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Original Article

Prevalence and Determinants of Consanguinity among the Libyan Population in Misurata as an Important Family and Child Health Issue

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ABSTRACT

Background: Consanguineous marriage is a deeply rooted cultural practice in many Mediterranean and Middle Eastern populations, including Libya, and it plays a significant role in the burden of genetic diseases and public health**. The aim** of this study was to estimate the prevalence and patterns of consanguineous marriages in Misurata, Libya, and to assess their potential role in increasing the risk of inherited disorders. **Material and Methods:** A cross-sectional survey was conducted from May to June 2025 at zero-dose vaccine centers in Misurata. A total of 500 fathers accompanying their children for vaccination were interviewed using a structured, pre-tested questionnaire that gathered information on demographic characteristics, marital relationships, and consanguinity status. **Results:** Out of the 500 couples, consanguinity was observed in 180 cases (36%), including paternal first cousins (8.6%), maternal first cousins (6.8%), double first cousins (2.6%), second cousins from the father's side (3.8%) and mother's side (3.4%), and more distant relatives (10.8%). The average age was 31.4±6.9 years for wives and 39.7±7.9 years for husbands. A family history of inherited disease was reported in 9.6% of the couples. **Conclusions:** Consanguineous marriages, especially first-cousin unions, remain highly prevalent in Misurata. Targeted genetic counseling, culturally sensitive awareness programs, and updated research are urgently needed to reduce the incidence of inherited disorders in the Libyan population.

Keywords: Consanguinity, Misurata, Libya, Genetic Disorders, Consanguineous Marriage,

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INTRODUCTION

Consanguineous marriage, a deeply rooted tradition in many Mediterranean and Middle Eastern populations, presents a significant public health challenge due to its association with an increased burden of genetic disease. Misurata, located on the Mediterranean coast of western Libya, is a culturally diverse city of approximately 95,448 families, with a population of 239,085 males and 236,372 females. Understanding the prevalence and determinants of consanguinity in this population is vital for guiding public health policies and targeted genetic counseling. Consanguineous marriage refers to a union between individuals who are biologically related. In clinical genetics, this term is used to describe marriages between couples who are second cousins or closer relatives [1] . Brothers and sisters are collectively termed sibs or siblings, and a group of siblings constitutes a sibship. Relatives are classified by their degree of biological proximity to the proband: first-degree relatives include the parents, siblings, and direct offspring of the proband; second-degree relatives comprise grandparents, grandchildren, aunts, uncles, nephews, nieces, and half-siblings; and third-degree relatives encompass first cousins. The offspring of first cousins are referred to as second cousins, while the child of a first cousin is termed a first cousin once removed relative to the parent's first cousin. Couples who share one or more common ancestors are defined as consanguineous (2).Arab populations have a long-standing tradition of consanguinity rooted in deep socio-cultural norms. In many Arab countries, first-cousin marriages are especially common, accounting for approximately 25–30% of all unions and representing some of the highest consanguinity rates globally [1]. Consanguinity is associated with a higher incidence of autosomal recessive genetic disorders, with over 500 genetic diseases reported in North Africa [3]. The risk of congenital anomalies and new genetic syndromes is notably increased in offspring from consanguineous marriages [4]. Although consanguinity is widely practiced, there is insufficient data on its global incidence and demographic implications, particularly in different Libyan health regions where such marriages occur frequently. This pilot study aims to determine the prevalence and analyze the patterns of consanguinity in Misurata as a baseline for a broader investigation across Libya. Its findings will highlight region-specific genetic disorders and their potential impact on public health, ultimately guiding the development of targeted prevention, early detection, and culturally informed intervention strategies.

MATERAIAL AND METHOD:

Study Design, Setting, and period

This cross-sectional study was conducted in Misurata, Libya, in the period from May to June 2025, with the aim of estimating the prevalence and determinants of consanguinity within the local population. The study was implemented at the city's zero-dose vaccine centers, which serve as primary entry points for routine childhood immunization, providing access to a diverse and representative sample of families.

Study Population

The study included fathers attending the zero-dose vaccine centers with their children for immunization. A total of 500 questionnaires were administered to eligible participants. The inclusion criterion was being a Libyan father accompanying a child for vaccination during the study period. Fathers who were not Libyan or who had not brought their children for vaccinations at the participating centers were excluded from the study.

Data Collection

Data were collected using a structured pre-tested questionnaire administered through face to face interviews conducted by trained data collectors. The questionnaire gathered information on demographic characteristics, familial relationships, and details related to consanguineous marriages, including the degree of biological relatedness between spouses.

Ethical considerations

The study protocol received official approval, and ethical clearance was obtained through a formal letter issued by the vaccination center. This approval was supported by the Community and Family Medicine Department, Faculty of Medicine, Misurata University. Informed consent was obtained from all participants prior to data collection. Anonymity and confidentiality were strictly maintained throughout the study.

Statistical analysis

All completed questionnaires were reviewed for completeness and accuracy before data entry into the Statistical Package for the Social Sciences (SPSS). Descriptive statistics (frequencies and percentages) were used to summarize the demographic characteristics of participants and estimate the prevalence of consanguinity. No inferential statistical tests or significance levels were applied in this study.

RESULTS:

The demographic characteristics of the study participants are presented in Table 1. A total of 500 couples were included. The mean age of the wives was 31.4 ± 6.9 years, while the mean age of the husbands was 39.7 ± 7.9 years. The average number of offspring per couple was 3.8 ± 2.1 (range: 1–11). A positive family history of hereditary disease was observed in 48 participants (9.6%), underscoring the potential role of consanguinity and its clinical and public health significance within this population.

Table 1: Sociodemographic Characteristics of the Sample (500 couples)

Characteristics	Result
Age of the wives	**31.4 ± 6.9 years**
Age of the husbands	**39.7 ± 7.9 years**
Number of offspring per couple	**3.8 ± 2.1**
History of hereditary disease	**48 participants 9.6%**
Total	**500 couples**

Consanguinity was observed in 180 couples (36%), with first-cousin marriages being the most common type: 43 couples (8.6%) were paternal first cousins and 34 couples (6.8%) were maternal first cousins. Double first-cousin consanguinity accounted for 13 couples (2.6%), while second-cousin marriages comprised 19 couples (3.8%) from the father's side and 17 couples (3.4%) from the mother's side. Far consanguineous couples accounted for 54 couples (10.8%), and the remaining 320 couples (64.0%) were not consanguineously related Table 2.

Table 2: Consanguinity Status of Couples (500 couples)

Consanguinity status	Frequency	Percent
First cousin (father side)	43	8.6%
First cousin (mother side)	34	6.8%
Double first cousin consanguinity	13	2.6%
Second cousin (father side)	19	3.8%
Second cousin (mother side)	17	3.4%
Far consanguineous couples	54	10.8%
Not consanguineous	320	64.0%
Total	500	100.0%

DISCUSSION:

This study estimated a consanguinity rate of 36% among couples in Misurata, Libya, with first-cousin marriages (15.4%) being the most common type. These findings directly address the study objective and align with previous research across Arab and North African countries, where consanguinity rates typically range between 20% and 50%, and earlier reports from Libya documented rates as high as 48.4% [1]. As illustrated in Table 3, Libya ranks among the Arab countries with the highest documented consanguinity rates, which reinforces the importance of identifying its determinants and public health implications.

Table 3: Consanguinity rates in Arab populations. Minimum and maximum reported rates are indicated when available

	First Cousin Marriages (>1C, 1C)	Overall Consanguinity (%)
Algeria	11.3	22.6–34%
Bahrain	24.5	39.4–45.5%
Egypt	14.3–23.2	20.9–32.8%
Egypt (Nubia)	39–47.2	60.5–80.4%
Iraq	29–33	47–60%
Jordan	19.5–39	28.5–63.7%
Kuwait	16.9–31.7	22.5–64.3%
Lebanon	6.7–31.6	12.8–42%
Libya	—	48.4%
Mauritania	—	47.2%
Morocco	8.6–10	19.9–28%
Oman	24.1	56.3%
Palestine	13.6–34.2	17.5–66.3%
Qatar	34.8	54%
Saudi Arabia	24.6–42.3	42.1–66.7%
Sudan	44.2–49.5	44.2–63.3%
Syria	28.7	30.3–39.8%
Tunisia	17.4–23	20.1–39.3%
United Arab Emirates	20.7–28.2	40–54.2%
Yemen	32–34	40–44.7%

Abbreviations: [>1C] = Double first-cousin marriage; [1C] = First-cousin marriage

Consanguineous marriages in Misurata appear to be influenced by well-established cultural, religious, and socioeconomic factors. These unions are traditionally viewed as a way to preserve family bonds, simplify marital arrangements, and foster trust within extended families [1,8]. In the Islamic context, cousin marriages are allowed under Sharia law, as long as they do not breach ethical or legal boundaries [9]. This religious permissibility, combined with traditional social norms, likely sustains the prevalence of such marriages in Misurata and similar communities.

Despite their acceptability, consanguineous marriages present recognized genetic health risks. In this study, 9.6% of participants reported a positive family history of hereditary disease, suggesting an increased risk of autosomal recessive disorders, including hematological and metabolic conditions, and congenital anomalies [7,10]. Although the majority of children born to consanguineous couples are healthy, the probability of recessive disorders increases due to the shared inheritance of pathogenic variants within extended families [7].

The study also identified a relatively high average number of offspring per couple (3.8 ± 2.1), which is consistent with findings from countries like Qatar, Tunisia, and Kuwait. Some research suggests consanguineous unions may be associated with higher fertility, due to early marriage, extended reproductive periods, and strong social support [1]. However, in larger families, the cumulative risk of expressing recessive conditions may also increase.

From an Islamic bioethical perspective, preventive approaches such as genetic counseling and premarital screening are supported and even encouraged under Sharia when they aim to protect future generations and promote family health [9]. These modern interventions are increasingly being promoted—and in some nations, mandated—to reduce inherited disease burdens.

In light of these determinants, public health strategies are crucial. Experts recommend implementing community-wide education programs, genetic risk assessment, and culturally sensitive counseling as measures to reduce health risks without disrupting established social norms [1,8,10]. Countries like the UAE and Tunisia have shown promising outcomes through integrated national screening programs that respect cultural and religious values [10]. The current findings from Misurata are echoed in regional data. A study in

Saudi Arabia reported a similar consanguinity rate of 38.9% and linked it to increased developmental disorders, supporting our observation of a 9.6% positive family history of hereditary disease [11]. The high proportion of first-cousin marriages also reflects patterns in Algeria, where a study documented a 40.2% consanguinity rate dominated by cousin unions [12]. Moreover, our findings on offspring number align with a genome-wide study in Tunisia, which reported that larger families in consanguineous unions increased the likelihood of expressing recessive disorders due to extended runs of homozygous [13]. Our data on hereditary disease frequency further reflect broader evidence that consanguinity heightens the risk of autosomal recessive conditions [14]. While cultural and religious norms continue to support consanguineous unions, emerging trends suggest changing perceptions. For instance, a 2021 Jordanian survey revealed that nearly 48% of university students opposed cousin marriages due to concerns about genetic diseases [15]. This indicates a potential shift in attitudes, especially among younger populations.

Given the persistently high prevalence of consanguinity in Libya, national strategies that integrate premarital genetic counseling and culturally informed public education—similar to successful programs in the UAE and Tunisia—could help reduce the burden of inherited disorders without challenging deeply held values [16].

CONCLUSION:

The results of present study will reinforce the need for multidisciplinary public health strategies in Libya. These should include genetic counseling, community education, religious engagement, and legal frameworks that empower individuals to make informed reproductive choices. Future research should further explore the long-term burden of genetic disorders associated with consanguinity and assess the effectiveness of screening programs and bioethical interventions in Arab contexts.

RECOMMENDATION

Future policies and clinical practices in Libya should integrate targeted genetic counseling services; premarital screening, and culturally tailored public health interventions. Additionally, further studies incorporating genetic analyses are encouraged to deepen understanding of the long-term impacts of consanguinity.

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DISCLOSURE OF CONFLICT OF INTEREST

The authors declare no conflicts of interest.

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