
The Genetic, Ecological, and Evolutionary Implications of Inbreeding: A Comprehensive Analysis of Costs, Benefits, and Conservation Strategies

Muhammad Muzammal,¹ Maria Shafiq,²
Shafiqua Ishtiaq,¹ Umar Raoun,¹ Mehak Fazal,¹
Murtaiz Hussain,¹ Faria Batool,¹ Pervaiz Ali,¹
Aiman Saeed Khan,¹ Muhammad Kamran
Khalid,² Muzammil Ahmad Khan¹

¹ Gomal Centre of Biochemistry and Biotechnology,
Gomal University, Dera Ismail Khan, Pakistan

² Gomal Medical College, Dera Ismail Khan, Pakistan

ABSTRACT

Inbreeding – the mating of closely related individuals – is a most important phenomenon for genetics, ecology, evolution, and even human societies. This review addresses all aspects of the genetic consequences of inbreeding, ecological and evolutionary implications, and conservation biology, and also provides cultural and religious perspectives on inbreeding, as shaped by varying traditions in marriage traditions and genetic outcomes. Genetic results of inbreeding include increased homozygosity, inbreeding depression, and a greater frequency of genetic disorders. Conservation technologies currently engaged include genetic rescue, translocation, and assisted gene flow to oppose inbreeding in endangered species. A wide variety of perspectives on inbreeding is exhibited in various religious and cultural beliefs. For Islam, cousin marriages form part of common practice and culture,

Recommended citation: Muzammal M. *et al.* The Genetic, Ecological, and Evolutionary Implications of Inbreeding: A Comprehensive Analysis of Costs, Benefits, and Conservation Strategies. *Social Evolution & History*, Vol. 25 No. 2, September 2026, pp. 127–149. DOI: 10.30884/seh/2026.02.05.

© 2026 ‘Uchitel’ Publishing House

with awareness of genetic risks growing. Historically, Christianity prohibited marriages between close kin, while Judaism and Hinduism uphold complex traditions in incorporating cultural practices vis-à-vis genetic concerns. Much new genetic knowledge has now created genetic counseling and premarital screening programs in several communities for health risks due to consanguinity. In conclusion, this review discussed the advantages and disadvantages of inbreeding, depending on the circumstances. Although inbreeding usually brings about disadvantages, it may lead to local adaptations, attachment to a territory, and consolidation of culture.

Keywords: *inbreeding, inbreeding depression, genetic rescue, consanguineous marriage, conservation biology, religious perspectives, genetic disorders.*

1. INTRODUCTION

Inbreeding is a critical biological process with significant implications for genetics, ecology, and evolution. Mating between closely related individuals increases homozygosity and brings about the expression of recessive alleles. Inbreeding is generally believed to have undesirable consequences in terms of inbreeding depression or low fitness; however, it can also assist evolutionarily and from a conservation perspective. For instance, the process of inbreeding became central to crop and livestock domestication, whereby selective breeding helped fix characters of interest (Adams *et al.* 2011). By sharp contrast, inbreeding among wild populations, particularly those that are small or isolated, leads to declining population size and a heightened risk of extinction. An understanding of inbreeding is essential to appreciate and address issues related to biodiversity conservation, the management of endangered species, and the control of genetic disorders in populations of humans and animals (Manolio *et al.* 2009; Varshney *et al.* 2014).

Inbreeding refers to the mating of individuals who have a recent common ancestor such that the offspring show a higher degree of genetic similarity. The degree of inbreeding may be quantified by the inbreeding coefficient (F) defined as the probability that two alleles at any locus in an individual are identical by descent. For example, given wolves that are siblings mating, their offspring would have an inbreeding coefficient of 0.25, meaning there is a 25 % chance any two alleles are identical by descent. Occasionally, inbreeding occurs naturally among small or isolated populations, while it can be brought about through controlled breeding (Allendorf *et al.* 2010).

1.2. Historical Context and Early Studies

The earliest investigations into inbreeding were done by Charles Darwin, who noticed the presence of inbreeding in plants and animals and documented its effects therein. In his book, titled *The Effects of Cross and Self-Fertilization in the Vegetable Kingdom*, published in 1876, Darwin noted the reduced vigor and fertility of self-fertilized plants relative to cross-pollinated plants. Early geneticists such as Gregor Mendel and Sewall Wright added to the understanding of the mechanisms of inbreeding and how much it contributes to the genetic composition of a population. The experiments of Wright on inbreeding coefficients and population structure form the basis of contemporary genetic studies. An instance is Wright's Island Model (1931), which illustrates how genetic drift and inbreeding may lead to genetic differences among populations (Wright 1943). This review looks to answer the following questions: What are the genetic consequences of inbreeding, and how are these expressed in different species? Under what ecological conditions does inbreeding take place, and what are the evolutionary consequences? How can inbreeding be managed in conservation biology to guarantee the survival of endangered species? What are the ethical and practical implications regarding the mitigation of its effects?

2. GENETIC CONSEQUENCES OF INBREEDING

Inbreeding causes more homozygosity, where deleterious recessive genes are more likely to be expressed. In small populations, genetic drift – that is, an unpredictable shift in allele frequencies – further diminishes genetic diversity. The Florida panther (*Puma concolor coryi*), for example, experienced increased homozygosity with the expression of harmful recessive alleles such as kinked tail and cardiac defects due to small population size (Johnson *et al.* 2010).

Inbreeding depression is a term used to describe the reduced fitness and viability of offspring due to inbreeding. This condition is a result of the expression of harmful recessive alleles and the elimination of heterozygote advantages. Symptoms of this condition manifest as lower fertility rates, increased mortality rates, and greater susceptibility to diseases. For example, inbred populations of Scandinavian wolves (*Canis lupus*) show reduced litter size and increased juvenile mortality rates compared with outbred populations (Liberg *et al.* 2005).

Inbreeding can lead to the accumulation of disorders, such as cystic fibrosis in humans or hip dysplasia in dogs. Such disorders decrease

the general fitness of the population, resulting in a drop in population. For instance, the Cheetah (*Acinonyx jubatus*) has become population-poor due to ancient inbreeding and thus finds itself at an ever-increasing risk of diseases, for example, feline infectious peritonitis (O'Brien *et al.* 1985).

3. INBREEDING AND INFERTILITY IN HUMAN POPULATIONS

Inbreeding, defined as reproduction between genetically related individuals, is a long-standing social and biological phenomenon with significant consequences for human health. One of the most critical implications of inbreeding in human populations is its contribution to infertility – a condition affecting millions worldwide. The genetic basis of this relationship stems from inbreeding's tendency to increase homozygosity across the genome, which raises the likelihood that harmful recessive alleles will be expressed (Peterson *et al.* 2007; Spotin *et al.* 2017; Sultana and Mannen 2004; Thoma *et al.* 2021). When present in homozygous form, many of these recessive genes can impair reproductive processes in both males and females. For instance, in males, inbreeding has been associated with non-obstructive azoospermia (a complete absence of sperm in semen) and severe oligospermia (very low sperm count), often due to genetic mutations that disrupt the Y chromosome or spermatogenesis pathways. In some populations, microdeletions in the AZF (azoospermia factor) regions of the Y chromosome have been found more frequently in men from consanguineous families, leading to defective sperm production and male infertility (Goldstein and Pollock 1997; Plotnikov and Guggenheim 2019; Vander Borcht and Wyns 2018).

Women also face elevated reproductive risks in inbred populations. Conditions such as premature ovarian failure, recurrent pregnancy loss, and congenital uterine anomalies are more common in women with a background of consanguineous lineage, often due to inherited mutations in genes involved in hormonal regulation or embryonic development. These genetic defects can also manifest as autosomal recessive disorders that indirectly affect fertility by impairing systemic health. For example, congenital adrenal hyperplasia, a condition more prevalent in consanguineous populations, is known to disrupt normal reproductive development and menstrual function, leading to subfertility or infertility in affected women (Carson and Kallen 2021; O'Flynn, O'Brien *et al.* 2010; Sokol 2009).

Globally, the impact of consanguinity on infertility is most pronounced in regions where cousin marriages are culturally endorsed and practiced across generations, such as the Middle East, North Africa, and South Asia (Obeagu *et al.* 2023; Yin *et al.* 2023). In Pakistan, where the prevalence of cousin marriage exceeds 50 % in some communities, studies have shown significantly higher rates of infertility and perinatal loss among consanguineous couples compared to unrelated pairs. Similar trends have been observed in rural areas of Iran, Egypt, and Saudi Arabia, where limited genetic diversity within isolated populations exacerbates the risk of reproductive complications (Hwang *et al.* 2010; Pritchard *et al.* 2000).

The effects of inbreeding on reproductive health also carry important psychosocial and public health implications. Infertility often carries a heavy emotional and social burden, particularly in societies where parenthood is strongly tied to social status, marital stability, and religious expectations. Women, in particular, may face blame, stigma, or ostracism for reproductive failure, even when the underlying cause is genetic or male-related. These social pressures can delay or prevent access to proper medical care, compounding the problem further (Al-yahya *et al.* 2022; Manzoor *et al.* 2018).

Recognizing the role of inbreeding in infertility underscores the importance of integrating genetic education and counseling into public health strategies, especially in regions with high consanguinity rates (Fareed *et al.* 2017). Premarital genetic screening, community-based education programs, and culturally sensitive counseling can empower couples to make informed reproductive decisions and help reduce the incidence of inherited infertility disorders (Bobdjonova and Abdurakhmanova 2020; Chaudhry and Arif 2024; Özman and Bakırcıoğlu 2020). Additionally, further research is needed to identify population-specific mutations and to develop personalized medical interventions. Ultimately, understanding the complex relationship between inbreeding and infertility not only advances reproductive medicine but also highlights the evolutionary consequences of limited mate selection and the importance of genetic diversity in maintaining population health. Table 1 shows the risk alleles causing infertility.

Table 1

**Risk Alleles and Genetic Mutations Linked to Infertility
in Inbred Populations**

Sex	Gene / Region	Mutation / Risk Allele	Associated Condition	Effect on Fertility
Male	<i>DAZ</i> (Y chromosome)	Deletion in AZFc region	Non-obstructive azoospermia	Absence of sperm due to impaired spermatogenesis
Male	<i>USP9Y</i>	Point mutations or deletions	Severe oligospermia or azoospermia	Reduced or absent sperm production
Male	<i>CFTR</i>	$\Delta F508$ and other mutations	Congenital bilateral absence of vas deferens (CBAVD)	Infertility due to blockage of sperm transport
Male	<i>NR5A1</i> (<i>SF1</i>)	Missense mutations	Hypogonadism, testicular dysgenesis	Hormonal imbalance, impaired sperm development
Male	<i>TEX11</i>	Frameshift or nonsense mutations	Meiotic arrest	Arrest in sperm development during meiosis
Female	<i>FSHR</i>	Variants: c.566C>T (p.Ala189Val), others	Poor ovarian response, premature ovarian failure	Impaired follicular development, infertility
Female	<i>NOBOX</i>	Loss-of-function mutations	Premature ovarian insufficiency	Early depletion of ovarian reserve
Female	<i>GDF9</i>	SNPs in promoter/coding regions	Anovulation, poor oocyte quality	Disrupted folliculogenesis and oocyte maturation
Female	<i>CYP21A2</i>	Mutations causing 21-hydroxylase deficiency	Congenital adrenal hyperplasia (CAH)	Hormonal imbalance, anovulation, reduced fertility
Both	<i>MSH5</i> , <i>MLH1</i>	Mutations in DNA mismatch repair genes	Meiotic arrest or chromosomal abnormalities	Gamete failure due to chromosomal segregation errors

4. CASE STUDIES: INBREEDING IN HUMAN POPULATIONS AND DOMESTICATED SPECIES

Studies conducted on isolated communities, such as the Amish or royal families in Europe, highlighted the negative effects of inbreeding on genetic health. For example, deleterious genes expressed recessively were very prevalent in Habsburg royalty because of consanguineous marriage practices (Alvarez *et al.* 2009).

Inbreeding in livestock and pets has led to the proliferation of genetic disorders, meriting the need for well-considered breeding strategies. For example, inbreeding was held responsible for the incidence of bovine leukocyte adhesion deficiency (BLAD) in dairy cattle (Shuster *et al.* 1992).

An example of heterosis is when hybrids produced by crossing bestow greater fitness on the progeny. Genetic rescue consists of the introduction of new genetic material into an inbred population as a way to counteract inbreeding depression. The introduction of Texas cougars into the Florida panther population increased the genetic variation and the fitness of the population (Hedrick 1995). Table 2 shows the most common genetic conditions due to inbreeding.

Table 2

Genetic Disorders Associated with Inbreeding

Disorder	Description	Species / Population Affected	References
Cystic Fibrosis	Autosomal recessive disorder affecting the lungs and digestive system	Humans (<i>e.g.</i> , European populations)	Bittles 2012
Thalassemia	Genetic blood disorder causing anemia	Humans (<i>e.g.</i> , Middle Eastern and Mediterranean populations)	Hamamy 2012
Hip Dysplasia	Developmental disorder affecting the hip joint	Dogs (<i>e.g.</i> , German Shepherds)	Shuster <i>et al.</i> 1992
Devil Facial Tumor Disease	Contagious cancer affecting Tasmanian devils	Tasmanian devils	McCallum <i>et al.</i> 2009
Mandibular Prognathism	Jaw deformity (<i>e.g.</i> , 'Habsburg jaw')	Humans (<i>e.g.</i> , Habsburg dynasty)	Alvarez <i>et al.</i> 2009

5. COMMON INBREEDING PROBLEMS IN HUMANS

5.1. Royal Families of Europe

The Habsburg dynasty, which ruled parts of Europe for centuries, is a prime example of the consequences of inbreeding. Successive generations of royal intermarriage led to a high frequency of genetic disorders, including the infamous 'Habsburg jaw' (mandibular prognathism) and other hereditary diseases. Charles II of Spain suffered from severe health problems and was sterile, possibly due to extensive inbreeding (Peacock *et al.* 2014; Vilas *et al.* 2019).

5.2. Isolated Human Populations

The Amish communities in the United States often marry within a closed group due to religious and cultural isolation. This has led to a higher incidence of certain rare genetic disorders, such as Ellis-van Creveld syndrome (dwarfism and polydactyly), among others. Isolation can reduce genetic diversity and increase the prevalence of autosomal recessive diseases.

5.3. Consanguineous Marriages in Certain Cultures

In some parts of the Middle East, North Africa, and South Asia, cousin marriages are relatively common. Studies have shown increased risks of genetic disorders, including congenital heart defects and autosomal recessive diseases, in offspring from these unions. While these practices may have social or economic benefits, they come with increased genetic risks and require public health consideration (Ahmad *et al.* 2022; Ahmed *et al.* 2024; Muzammal, Ahmad *et al.* 2021; Muzammal, Ali *et al.* 2021).

5.4. The Pingelapese People (Micronesia)

The Pingelapese people of Micronesia are known for an unusually high prevalence of achromatopsia, a rare genetic disorder causing complete color blindness, extreme light sensitivity, and poor visual acuity. This phenomenon is the result of a historical bottleneck following a catastrophic typhoon in the eighteenth century that reduced the island's population to about 20 individuals, one of whom is believed to have carried the recessive gene for the condition. Due to the island's isolation and the founder effect, the gene became concentrated over generations, now affecting roughly 1 in 30 residents – an incidence vastly higher than the global average of 1 in 30,000 (Barris 1997; Winick *et al.* 1999). Those with achromatopsia are often called ‘night people’ due to their improved night vision, a trait that helps them adapt to the intense sunlight that impairs their vision during the day. The community has culturally adapted to the condition, offering social inclusion and practical accommodations like homemade visors and sunglasses. The case has become a key example in genetics and anthropology, highlighting how isolation and genetic drift can shape human populations (Lowndes *et al.* 2021; McKyton *et al.* 2023). It also raises ethical questions regarding intervention, genetic counseling, and the preservation of cultural identity. This rare instance of genetic concentration illustrates the complex interplay between biology, environment, and culture in human adaptation (Sundin *et al.* 2000).

5.5. Ashkenazi Jewish Population

Due to historical population bottlenecks and endogamy, Ashkenazi Jews have a higher carrier frequency for certain genetic disorders like Tay-Sachs disease and Gaucher disease. Community-wide carrier screening programs have dramatically reduced the birth of affected individuals. Targeted genetic interventions can mitigate the consequences of long-term inbreeding (Behar *et al.* 2004; Guha *et al.* 2012; Manchanda *et al.* 2017). Table 3 shows the high-frequency risk alleles in inbred or isolated Human Populations.

Table 3

**High-Frequency Risk Alleles in Inbred
or Isolated Human Populations**

Population	Disorder	Gene / Mutation	Carrier / Affected Frequency	Cause
Ashkenazi Jews	Tay-Sachs disease	<i>HEXA</i> (1278insTATC)	~1 in 30 carriers	Founder effect, endogamy
Ashkenazi Jews	Gaucher disease type I	<i>GBA</i> (N370S)	~1 in 15 carriers	Founder effect
Amish (USA)	Ellis-van Creveld syndrome	<i>EVC</i> , <i>EVC2</i>	~1 in 200 affected in some communities	Genetic drift, inbreeding
Amish	Maple syrup urine disease	<i>BCKDHA</i> , <i>BCKDHB</i>	~1 in 12 carriers in some settlements	Founder effect, inbreeding
Hutterites	Severe combined immunodeficiency (SCID)	<i>IL2RG</i> , <i>ADA</i>	Clustered cases, very rare elsewhere	Closed breeding pool
Pingelapese (Micronesia)	Achromatopsia	<i>CNGB3</i>	~5–10 % affected	Bottleneck, inbreeding
Finnish	Congenital nephrotic syndrome	<i>NPHS1</i>	~1 in 10,000 affected	Finnish disease heritage
French Canadians (Quebec)	Tyrosinemia type I	<i>FAH</i>	~1 in 20–25 carriers in Saguenay region	Founder effect
French Canadians	LCHAD deficiency	<i>HADHA</i>	Elevated in certain subpopulations	Founder effect
Bedouins (Middle East)	Bardet-Biedl syndrome, Meckel syndrome	<i>BBS1</i> , <i>TMEM67</i> , etc.	10–20x higher than global average	Consanguinity, large family structure

Table 3 (continued)

Population	Disorder	Gene / Mutation	Carrier / Affected Frequency	Cause
Roma (Gypsies)	Congenital myasthenic syndrome	RAPSN	High in Eastern European Roma	Endogamy, drift
Roma	Non-syndromic hearing loss	<i>GJB2</i> (35delG)	High in certain clans	Founder mutations, endogamy
South Indians (Tamil Nadu)	Congenital heart defects, thalassemia	<i>GATA4</i> , <i>HBB</i>	Elevated in some caste-based marriages	Consanguinity
Icelanders	Hemochromatosis	<i>HFE</i> (c.C282Y)	~10–15 % carrier rate	Founder effect, small gene pool
Sardinians (Italy)	β -Thalassemia	<i>HBB</i>	~10–12 % carrier rate	Isolation, malaria selection pressure
Yakuts (Siberia)	Spinal muscular atrophy (SMA)	<i>SMN1</i> deletion	Elevated regional incidence	Bottleneck, isolation
Cape Coloureds (South Africa)	Porphyria variegata	<i>PPOX</i>	~3 in 1,000 affected	Founder mutation
Sephardic Jews (North Africa)	Familial Mediterranean Fever	<i>MEFV</i>	Up to 1 in 7 carriers	Endogamy, regional isolation

6. ECOLOGICAL AND EVOLUTIONARY PERSPECTIVES

6.1. Inbreeding in Natural Populations: Prevalence and Patterns

Inbreeding is common among small isolated populations with few options for mating; these include island species or those that have fragmented habitats due to human activities. An example would be the Tasmanian devil (*Sarcophilus harrisii*), which has undergone a population bottleneck due to inbreeding and the development of transmissible cancers (McCallum *et al.* 2009).

Inbreeding incidence is dependent on habitat fragmentation, population size, and dispersal ability. For example, among inbreeding species, those that do not possess mobility would be expected to have

fewer opportunities to mate. The Iberian lynx (*Lynx pardinus*) is a perfect example of such a situation. Due to the phenomenon of habitat fragmentation, inbreeding has increased, leading to decreased genetic variability (Palomares *et al.* 2012).

Inbreeding often bears a short-term cost, but it may confer long-term adaptation benefits by raising the frequency of beneficial alleles in a population. This trade-off is more prominent where local adaptation is beneficial to the population, especially in stable environments. For example, inbred populations of the house sparrow (*Passer domesticus*) have shown increased adaptation to their local environments (Jensen *et al.* 2007).

Inbreeding could eventually lead to speciation by promoting reproductive isolation and genetic divergence. It can also contribute to increased local adaptation through increasing the frequency of alleles adapted to particular local environmental conditions. For instance, inbred populations of the three-spined stickleback (*Gasterosteus aculeatus*) adapted rapidly to freshwater (Reynolds *et al.* 1995). Evolutionary trade-offs of inbreeding are shown in Table 4.

Table 4

Evolutionary Trade-offs of Inbreeding

Aspect	Short-term Costs	Long-term Benefits	Examples	References
Genetic Diversity	Reduced heterozygosity, increased expression of deleterious alleles	Increased frequency of beneficial alleles in stable environments	House sparrow adaptation to local environments	Jensen <i>et al.</i> 2007
Fitness	Inbreeding depression (reduced fertility, higher mortality)	Local adaptation and speciation in isolated populations	Three-spined stickleback adaptation to freshwater habitats	Reynolds <i>et al.</i> 1995
Disease Susceptibility	Increased vulnerability to diseases due to reduced immune system diversity	Potential for disease resistance in stable, isolated populations	Tasmanian devil population bottleneck and disease spread	McCallum <i>et al.</i> 2009
Population Viability	Reduced population growth and increased extinction risk	Potential for rapid adaptation in small, isolated populations	Florida panther genetic rescue	Johnson <i>et al.</i> 2010

6.2. Case Studies: Inbreeding in Endangered Species and Island Populations

Being a historical inbreeder, the cheetah's low genetic variability renders it susceptible to diseases (O'Brien *et al.* 1985). The Tasmanian devil has undergone several population bottlenecks, which has led to inbreeding and transmission of malignant tumors (McCallum *et al.* 2009).

6.2.1. Inbreeding in Conservation Biology

Furthermore, small populations are especially prone to inbreeding since they have low levels of genetic variation, resulting in reduced adaptability and an increased chance of extinction. For instance, the Mauritius kestrel (*Falco punctatus*) experienced a population bottleneck with inbreeding and a subsequent decline in genetic diversity (Groombridge *et al.* 2000).

Inbreeding is minimized through the careful application of pedigree analysis and genetic monitoring during captive breeding programs. Mate pairing and artificial insemination techniques are employed to assist in the maintenance of genetic diversity. For example, genetic management of the California condor (*Gymnogyps californianus*) captive breeding program has facilitated increases in both population size and genetic diversity (Ralls and Ballou 2004). Assisted gene flow, which translocates individuals from one population to another for the purpose of introducing genetic material, has successfully been employed in the Florida panther (Hedrick 1995). In this respect, the manipulation of genetic diversity brings up ethical concerns regarding interventions in natural processes and animal welfare (Fraser 2008).

6.2.2. Case Studies: Successes and Failures in Inbreeding Management

Two well-known examples illustrate contrasting outcomes of genetic rescue efforts. Florida panthers were successfully rescued genetically by introducing Texas cougars in 1995 (Hedrick).

Isle Royale wolves dwindled from inbreeding after a temporary genetic rescue failed (Adams *et al.* 2011). Table 5 shows the conservation strategies to mitigate inbreeding.

Table 5

Conservation Strategies to Mitigate Inbreeding

Strategy	Description	Example	Outcome	References
Genetic Rescue	Introduction of new genetic material into an inbred population	Florida panther (introduction of Texas cougars)	Increased genetic diversity and population viability	Hedrick 1995
Translocation	Moving individuals from one population to another to increase genetic diversity	Iberian lynx (translocation to new habitats)	Improved genetic health and population growth	Palomares <i>et al.</i> 2012
Assisted Gene Flow	Facilitating gene flow between isolated populations	Scandinavian wolf (migration between populations)	Reduced inbreeding depression	Liberg <i>et al.</i> 2005
Captive Breeding Programs	Controlled breeding to maintain genetic diversity	California condor (captive breeding and reintroduction)	Population recovery and increased genetic diversity	Ralls & Ballou 2004
Habitat Restoration	Restoring habitats to reduce fragmentation and increase population connectivity	Mauritius kestrel (habitat restoration and reintroduction)	Improved population size and genetic health	Groombridge <i>et al.</i> 2000

7. MITIGATING THE EFFECTS OF INBREEDING

Genetic monitoring tools such as microsatellite analysis and whole-genome sequencing are used to measure inbreeding levels and predict population viability (Frankham 2005). Translocation of individuals and re-establishment of habitats can increase population size and connectivity, thereby reducing inbreeding (Fischer and Lindenmayer 2000). Technologies such as CRISPR and genomic selection have opened up new avenues for the management of genetic diversity, including alleviating inbreeding depression. Habitat conservation, genetic monitoring, and most importantly, the use of assisted gene flow should be prioritized to prevent inbreeding in endangered species (Frankham 2005). Research in the future has to look into further studies regarding the long-term effects of inbreeding, the impacts of epigenetics, and the development of new tools in genetic conservation (Allendorf *et al.* 2010).

8. THE CONCEPT OF INBREEDING IN DIFFERENT RELIGIONS

Inbreeding or consanguineous marriage has been, in fact, an area of concern and regulation over centuries-old religious traditions. Each religion regards it differently based on the relevant cultural, social, or genetic factors. This segment will analyze the traditions regarding inbreeding under the world's prominent religions, including but not limited to Islam, Christianity, Judaism, and Hinduism.

8.1. Inbreeding in Islam

Islam has set certain rules on the laws of marriage, which include the position on consanguinity. Cousin marriages, especially the ones between first cousins, are quite common in many parts of the Muslim world. The Quran does not expressly forbid cousin marriages; instead, it is usually accepted because of culture and preserving family ties. Islamic scholars, however, stress genetic counseling and awareness of the possible health risks associated with inbreeding. Research conducted on these populations has indicated that consanguinity-associated marriages are linked with higher prevalence rates of genetic disorders like thalassemia and congenital malformations (Hamamy 2012).

8.2. Inbreeding in Christianity

Christianity discourages consanguineous marriages for both religious and social reasons. The Catholic Church, for example, has historically outlawed marriages between close relatives, *i.e.*, first cousins according to 1983 canon law. The rationale is that such unions could lead to moral and genetic deficiencies. The rigor of these prohibitions has, however, fluctuated in space and time across different Christian denominations. There have been occasions when dispensations have been granted to cousin marriages, especially for purposes of political alliance-making among royalty and nobility and keeping wealth within families (Port and Bittles 2001).

8.3. Inbreeding in Judaism

Jewish marriage and kinship rights are esoterically defined within the Torah while further elaborated in the Talmud. While the Torah explicitly chastises certain close-kin marriages, such as those involving siblings or parent-child unions, there is no explicit condemnation of cousin marriages. In fact, marriage between cousins was a widespread practice in Jewish communities all over, especially those in the Middle East and North Africa, where it served to strengthen family ties

and preserve culture. This practice has largely become less common among modern Jewish communities, especially those in the West, as awareness of genetic risks has spread (Bittles 1994; 'Forbidden Relatives: The American Myth of Cousin Marriage' 1997; Shimony *et al.* 2009; Treister-Goltzman and Peleg 2019; Zhivotovsky *et al.* 2001).

8.4. Inbreeding in Hinduism

Traditionally, Hinduism discourages marriages within the immediate family, while endogamy, or marriage within one's group, is usually encouraged. The Manusmriti, one of the ancient texts concerned with Hindu law, lays down regulations about permissible and prohibited types of unions. Hence, while there is no prohibitory injunction on cousin marriages, they are generally uncommon in most Hindu communities. Instead, arranged marriages often occur within the same caste but outside a family to prevent genetic disorders. On the other hand, in parts of India, especially the South, consanguineous marriages are actually quite common, particularly between cross-cousins, for cultural and economic reasons (Rao and Inbaraj 1977).

8.5. Inbreeding in Other Religions and Cultures

Zoroastrianism in antiquity had strongly prescriptive views favoring consanguineous marriage within the nuclear and extended family to sustain blood purity in the family and foster tie-bonding. Such marriages were called Xwedodah and were believed to be beneficial from a spiritual perspective, although they virtually disappeared in the present day (Bittles and Neel 1994; Boyce 1979). Buddhism does not specifically oppose cousin marriages, and cousin marriage practices differ widely across Buddhist cultures. In some populations, cousin marriages are accepted, whereas in others, they are discouraged on sociological and genetic grounds (Fortunato *et al.* 2006). Historically, marriage traditions have been dissected under the lens of religion. In more recent years, advances in genetics have elucidated the hazards accompanying consanguineous marriages that lead to a higher incidence of autosomal recessive disorders. Several religious communities are beginning to address this concern with genetic counseling and education. Muslim-majority countries are already beginning to start premarital genetic screening programs for the prevention of genetic disorders (Al-Gazali *et al.* 2006). Table 6 shows the religious perspectives on consanguineous marriage, while Table 7 shows the prevalence of consanguineous marriages in different regions.

Table 6

Religious Perspectives on Consanguineous Marriage

Religion	Attitude Toward Cousin Marriage	Genetic Risks Addressed?	References
Islam	Permitted and common in many Muslim-majority countries	Increasing use of genetic counseling and premarital screening	Hamamy 2012
Christianity	Historically discouraged, though dispensations were granted in some cases (<i>e.g.</i> , royalty)	Genetic risks recognized, leading to avoidance of close-kin marriages	Alvarez <i>et al.</i> 2009
Judaism	Permitted, though less common in modern times	Genetic counseling increasingly used in Jewish communities	Treister-Goltzman and Peleg 2019
Hinduism	Generally discouraged, though practiced in some regions (<i>e.g.</i> , South India)	Emphasis on caste endogamy without close-kin marriages	Rao and Inbaraj 1977
Zoroastrianism	Encouraged in ancient times (xwedodah), now rare	Historical practice with spiritual significance, no longer common	Boyce 1979

Table 7

Prevalence of Consanguineous Marriages in Different Regions

Region	Prevalence of Cousin Marriages	Cultural / Religious Context	Genetic Outcomes	References
Middle East	High (20–50 %)	Common in Muslim-majority countries, culturally accepted	Increased prevalence of autosomal recessive disorders (<i>e.g.</i> , thalassemia)	Hamamy 2012
South Asia (India, Pakistan)	High (30–60 %)	Common in some Hindu and Muslim communities, especially in rural areas	Higher rates of genetic disorders (<i>e.g.</i> , congenital malformations)	Rao and Inbaraj 1977
Europe	Low (< 1 %)	Historically practiced among royalty, now rare due to social and genetic concerns	Limited impact on genetic health	Alvarez <i>et al.</i> 2009
North America	Low (< 1 %)	Socially discouraged, legal restrictions in some states	Minimal impact on genetic health	Bittles 2012
Sub-Saharan Africa	Moderate (10–20 %)	Practiced in some communities to strengthen family ties	Increased prevalence of sickle cell anemia and other genetic disorders	Port and Bittles 2001

9. CONCLUSION

The concept of inbreeding is viewed on quite an array of scales with different interpretations depending on the dogmas involved along that spectrum, with social, cultural, and genetic influences at play. For the most part, religions like Islam have historically sanctioned consanguinity, whereas in some sects within Christianity, consanguineous marriages have been condemned. With increased knowledge regarding inbreeding risks through modern genetic research, many religious groups are beginning to institute genetic counseling and educational programs. This comprehensive understanding of religion and genetics is vital in addressing health and social issues related to consanguineous marriages. Future studies should focus on these religions/cultures concerning their influence on marriage patterns on various fronts dealing with genetic diversity and public health. Studies in the future should consider the assessment of genetic counseling programs within religious communities, education in changing marriage practices, and the ethical aspects concerning genetic screening in various cultural contexts.

ACKNOWLEDGMENTS

All lab members.

CONFLICT OF INTEREST

Not declared by the author.

REFERENCES

- Adams, J. R., Vucetich, L. M., Hedrick, P. W., Peterson, R. O., and Vucetich, J. A. 2011. Genomic Sweep and Potential Genetic Rescue during Limiting Environmental Conditions in an Isolated Wolf Population. *Proceedings of the Royal Society B: Biological Sciences* 278 (1723): 3336-44. <https://doi.org/10.1098/rspb.2011.0261>.
- Ahmad, S., Ali, M. Z., Muzammal, M., Mir, F. A., and Khan, M. A. 2022. The Molecular Genetics of Human Appendicular Skeleton. *Molecular Genetics and Genomics* 297 (5): 1195–1214. <https://doi.org/10.1007/s00438-022-01930-1>.
- Ahmed, I., Muzammal, M., Khan, M. A., Ullah, H., Farid, A., Yasin, M., Khan, J., Alam, K., and Mir, A. 2024. Identification of Four Novel Candidate Genes for Non-syndromic Intellectual Disability in Pakistani Families. *Biochemical Genetics* 62 (4): 2571–2586. <https://doi.org/10.1007/s10528-023-10556-w>.

- Al-Gazali, L., Hamamy, H., and Al-Arrayad, S. 2006. Genetic Disorders in the Arab World. *British Medical Journal* 333 (7573): 831–834. <https://doi.org/10.1136/bmj.38982.704931.AE>.
- Allendorf, F. W., Hohenlohe, P. A., and Luikart, G. 2010. Genomics and the Future of Conservation Genetics. *Nature Reviews Genetics* 11 (10): 697–709. <https://doi.org/10.1038/nrg2844>.
- Alvarez, G., Ceballos, F. C., and Quinteiro, C. 2009. The Role of Inbreeding in the Extinction of a European Royal Dynasty. *PLoS ONE* 4 (4): e5174. <https://doi.org/10.1371/journal.pone.0005174>.
- Alayahya, M., Aloraini, T., Al-Harbi, Y., Alsubaie, L., Alswaid, A., Eyaid, W., Mutairi, F., Ababneh, F., Alfadhel, M., and Alfares, A. 2022. Genetic Impact of Non-consanguineous Marriages in Saudi Arabia. *Journal of Biochemical and Clinical Genetics* 5 (2): 37–42. <https://doi.org/10.24911/jbcgenetics/183-1664872492>.
- Barris, M. C. 1997. The Island of the Colorblind. Book review. *Optometry and Vision Science* 74 (3): 125. <https://doi.org/10.1097/00006324-199703000-00002>.
- Behar, D. M., Hammer, M. F., Garrigan, D., Vilems, R., Bonne-Tamir, B., Richards, M., Gurwitz, D., Rosengarten, D., Kaplan, M., Della Pergola, S., Quintana-Murci, L., and Skorecki, K. 2004. MtDNA Evidence for a Genetic Bottleneck in the Early History of the Ashkenazi Jewish Population. *European Journal of Human Genetics* 12 (5): 355–364. <https://doi.org/10.1038/sj.ejhg.5201156>.
- Bittles, A. H. 1994. The Role and Significance of Consanguinity as a Demographic Variable. *Population and Development Review* 20 (3): 561–584. <https://doi.org/10.2307/2137601>.
- Bittles, A. H. 2012. *Consanguinity in Context*. Cambridge: Cambridge University Press. <https://doi.org/10.1017/cbo9781139015844.015>.
- Bittles, A. H., and Neel, J. V. 1994. The Costs of Human Inbreeding and Their Implications for Variations at the DNA level. *Nature Genetics* 8 (2). <https://doi.org/10.1038/ng1094-117>.
- Bobdjonova, O. B., and Abdurakhmanova, F. M. 2020. Consanguineous Marriage as Socio-Medical Problem. *I. P. Pavlov Russian Medical Biological Herald* 28 (2): 249–258. <https://doi.org/10.23888/PAVLOVJ2020282249-258>.
- Boyce, M. 1979. *Zoroastrians, Their Religious Beliefs and Practices*. Library of Religious Beliefs and Practices. London: Routledge & Kegan Paul.
- Carson, S. A., and Kallen, A. N. 2021. Diagnosis and Management of Infertility: A Review. *JAMA (Journal of the American Medical Association)* 326 (1): 65–76. <https://doi.org/10.1001/jama.2021.4788>.

- Chaudhry, T., and Arif, R. 2024. The Impact of Consanguineous Marriage on Children's Human Capital in Pakistan. *Journal of South Asian Development* 19 (1): 112–137. <https://doi.org/10.1177/09731741231200380>.
- Fareed, M., Kaisar Ahmad, M., Azeem Anwar, M., and Afzal, M. 2017. Impact of Consanguineous Marriages and Degrees of Inbreeding on Fertility, Child Mortality, Secondary Sex Ratio, Selection Intensity, and Genetic Load: A Cross-Sectional Study from Northern India. *Pediatric Research* 81 (1): 18–26. <https://doi.org/10.1038/pr.2016.177>.
- Fischer, J., and Lindenmayer, D. B. 2000. An Assessment of the Published Results of Animal Relocations. *Biological Conservation* 96 (1): 1–11. [https://doi.org/10.1016/S0006-3207\(00\)00048-3](https://doi.org/10.1016/S0006-3207(00)00048-3).
- Forbidden Relatives: The American Myth of Cousin Marriage. 1997. *Choice Reviews Online* 34 (09): <https://doi.org/10.5860/choice.34-5171>.
- Fortunato, L., Holden, C., and Mace, R. 2006. From Bridewealth to Dowry? *Human Nature* 17 (4): 355–376. <https://doi.org/10.1007/s12110-006-1000-4>.
- Frankham, R. 2005. Genetics and Extinction. *Biological Conservation* 126 (2): 131–140. <https://doi.org/10.1016/j.biocon.2005.05.002>.
- Fraser, D. 2008. Understanding Animal Welfare. *Acta Veterinaria Scandinavica* 50 (SUPPL. 1): S1. <https://doi.org/10.1186/1751-0147-50-S1-S1>.
- Goldstein, D. B., and Pollock, D. D. 1997. Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. *Journal of Heredity* 88 (5): 335–342. <https://doi.org/10.1093/oxfordjournals.jhered.a023114>.
- Groombridge, J. J., Jones, C. G., Bruford, M. W., and Nichols, R. A. 2000. Conservation Biology – ‘Ghost’ Alleles of the Mauritius Kestrel. *Nature* 403 (6770): 616. <https://doi.org/10.1038/35001148>.
- Guha, S., Rosenfeld, J. A., Malhotra, A. K., Lee, A. T., Gregersen, P. K., Kane, J. M., Pe’er, I., Darvasi, A., and Lencz, T. 2012. Implications for Health and Disease in the Genetic Signature of the Ashkenazi Jewish Population. *Genome Biology* 13 (1): R2. <https://doi.org/10.1186/gb-2012-13-1-r2>.
- Hamamy, H. 2012. Consanguineous Marriages Preconception Consultation in Primary Health Care Settings. *Journal of Community Genetics* 3 (3): 185–192. <https://doi.org/10.1007/s12687-011-0072-y>.
- Hedrick, P. W. 1995. Gene Flow and Genetic Restoration: The Florida Panther as a Case Study. *Conservation Biology* 9: 996–1007. <https://doi.org/10.1046/j.1523-1739.1995.9050988.x-i1>.
- Hwang, K., Yatsenko, A. N., Jorgez, C. J., Mukherjee, S., Nalam, R. L., Matzuk, M. M., and Lamb, D. J. 2010. Mendelian Genetics of Male Infertility. *Annals of the New York Academy of Sciences* 1214: E1–E17. <https://doi.org/10.1111/j.1749-6632.2010.05917.x>.

- Jensen, H., Bremset, E. M., Ringsby, T. H., and Sæther, B. E. 2007. Multi-locus Heterozygosity and Inbreeding Depression in an Insular House Sparrow Metapopulation. *Molecular Ecology* 16: 4066–4078. <https://doi.org/10.1111/j.1365-294X.2007.03452.x>.
- Johnson, W. E., Onorato, D. P., Roelke, M. E., Land, E. D., Cunningham, M., Belden, R. C., McBride, R., Jansen, D., Lotz, M., Shindle, D., Howard, J. G., Wildt, D. E., Penfold, L. M., Hostetler, J. A., Oli, M. K., and O'Brien, S. J. 2010. Genetic Restoration of the Florida Panther. *Science* 329 (5999): 1641–1645. <https://doi.org/10.1126/science.1192891>.
- Liberg, O., Andrén, H., Pedersen, H. C., Sand, H., Sejberg, D., Wabakken, R., Åkesson, M., and Bensch, S. 2005. Severe Inbreeding Depression in a Wild Wolf (*Canis lupus*) Population. *Biology Letters* 1 (1): 17–20. <https://doi.org/10.1098/rsbl.2004.0266>.
- Lowndes, R., Molz, B., Warriner, L., Herbik, A., de Best, P. B., Raz, N., Gouws, A., Ahmadi, K., McLean, R. J., Gottlob, I., Kohl, S., Choritz, L., Maguire, J., Kanowski, M., Käsmann-Kellner, B., Wieland, I., Banin, E., Levin, N., Hoffmann, M. B., ... Baseler, H. A. 2021. Structural Differences across Multiple Visual Cortical Regions in the Absence of Cone Function in Congenital Achromatopsia. *Frontiers in Neuroscience* 15: 718958. <https://doi.org/10.3389/fnins.2021.718958>.
- Manchanda, R., Patel, S., Antoniou, A. C., Levy-Lahad, E., Turnbull, C., Evans, D. G., Hopper, J. L., Macinnis, R. J., Menon, U., Jacobs, I., and Legood, R. 2017. Cost-Effectiveness of Population Based BRCA Testing with Varying Ashkenazi Jewish Ancestry. *American Journal of Obstetrics and Gynecology* 217 (5): 578.e1–578.e12. <https://doi.org/10.1016/j.ajog.2017.06.038>.
- Manolio, T. A., Collins, F. S., Cox, N. J., Goldstein, D. B., Hindorff, L. A., Hunter, D. J., McCarthy, M. I., Ramos, E. M., Cardon, L. R., Chakravarti, A., Cho, J. H., Guttmacher, A. E., Kong, A., Kruglyak, L., Mardis, E., Rotimi, C. N., Slatkin, M., Valle, D., Whittemore, A. S., ... Visscher, P. M. 2009. Finding the Missing Heritability of Complex Diseases. *Nature* 461 (7265): 747–753. <https://doi.org/10.1038/nature08494>.
- Manzoor, R., Imran, W., Murtaza Maken, A., and Hasan Syed, T. 2018. Consanguineous Marriages: Effects on Pregnancy Outcomes in Pakistan. *Journal of Development Policy, Research & Practice (JoDPRP)* 2 (1): 78–105. <https://doi.org/10.59926/jodprp.vol02/06>.
- McCallum, H., Jones, M., Hawkins, C., Hamede, R., Lachish, S., Sinn, D. L., Beeton, N., and Lazenby, B. 2009. Transmission Dynamics of Tasmanian Devil Facial Tumor Disease may Lead to Disease-Induced Extinction. *Ecology* 90 (12). <https://doi.org/10.1890/08-1763.1>.
- McKyton, A., Marks Ohana, D., Nahmany, E., Banin, E., and Levin, N. 2023. Seeing Color Following Gene Augmentation Therapy in Achromatopsia.

- Current Biology* 33 (16): p3489–3494. <https://doi.org/10.1016/j.cub.2023.06.041>.
- Muzammal, M., Ahmad, S., Ali, M. Z., and Khan, M. A. 2021. Alopecia-retardation Syndrome: Molecular Genetics of a Rare Neuro-Dermal Disorder. *Annals of Human Genetics* 85 (5): 147–154. <https://doi.org/10.1111/ahg.12425>.
- Muzammal, M., Ali, M. Z., Ahmad, S., Huma, S., Rizwan, Ahmad, S., Abbasi, A. A., Khan, S., and Khan, M. A. 2021. The Molecular Genetics of UV-Sensitive Syndrome: A Rare Dermal Anomaly. *Journal of the Pakistan Medical Association* 71 (10): 2391–2396. <https://doi.org/10.47391/JPM.A.03-476>.
- Obeagu, E. I., Njar, V. E., and Obeagu, G. U. 2023. Infertility: Prevalence and Consequences. *International Journal of Current Research in Chemistry and Pharmaceutical Sciences* 10 (7): 43–50.
- O'Brien, S. J., Roelke, M. E., Marker, L., Newman, A., Winkler, C. A., Meltzer, D., Colly, L., Evermann, J. F., Bush, M., and Wildt, D. E. 1985. Genetic Basis for Species Vulnerability in the Cheetah. *Science* 227 (4693): 1428–1434. <https://doi.org/10.1126/science.2983425>.
- O'Flynn O'Brien, K. L., Varghese, A. C., and Agarwal, A. 2010. The Genetic Causes of Male Factor Infertility: A Review. *Fertility and Sterility* 93 (1): 1–12. <https://doi.org/10.1016/j.fertnstert.2009.10.045>.
- Özman, O., and Bakırcıoğlu, M. E. 2020. Clinical Impact of Parental Consanguineous Marriage in Idiopathic Nonobstructive Azoospermia. *F and S Reports* 1 (3): 209–212. <https://doi.org/10.1016/j.xfre.2020.07.002>.
- Palomares, F., Godoy, J. A., López-Bao, J. V., Rodríguez, A., Roques, S., Casas-Marce, M., Revilla, E., and Delibes, M. 2012. Possible Extinction Vortex for a Population of Iberian Lynx on the Verge of Extirpation. *Conservation Biology* 26 (4): 689–97. <https://doi.org/10.1111/j.1523-1739.2012.01870.x>.
- Peacock, Z. S., Klein, K. P., Mulliken, J. B., and Kaban, L. B. 2014. The Habsburg Jaw-Re-examined. *American Journal of Medical Genetics, Part A*, 164 (9): 2263–2269. <https://doi.org/10.1002/ajmg.a.36639>.
- Peterson, B. D., Gold, L., and Feingold, T. 2007. The Experience and Influence of Infertility: Considerations for Couple Counselors. *The Family Journal* 15 (3): 251–257. <https://doi.org/10.1177/1066480707301365>.
- Plotnikov, D., and Guggenheim, J. A. 2019. Mendelian Randomisation and the Goal of Inferring Causation from Observational Studies in the Vision Sciences. *Ophthalmic and Physiological Optics* 39 (1): 11–25. <https://doi.org/10.1111/opo.12596>.

- Port, K., and Bittles, A. H. 2001. A Population-Based Estimate of the Prevalence of Consanguineous Marriage in Western Australia. *Community Genetics* 4 (2): 97–101. <https://doi.org/10.1159/000051166>.
- Pritchard, J. K., Stephens, M., and Donnelly, P. 2000. Inference of Population Structure Using Multilocus Genotype Data. *Genetics* 155 (2): 945–959. <https://doi.org/10.1093/genetics/155.2.945>.
- Ralls, K., and Ballou, J. D. 2004. Genetic Status and Management of California Condors. *Condor* 106 (2): 215–228. <https://doi.org/10.1650/7348>.
- Rao, P. S. S., and Inbaraj, S. G. 1977. Inbreeding in Tamil Nadu, South India. *Social Biology* 24 (4): 281–288. <https://doi.org/10.1080/19485565.1977.9988298>.
- Reynolds, J. D., Bell, M. A., and Foster, S. A. 1995. The Evolutionary Biology of the Threespine Stickleback. *The Journal of Animal Ecology* 64 (3): 418–419. <https://doi.org/10.2307/5902>.
- Shimony, A., Afawi, Z., Asher, T., Mahajnah, M., and Shorer, Z. 2009. Epidemiological Characteristics of Febrile Seizures – Comparing between Bedouin and Jews in the Southern part of Israel. *Seizure* 18 (1): 26–29. <https://doi.org/10.1016/j.seizure.2008.05.011>.
- Shuster, D. E., Kehrli, M. E., Ackermann, M. R., and Gilbert, R. O. 1992. Identification and Prevalence of a Genetic Defect that Causes Leukocyte Adhesion Deficiency in Holstein Cattle. *Proceedings of the National Academy of Sciences of the United States of America* 89 (19): 9225–9229. <https://doi.org/10.1073/pnas.89.19.9225>.
- Sokol, R. Z. 2009. Endocrinology of Male Infertility: Evaluation and Treatment. *Seminars in Reproductive Medicine* 27 (2): 149–158. <https://doi.org/10.1055/s-0029-1202303>.
- Spotin, A., Mahami-Oskouei, M., Harandi, M. F., Baratchian, M., Bordbar, A., Ahmadpour, E., and Ebrahimi, S. 2017. Genetic Variability of Echinococcus Granulosus Complex in Various Geographical Populations of Iran Inferred by Mitochondrial DNA Sequences. *Acta Tropica* 165: 10–16. <https://doi.org/10.1016/j.actatropica.2016.03.002>.
- Sultana, S., and Mannen, H. 2004. Polymorphism and Evolutionary Profile of Mitochondrial DNA Control Region Inferred from the Sequences of Pakistani Goats. *Animal Science Journal* 75 (4): 303–309. <https://doi.org/10.1111/j.1740-0929.2004.00190.x>.
- Sundin, O. H., Yang, J. M., Li, Y., Zhu, D., Hurd, J. N., Mitchell, T. N., Silva, E. D., and Maumenee, I. H. 2000. Genetic Basis of Total Colourblindness among the Pingelapese Islanders. *Nature Genetics* 25 (3): 289–293. <https://doi.org/10.1038/77162>.
- Thoma, M., Fledderjohann, J., Cox, C., and Kantum Adageba, R. 2021. Biological and Social Aspects of Human Infertility: A Global Perspective.

- Oxford Research Encyclopedia of Global Public Health*. <https://doi.org/10.1093/acrefore/9780190632366.013.184>.
- Treister-Goltzman, Y., and Peleg, R. 2019. Caution is Needed in Interpreting Hemoglobin A1c Levels in the Muslim Bedouin Population of Southern Israel. *Israel Medical Association Journal* 21 (8): 546–551.
- Vander Borght, M., and Wyns, C. 2018. Fertility and Infertility: Definition and Epidemiology. *Clinical Biochemistry* 62: 2–10. <https://doi.org/10.1016/j.clinbiochem.2018.03.012>.
- Varshney, R. K., Terauchi, R., and McCouch, S. R. 2014. Harvesting the Promising Fruits of Genomics: Applying Genome Sequencing Technologies to Crop Breeding. *PLoS Biology* 12 (6): e1001883. <https://doi.org/10.1371/journal.pbio.1001883>.
- Vilas, R., Ceballos, F. C., Al-Soufi, L., González-García, R., Moreno, C., Moreno, M., Villanueva, L., Ruiz, L., Mateos, J., González, D., Ruiz, J., Cinza, A., Monje, F., and Álvarez, G. 2019. Is the ‘Habsburg Jaw’ Related to Inbreeding? *Annals of Human Biology* 46 (7–8): 553–561. <https://doi.org/10.1080/03014460.2019.1687752>.
- Winick, J. D., Blundell, M. L., Galke, B. L., Salam, A. A., Leal, S. M., and Karayiorgou, M. 1999. Homozygosity Mapping of the a Chromatopsia Locus in the Pingelapese. *American Journal of Human Genetics* 64 (6): 1679–1685. <https://doi.org/10.1086/302423>.
- Wright, S. 1943. Isolation by Distance. *Genetics* 28 (2): 114–138. <https://doi.org/10.1093/genetics/28.2.114>.
- Yin, M. X. C., Chen, X. Y., Shen, X. L., Lin, H. D., Xi, H. T., and Qiu, L. 2023. Illness Anxiety, Infertility Stress, Resilience and Thyroid-Stimulating Hormone among Infertile People Undergoing ART Treatment in China. *Psychology and Health* 40 (2): 217–230. <https://doi.org/10.1080/08870446.2023.2214161>.
- Zhivotovsky, L. A., Ahmed, S., Wang, W., and Bittles, A. H. 2001. The Forensic DNA Implications of Genetic Differentiation between Endogamous Communities. *Forensic Science International* 119 (3): 269–272. [https://doi.org/10.1016/S0379-0738\(00\)00442-4](https://doi.org/10.1016/S0379-0738(00)00442-4).