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Review Article

Ethnic Differences in Genetic and Epigenetic Factors Related to Male Infertility: A Narrative Review

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Abstract

Male infertility causes problems in 7% of worldwide men which creates major difficulties for reproductive health and family planning. A combination of genetic factors and epigenetic factors with environmental elements and lifestyle choices creates causes of this condition. The treatment options available through assisted reproductive technologies (ART) give hope to couples yet we still know only a few aspects of genetic and epigenetic influences related to male infertility. Studies regarding ethnic differences have demonstrated that infertility incidence rates together with biological causes show substantial variation between different cultural groups. The differences become visible through both genetic mutation frequencies along with alterations in epigenetic controls of reproductive functions.

Male infertility suffers from genetic elements that comprise Y-chromosome microdeletions and gene mutations in addition to single nucleotide polymorphisms (SNPs). Fewer studies have been conducted on different ethnic groups because their occurrence rates between populations show significant differences. The development of sperm cells depends critically on epigenetic processes which include DNA methylation and histone modification mechanisms. The modifications affect spermatogenesis and result from genetic factors along with environmental conditions that include diet and lifestyle habits and toxic exposures where these variances differ among ethnic groups.

The understanding of genetic and epigenetic variations across ethnic populations creates essential effects on diagnosing and treating male infertility. The use of ethnic-specific profiles for diagnostic and treatment selection enhances both accuracy rates and treatment success outcomes. The analysis of ethnic differences makes the possibility of developing targeted reproductive healthcare initiatives along with methods to decrease reproductive health inequality.

The article investigates the ways that genetic along epigenetic variations between ethnic populations affect male infertility rates. This review brings together existing knowledge while demonstrating unmet needs to underline the need for ethnic perspectives in studies involving infertility. The research advances methods for developing better specific diagnoses and treatment options for male infertility worldwide.

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1. Introduction

Male infertility is a multifactorial condition that affects approximately 7% of men globally, with significant implications for reproductive health and family planning. The underlying causes of male infertility are complex and can involve a range of genetic, epigenetic, environmental, and lifestyle factors. While advances in assisted reproductive technologies (ART) have offered solutions for many infertile couples, the genetic and epigenetic factors influencing male infertility remain incompletely understood. Among these, ethnic differences have emerged as a crucial area of interest, revealing that the prevalence and manifestation of male infertility may vary significantly across different ethnic groups. These ethnic variations are not only observed in the frequency of genetic mutations but also in the epigenetic modifications that influence fertility outcomes [1, 2].

1.1. Overview of male infertility

Genetic factors, such as Y-chromosome microdeletions, gene mutations, and single nucleotide polymorphisms (SNPs), have long been associated with male infertility. However, the distribution and impact of these genetic anomalies often differ across populations, highlighting the need for population-specific studies [3, 4].

1.2. Genetic and epigenetic factors in male infertility

Similarly, epigenetic factors, which involve heritable changes in gene expression without alterations in the DNA sequence, have been shown to play an essential role in spermatogenesis and fertility. These modifications, such as DNA methylation and histone modifications, can be influenced by both genetic predisposition and environmental exposures, which may vary widely between ethnic groups due to differences in lifestyle, diet, and environmental factors [5].

1.3. Ethnic differences in male infertility

The significance of ethnic differences in genetic and epigenetic factors lies in their potential implications for the diagnosis, management, and treatment of male infertility. Tailored diagnostic approaches, based on ethnic-specific genetic and epigenetic profiles, could enhance the accuracy of infertility assessments and improve the effectiveness of treatment strategies. Moreover, understanding these differences could lead to more personalized healthcare practices and help reduce disparities in reproductive health outcomes across diverse populations [2].

This narrative review seeks to explore the ethnic differences in genetic and epigenetic factors related to male infertility, synthesizing findings from recent global studies to highlight the role of genetic mutations,

epigenetic modifications, and environmental influences. By reviewing the current state of knowledge and identifying areas for future research, this article aims to underscore the importance of considering ethnic diversity in the study of male infertility. Ultimately, the goal is to contribute to the development of more effective and personalized strategies for the diagnosis and treatment of male infertility worldwide.

2. Methodology

This narrative review explores ethnic differences in genetic and epigenetic factors related to male infertility. The goal was to synthesize and summarize findings from various studies that examine how these factors vary across different populations.

2.1. Search strategy

To conduct this review, a systematic search was performed across multiple academic databases, including PubMed, Scopus, EMBASE, Cochrane Library, and Google Scholar, focusing on peer-reviewed articles published within the past 15 years (2008-2023). The search terms used included “male infertility,” “genetics,” “epigenetics,” “ethnic differences,” “Y chromosome deletions, “ethnic groups” AND “DNA methylation” and “single nucleotide polymorphisms (SNPs).” Only studies that provided data on ethnic variations in genetic or epigenetic factors were considered for inclusion.

2.2. Inclusion and exclusion criteria

The inclusion criteria were as follows:

- Studies that focused on male infertility and the associated genetic or epigenetic factors.
- Research that addressed ethnic or population-based differences in these factors. Studies published in English and peer-reviewed journals.

Exclusion criteria included:

- Studies with insufficient data on ethnic variations.
- Non-peer-reviewed articles, dissertations, or conference abstracts.
- Studies focused on female infertility or other aspects of reproductive health unrelated to male infertility.

2.3. Data analysis

The selected articles were reviewed for their relevance and quality. The analysis included a mix of original research, meta-analyses, and comprehensive reviews. Each study was evaluated for its methodology, sample size, and the significance of its findings regarding ethnic differences in male infertility. This process

allowed for a broad synthesis of evidence from different ethnic groups, contributing to the understanding of genetic and epigenetic factors in male infertility across populations [6-10].

3. Genetic Factors in Male Infertility

Genetic factors are a critical determinant of male fertility, accounting for a substantial proportion of infertility cases. Male infertility due to genetic abnormalities can arise from chromosomal abnormalities, gene mutations, and polymorphisms, all of which can significantly influence spermatogenesis and sperm function. The genetic makeup of different populations varies, and as a result, the prevalence and types of genetic factors affecting male infertility can differ markedly across ethnic groups [10-15]. For instance, studies have shown that certain ethnic populations may have higher frequencies of Y chromosome microdeletions or specific gene mutations, which are closely associated with male infertility [11, 12, 14]. Additionally, polymorphisms in genes such as PRM1 and PRM2, which are involved in sperm function, have been found to be linked to infertility in certain ethnic groups [13]. These ethnic differences underscore the importance of considering genetic factors in the diagnosis and management of male infertility.

3.1. Y chromosome microdeletions

Y chromosome microdeletions, particularly in the Azoospermia Factor (AZF) region, are well-documented causes of male infertility, especially in cases of azoospermia and severe oligozoospermia. These microdeletions can impair sperm production and lead to complete infertility. However, studies have revealed considerable ethnic variation in the frequency and distribution of Y chromosome microdeletions. For example, research in East Asian populations, such as Chinese and Japanese men, has identified specific microdeletion patterns that are relatively rare in Caucasian populations. Notably, the gr/gr deletion in the AZFc region has been reported more frequently in Indian and Chinese infertile men than in Caucasian men, indicating potential ethnic differences in susceptibility to infertility due to Y chromosome deletions [11, 16, 17]. This suggests that ethnic-specific screening for Y chromosome microdeletions should be considered in clinical practice, as different populations may exhibit different genetic profiles that affect fertility [18-20].

3.2. Single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) represent one of the most common types of genetic variation in the human genome and are crucial in understanding male infertility. Various studies have identified SNPs in genes related to spermatogenesis, hormone regulation, and sperm function, which are associated with male infertility. However, the presence and impact of these SNPs on fertility often vary between ethnic

groups. For instance, the MTHFR gene, involved in folate metabolism, has been linked to male infertility, but its influence appears to be stronger in Asian populations compared to Caucasians [16, 17]. Other notable genes, such as those involved in oxidative stress (e.g., SOD1) and DNA repair mechanisms (e.g., TP53), exhibit population-specific patterns of polymorphisms that may influence male fertility outcomes [18-20]. These findings underscore the importance of considering ethnic differences when investigating the genetic underpinnings of male infertility, as the prevalence of specific SNPs and their associations with infertility may vary considerably between populations [18, 21].

3.3. Y chromosome haplogroups

Haplogroup Q, which is commonly found among Native American populations, is indeed an interesting example. This haplogroup is thought to have originated in Central Asia and is linked to the early migration of humans into the Americas via the Bering Land Bridge during the last Ice Age. The stability of the AZFc region on the Y chromosome, often associated with male fertility, has been observed in certain subclades of haplogroup Q. This connection could provide insight into how genetic adaptations may have played a role in the survival and expansion of early Native American population [22, 23].

Additionally, studying ethnic-specific haplogroups like Q can help uncover patterns of genetic drift, natural selection, and even historical events that shaped the genetic makeup of populations over time. It's also worth noting that while haplogroups can highlight broad ancestral trends, they represent only a small fraction of our genome and should be considered alongside other genetic and cultural factors for a more comprehensive understanding [24].

3.4. Ethnic-Specific CFTR mutations

3.4.1. CFTR mutations and CBAVD

The CFTR gene (Cystic Fibrosis Transmembrane Conductance Regulator) is a crucial gene located on chromosome 7. It encodes a protein that functions as a channel for chloride ions across epithelial cell membranes. This protein plays a significant role in maintaining the balance of salt and water in various tissues, particularly in the lungs, pancreas, and intestines. Congenital bilateral absence of the vas deferens (CBAVD) is strongly associated with mutations in the CFTR gene [25]. Over 2,000 variants have been identified, with ethnic-specific distributions:

Caucasians: ΔF508 mutation accounts for 72–88% of CBAVD cases, often in compound heterozygosity with mild variants like R117H3 [25].

South Asians: Higher prevalence of splice-site mutations (e.g., 3272–26A→G in 31% of cases) and lower ΔF508 frequency (18%) 813 [26].

East Asians: Novel missense variants (e.g., D110H, Q1352H) dominate, but many are absent in Western populations [25].

4. Epigenetic Factors in Male Infertility

Epigenetic factors have emerged as significant contributors to male infertility, as they regulate gene expression without altering the DNA sequence itself. Epigenetic modifications, such as DNA methylation, histone modification, and non-coding RNA regulation, play pivotal roles in spermatogenesis and sperm function. Abnormalities in these epigenetic processes can disrupt normal sperm production and function, leading to infertility [27, 28]. Recent research has shown that epigenetic alterations in sperm can be passed on to offspring, further complicating the understanding of male infertility [29, 30]. Additionally, studies have suggested that epigenetic modifications associated with infertility may vary across ethnic groups, indicating that the genetic and environmental factors influencing male infertility may be population-specific [31]. These findings underscore the importance of considering epigenetic factors in the diagnosis and treatment of male infertility, as well as in the development of personalized therapies [32, 33].

4.1. DNA methylation patterns

DNA methylation, one of the most studied forms of epigenetic modification, plays a critical role in regulating spermatogenesis. DNA methylation involves the addition of methyl groups to cytosine residues in DNA, which can silence gene expression. Disruptions in DNA methylation patterns have been linked to various male infertility conditions, including abnormal sperm motility, reduced sperm count, and impaired fertilization ability. Studies have shown that the overall methylation landscape is significantly altered in infertile men compared to fertile men [34].

However, these methylation changes are not uniform across all populations. For example, research comparing DNA methylation in infertile Chinese and Caucasian men has revealed significant differences in the methylation of key genes involved in spermatogenesis. These findings suggest that ethnic-specific factors may contribute to variations in epigenetic regulation. In particular, genes such as STK31, which are involved in sperm motility, exhibit different methylation patterns in various ethnic groups, potentially influencing fertility outcomes [35, 36].

Additionally, aberrant DNA methylation patterns in spermatozoa have been observed in men with idiopathic infertility, reinforcing the role of DNA methylation in male fertility [34]. Moreover, the methylation of genes like MTHFR has been associated with infertility, particularly in cases of idiopathic infertility [38), further emphasizing the importance of DNA methylation as a potential biomarker for male infertility and its relevance to assisted reproductive technologies [32].

4.2. Imprinted genes and epigenetic regulation

Imprinted genes, such as H19, MEST, and IGF2, are regulated by parent-of-origin DNA methylation, and defects in the imprinting of these genes have been strongly associated with male infertility. These genes play a crucial role in sperm development and function, and their proper epigenetic regulation is essential for maintaining fertility. Recent studies have highlighted that imprinting defects in these genes, particularly in H19 and MEST, can vary significantly across ethnic groups, with certain populations exhibiting higher rates of epimutations. For instance, research has found that men from African populations tend to have a higher frequency of imprinting defects in the H19 and MEST genes than men from European populations [38, 39]. These variations suggest that ethnic background plays a significant role in the prevalence of epigenetic defects that affect male fertility, emphasizing the need for more focused research on the ethnic-specific epigenetic mechanisms contributing to infertility [29, 40].

4.3. Sperm miRNA profiles

miR-34c is a specific microRNA that has been identified as critical for the process of spermatogenesis. miRNAs are small non-coding RNA molecules that play key roles in regulating gene expression. The involvement of miR-34c in spermatogenesis suggests that it may influence various aspects of sperm production and quality [41]. There are ethnic differences that highlight that the expression levels of miR-34c show significant variation between different ethnic groups, indicating that genetics and possibly environmental or lifestyle factors may lead to differing health outcomes related to fertility across these groups. For instance, miR-34c expression levels are 2.5 times lower in African men compared to European men, offering a clear quantitative comparison between these two ethnic groups [41].

This growing body of evidence underscores the importance of considering ethnic variations in the study of male infertility, as epigenetic regulation may be influenced by genetic, environmental, and lifestyle factors unique to each population.

5. Environmental and Lifestyle Factors

The interplay between environmental exposures, lifestyle factors, and genetic and epigenetic changes is crucial in understanding male infertility. Environmental toxins, diet, and lifestyle choices can impact both the genetic and epigenetic landscape of male fertility. These factors vary considerably across ethnic populations, influencing fertility outcomes in diverse ways. For example, Mima (2018) reviewed the evidence linking environmental toxins to male fertility, highlighting how such exposures can affect sperm quality and reproductive function [42]. Cescon (2020) further discussed how environmental factors, particularly epigenetic alterations, contribute to male infertility [43].

Lifestyle choices, such as smoking, alcohol consumption, and diet, also significantly influence male fertility. Osadchuk et al., (2023) examined how lifestyle factors can lead to reduced sperm quality and emphasized the importance of considering these factors in clinical practice [44]. Additionally, Martinović et al., (2024) highlighted the role of epigenetic interventions and lifestyle modifications in improving fertility outcomes [45].

Moreover, environmental factors interact with genetic regulation during sperm development, which can affect offspring health. Sengupta et al., (2023) explored how environmental and genetic influences play a role in sperm-to-embryo processes and their implications for reproductive health [46]. Finally, Guerrero-Bosagna et al., (2014) reviewed the epigenetic transgenerational inheritance of sperm alterations and their impact on male infertility, suggesting that paternal lifestyle could affect offspring health outcomes across generations [30].

5.1. Diet and nutrition

Diet plays a significant role in modulating male fertility, as essential nutrients can influence both genetic and epigenetic mechanisms that regulate spermatogenesis. Nutrients such as folate, zinc, selenium, and antioxidants are critical for DNA repair and methylation, which are essential for healthy sperm production [47, 48]. Dietary patterns differ significantly across ethnic groups, with some populations consuming higher levels of certain nutrients due to cultural dietary preferences. For example, Mediterranean diets rich in antioxidants have been shown to support sperm health [49], while certain Asian diets that are high in soy-based products may influence hormone levels and sperm function differently. These nutritional variations may contribute to the differences in male infertility observed between ethnic populations. Furthermore, epigenetic changes related to diet, such as methylation of key fertility-related genes, may differ between populations, emphasizing the need for population-specific dietary recommendations for fertility improvement [50, 51].

5.2. Environmental exposures

Environmental factors, such as exposure to endocrine-disrupting chemicals (EDCs), heavy metals, and pollutants, are significant contributors to male infertility [52]. These toxins can alter the epigenetic regulation of genes involved in spermatogenesis, leading to infertility. Environmental exposures often vary depending on geographic location, occupation, and socioeconomic status, making them highly relevant to understanding ethnic differences in infertility. For instance, men from industrialized regions may have higher exposure to environmental toxins like phthalates, which have been linked to decreased sperm count and motility [42, 43]. Conversely, men from rural or less industrialized areas may experience lower levels of exposure but could be at risk for other environmental stressors, such as agricultural chemicals [30,

32]. These differences highlight the need for ethnic-specific environmental risk assessments to address the unique factors contributing to male infertility in various populations [46, 53].

6. Implications for Diagnosis and Treatment

Understanding the ethnic variations in genetic and epigenetic factors associated with male infertility is essential for improving diagnostic and treatment strategies. As the genetic and epigenetic profiles of different populations vary, it is important to consider ethnicity when developing personalized treatment plans. Genetic testing for Y chromosome microdeletions, SNPs, and epigenetic changes should be tailored to the ethnic background of the patient to increase diagnostic accuracy and treatment efficacy [54, 55]. Moreover, environmental and lifestyle factors should be taken into account when designing fertility interventions, ensuring that treatments are culturally appropriate and effective for diverse populations [12, 56]. As research continues to uncover the complex relationships between genetics, epigenetics, and male infertility, future studies should focus on large-scale, multi-ethnic cohorts to provide more comprehensive insights into the ethnic-specific risk factors for male infertility [57, 58].

7. Discussion

7.1. Ethnic variations in genetic causes of male infertility

The genetic underpinnings of male infertility, particularly those involving Y chromosome microdeletions and SNPs, exhibit substantial ethnic heterogeneity. Previous studies have shown that specific deletions within the AZF region of the Y chromosome, such as the gr/gr deletion, are more prevalent in Asian populations compared to Caucasians, further emphasizing the ethnic specificity of genetic markers in male infertility [16, 59]. This is important because genetic testing, specifically for Y chromosome microdeletions, is a common diagnostic tool for male infertility. A standardized diagnostic approach that takes ethnic differences into account may enhance the precision of diagnosis and improve patient outcomes [60, 61].

Furthermore, SNPs in genes associated with spermatogenesis, such as the MTHFR gene, demonstrate population-specific risks that can inform clinical decision-making. For instance, the association of MTHFR polymorphisms with male infertility in Asian populations but not in Caucasians could guide targeted genetic screening for men from these regions [62, 63]. Understanding these ethnic-specific genetic variations can ultimately lead to more personalized diagnostic approaches, particularly for those seeking fertility treatments or sperm preservation [11].

While this review identified several key genetic markers, it is crucial to note that the genetic basis of male infertility is far from fully elucidated. Many genetic factors remain undiscovered, and the complexity of genetic interactions (such as epistasis) suggests that a multifactorial approach is needed to understand

infertility across different ethnic groups. For instance, the interplay between mutations in spermatogenesis-related genes and environmental factors may present a more intricate pathophysiological mechanism of infertility than previously anticipated. Future research should therefore focus on expanding genetic studies to include diverse ethnic cohorts, allowing for a comprehensive understanding of genetic variations in male infertility [11, 16].

7.2. The role of epigenetics in male infertility

Epigenetic mechanisms, including DNA methylation, histone modifications, and non-coding RNA regulation, are increasingly recognized as pivotal in the regulation of spermatogenesis and male fertility. The fact that epigenetic changes can be influenced by environmental factors and lifestyle choices makes them an essential focus for understanding the underlying causes of male infertility. The findings from this review highlight the significant role of DNA methylation in spermatogenesis, with specific gene loci showing altered methylation patterns in infertile men [29, 64]. These findings are particularly relevant in the context of ethnic differences, where varying environmental exposures and lifestyle habits may influence the epigenome in population-specific ways [29, 36].

For example, variations in global DNA methylation levels between Caucasian and Chinese populations suggest that epigenetic regulation of sperm function may vary across ethnic groups [43, 65]. These ethnic differences in methylation could have profound implications for male infertility diagnostics and treatment. More research is needed to identify specific epigenetic markers that correlate with infertility in diverse ethnic populations, with the goal of developing non-invasive diagnostic tests based on sperm DNA methylation profiles [46]. These epigenetic markers could eventually serve as biomarkers for early detection and prognosis of infertility, leading to more targeted therapeutic approaches.

The review also highlights the role of imprinted genes in male infertility, particularly in relation to epigenetic modifications. Defects in the imprinting of genes such as H19 and MEST have been observed to cause infertility in some populations, with distinct variations between ethnic groups [46]. Understanding how these imprinted genes are regulated in different populations could provide valuable insights into the genetic-epigenetic interactions that contribute to male infertility. These findings suggest that epigenetic analysis, in conjunction with genetic screening, could offer a more comprehensive approach to diagnosing and managing infertility.

7.3. Environmental and lifestyle factors: Implications for ethnic-specific differences

Environmental and lifestyle factors are known to influence both genetic and epigenetic mechanisms, potentially exacerbating the risk of infertility. This review emphasizes that ethnic differences in diet, occupational exposure to environmental toxins, and lifestyle habits are significant contributors to male

infertility. These factors not only affect the epigenetic regulation of sperm but also interact with genetic predispositions to increase the risk of infertility in certain populations. For example, the consumption of diets rich in folate has been shown to influence DNA methylation patterns and spermatogenesis, and differences in dietary habits between ethnic groups can explain some of the observed disparities in male infertility [53, 66].

In addition to dietary factors, exposure to environmental toxins such as pesticides, heavy metals, and endocrine-disrupting chemicals further complicates the etiology of male infertility. Men from certain ethnic backgrounds who are exposed to higher levels of these toxins due to occupational or environmental conditions may experience an increased risk of infertility. For instance, research has shown that farmers in rural regions of Southeast Asia, where pesticide use is prevalent, have higher rates of sperm DNA fragmentation and lower fertility. This finding points to the critical need for public health interventions that address environmental factors and their impact on male reproductive health, particularly in populations with high occupational exposure to toxic substances [67, 68].

Lifestyle habits such as smoking, alcohol consumption, and obesity are also important contributors to male infertility. These habits are influenced by cultural and socioeconomic factors, which vary across ethnic groups. For example, studies have shown that smoking rates are higher among certain ethnic groups, leading to increased DNA damage and abnormal epigenetic modifications in sperm. Similarly, obesity, which is linked to changes in sperm DNA methylation and oxidative stress, is more prevalent in some ethnic populations due to genetic predispositions and lifestyle factors [69, 70].

7.4. Clinical implications and the need for personalized approaches

The findings from this review underscore the importance of considering ethnic differences when diagnosing and treating male infertility. The integration of genetic and epigenetic screening into clinical practice could enable healthcare providers to offer more personalized and effective treatments to patients. Ethnicity-specific genetic markers and epigenetic profiles could serve as valuable tools for early detection and risk assessment in populations at higher risk for infertility [12, 71]. In particular, men from specific ethnic groups who carry genetic variants or epigenetic modifications that predispose them to infertility could benefit from targeted interventions aimed at improving sperm quality [26, 72]. Ethnic disparities in ICSI outcomes, particularly in sperm retrieval success rates among individuals with non-obstructive azoospermia, reveal notable differences between African and Caucasian populations. The reported data—72% success for Africans compared to 89% for Caucasians—underscores a critical issue that requires further exploration [73]. These differences may arise from various factors such as genetic variations, disparities in healthcare access, socioeconomic challenges, or differences in clinical practices. Identifying the underlying causes is crucial to achieving equitable treatment outcomes for all patients undergoing ICSI procedures.

Moreover, lifestyle and environmental interventions tailored to the unique needs of different ethnic populations could help mitigate the effects of infertility. Public health campaigns that promote healthier lifestyles, improved diets, and reduced exposure to environmental toxins could have a significant impact on male fertility rates across diverse populations [74, 75]. These strategies could be particularly beneficial when applied in populations with specific genetic predispositions, offering a personalized approach that enhances fertility outcomes.

8. Future Research Directions

While significant progress has been made in understanding the genetic and epigenetic factors contributing to male infertility, much remains to be discovered. Future research should prioritize large-scale, multi-ethnic studies to better capture the full extent of genetic and epigenetic diversity in male infertility. These studies should aim to identify novel genetic variants, epigenetic markers, and environmental factors that contribute to infertility across different ethnic groups [76, 77].

Additionally, the use of advanced omics technologies, such as epigenomics, transcriptomics, and proteomics, will be critical for further elucidating the molecular mechanisms of male infertility. These approaches will provide a deeper understanding of the complex interactions between genetic, epigenetic, and environmental factors and their collective impact on male reproductive health [78, 79]. We highly recommend that establishing a global male infertility biobank with ethnic cohorts would facilitate research on genetic, environmental, and lifestyle factors contributing to male infertility across diverse populations. Additionally, developing ethnic-specific sperm epigenome reference maps would provide insights into how various factors influence sperm quality and fertility, enabling more personalized and effective approaches for diagnosis and treatment.

In conclusion, this review highlights the importance of considering ethnic differences in the genetic and epigenetic factors related to male infertility. The complex interplay between genetic mutations, epigenetic modifications, and environmental influences underscores the need for a personalized, multi-faceted approach to diagnosing and treating male infertility. By incorporating ethnic-specific information into clinical practice, researchers and healthcare providers can improve outcomes for men affected by infertility and move towards more targeted and effective interventions [80].

9. Conclusion

Male infertility emerges from genetic, epigenetic, and environmental sources and takes different forms according to ethnic population makeup. Testing protocols require ethnicity-based genetic screening since genetic variation including Y chromosome defects and CFTR and AR gene mutations determines the need for separate examination strategies. Environmental and lifestyle factors together with DNA methylation

and histone modifications and non-coding RNAs play an active role in shaping infertility risk patterns between different populations.

The diagnostic process for male infertility needs both individual treatment strategies and specific knowledge about different ethnic groups to achieve better treatment results. Reproductive medicine benefits from the implementation of genetic along with epigenetic data specific to ethnic populations because it improves diagnostic outcomes and creates more effective treatment plans. Large-scale multi-ethnic research studies of the future must explore genetic, epigenetic, and environmental relationships to develop precision medicine techniques that address the reproductive health needs of multiple ethnicities.

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