small, N., Bittles, A. H., Petherick, E. S., & Wright, J. (2017). Endogamy, consanguinity and the health implications of changing marital choices in the UK Pakistani community. *J Biosoc Sci*, *49*(4), 435–46.

Solignac, M., Periquet, G., Anxolabehere, D., & Petit, C. (1995). Génétique et evolution 1: La variation des gènes dans les populations. *Collect Meth Herman Ed des Sciences et des Arts*, *289*.

Stoll, C., Alembik, Y., Roth, M. P., & Dott, B. (1999). Parental consanguinity as a cause for increased incidence of births defects in a study of 238,942 consecutive births. *Ann Genet*, *42*(3), 133–9.

Suen, L. J., Huang, H. M., & Lee, H. H. (2014). A comparison of convenience sampling and purposive sampling. *Hu Li Za Zhi*, *61*(3), 105–11.

Tadmouri, G. O., Nair, P., Obeid, T., Al Ali, T. M., Al Khaja, N., & Hamamy, H. A. (2009). Consanguinity and reproductive health among Arabs. *Reprod Health*, *6*, 17.

Talbi, J., Khadmaoui, A., Soulaymani, A., & Chafik, A. (2008). Caractérisation de l'évolution de la consanguinité dans la population des Doukkala (Maroc). *Antropo*, *17*, 7–13.

Temaj, G., Nuhii, N., & Sayer, J. A. (2022). The impact of consanguinity on human health and disease with an emphasis on rare diseases. *Journal of Rare Diseases*, *1*, 1–2.

Zlotogora, J. (1991). Problems in diagnosis and delineation of inherited disorders in highly inbred populations. *Am J Med Genet*, *41*(4), 451–453.

Further reading

Baris, H. N., Barnes-Kedar, I., Toledano, H., Halpern, M., Hershkovitz, D., Lossos, A, … Levi, Z. (2016). Constitutional mismatch repair deficiency in Israel: High proportion of founder mutations in MMR genes and consanguinity. *Pediatr Blood Cancer*, *63*(3), 418–27.

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