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ABOUT COVER

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The primary aim of *World Journal of Medical Genetics* (*WJMG*, *World J Med Genet*) is to provide scholars and readers from various fields of medical genetics with a platform to publish high-quality basic and clinical research articles and communicate their research findings online.

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CASE REPORT

Celiac sprue - a cryptic disease: A case report

Lisa R Maness

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Abstract

BACKGROUND

Celiac sprue, or celiac disease, is a relatively common disease whereby many are unaware that they have it. It often manifests with symptoms outside of the digestive system. Many health care providers are unaware of the wide variety of symptoms of celiac disease as well as diseases that are associated with it, often delaying diagnosis and treatment.

CASE SUMMARY

The following case indicates an otherwise healthy 20-year-old female who presents with a variety of symptoms and is ultimately diagnosed with shingles, infectious mononucleosis, and celiac disease

CONCLUSION

Although it is known that risk-factors are genetic as well as environmental, much more research is needed to better understand the relationship of potential causes. In addition, continuing education is needed in health care so that more practitioners better understand celiac disease.

Key Words: Celiac disease; Autoimmune disease; Shingles; Infectious mononucleosis; Case report

Core Tip: More studies are needed that correlate infectious agents such as Epstein-Barr virus and varicella zoster virus to celiac disease (CD). In addition, further in-depth studies on this particular patient, as well as others, may yield more information on immune status of patients with CD. This case and others demonstrate that more health care practitioners should understand that shingles can occur in patients outside of those recommended for vaccination; delaying treatment places patients more at risk. Practitioners also need to better understand CD, its wide range of symptoms, and its relationship to other infectious agents.

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INTRODUCTION

A 21-year-old female on a vegetarian diet was enrolled in graduate school and working at a local supermarket. She had a history of abdominal pain and bloody diarrhea with a colonoscopy several months previously indicating anal fissures and internal hemorrhoids. She visited a family physician complaining of a tingly, itchy rash on the forehead, eyelid, and eyebrow as well as multiple large, swollen lymph nodes in the neck and jaw, as well as fatigue. The family practitioner mistakenly denied shingles, caused by the varicella zoster virus (VZV), but took note of the large lymph nodes and ordered a rapid test for infectious mononucleosis, caused by Epstein-Barr virus (EBV), that initially turned out negative. The patient was referred to a dermatologist for the rashes.

CASE PRESENTATION

Chief complaints

The patient described to the dermatologist feeling a tingling sensation from the right eye to the right side of the scalp, but the physician stated that this could not be shingles due to her young age. Given the option to take a biopsy in order to determine the cause, the patient agreed. During the 2 wk wait for biopsy results, the patient developed symptoms of blurry vision, numbness in the extremities, night sweats, itchy skin, dizziness, headaches, extreme fatigue, bone and muscle pain in the hips, thighs, and arms along with left upper quadrant pain and an increasing number of lymph nodes enlarging.

Personal and family history

She had a history of abdominal pain and bloody diarrhea with a colonoscopy several months previously indicating anal fissures and internal hemorrhoids.

Physical examination

Multiple physicians were seen over several weeks and all claimed that "there is nothing wrong" with the patient. One ordered an X-ray of the left hip and no abnormalities were detected. Others repeated spot tests for infectious mononucleosis, strep throat, and human immunodeficiency virus, all of which were negative. 2 wk later, the biopsy results were positive for VZV. The same dermatologist who denied that it could be shingles then claimed that it was too late for treatment, that treatment for shingles should begin within 48 h.

Within days, the patient went to the emergency department (ED) with continuation of symptoms and increased abdominal, bone, and joint pain; a cat scan was performed on the abdominal area, with no obvious abnormalities, except for enlarged ovarian follicles. An ultrasound was performed on the head and neck soft tissues; several nodes were measured and reported to be "slightly prominent", one 2.2 cm in length. The spot mono and strep tests were repeated once again and were negative. Complete blood count (CBC), comprehensive metabolic panel, erythrocyte sedimentation rate, thyroid stimulating hormone, and lipase were all normal and pregnancy test was negative. The ED physician noticed the report of follicles in each ovary and discharged the patient with diagnosis of adenopathy and follicular cysts.

The patient visited her OB-GYN within the next several days and he stated that the sizes of the follicles were normal and of no concern. He stated that he believed the patient's primary problem was intestinal and recommended that she revisit the gastroenterologist. The white blood cell (WBC) count at OB-GYN visit was $3.8 \times 10^3/\mu L$ with the reference range of $4.0\text{-}11.0^3/uL$. The student quit her part-time job as she was unable to keep up with expectations.

Laboratory examinations

At several subsequent appointments with a family practitioner a month after onset of symptoms, a physician's assistant (PA) ordered tests for rocky mountain spotted fever, lyme antibodies, uric acid, CBC with differential, and EBV antibody profile. She also prescribed acyclovir to address the shingles diagnosis. The WBC count was still 3.8 × 10^3/μL and at this time EBV titers indicated abnormalities. The EBV Ab VCA, IgM was 81.6 (H) with the reference range of 0.0-35.9 U/mL, the EBV Ab VCA, IgG was 225.0 (H) with the reference range of 0.0-17.9 U/mL, and the EBV Nuclear Antigen Ab, IgG was 66.7 (H) with the reference range of 0.0-17.9 U/mL (Table 1). Results indicated that the patient likely experienced an infection from EBV sometime in the past or recent past[1].

The PA referred the patient to an infectious disease physician to discuss the symptoms of infectious mono and shingles as well as leukopenia. The infectious disease specialist suggested to continue resting adequately, have a CBC repeated in 4 wk if lymph node swelling persists, and to reassess the size of the spleen if necessary. The PA referred the patient for a magnetic resonance imaging; the head scan showed no abnormalities. The patient was referred for another ultrasound of the neck to check the lymph nodes and upon noting further enlargement was referred to an Ear/Nose/Throat specialist. This specialist was unable to know for certain the cause of the enlargements as more nodes were enlarging such as in the cheekbone, armpit, neck, and jaw. He felt it was likely due to the combination of viral infections, leaving it up to the patient to decide whether to have a biopsy performed. After a couple of weeks of symptoms not subsiding, the patient decided to have this performed on the largest lymph node just below the jaw; the result was that this was a reactive lymph node. 2 wk later, after declaring that the patient's symptoms were due to EBV and recent shingles, the PA orders celiac disease (CD) panel and Ova and Parasite test in response to patient symptoms of left upper quadrant abdominal pain and fatty, loose, yellow stools. Within a week the CD panel results indicated a t-transglutaminase (tTG) IgA level of > 100 U/mL, with a reference range of 0-3 U/mL (Table 2). The endomysial antibody IgA was positive. The Quantitative IgA level was 137 mg/dL, with the range of 87-352 mg/dL. The patient was referred to her gastroenterologist for upper gastrointestinal endoscopy.

Imaging examinations

An endoscopy was performed and impressions from the test were: Duodenal mucosal changes seen, suspicious for CD. Biopsies were taken and results from the biopsies indicated celiac disease, whereby the patient should be placed on a gluten free diet indefinitely and recommended to have gluten antibody levels checked periodically.

Two months after initial complaints, the patient had greater explanation for the prolonged and multiple symptoms, including swollen lymph nodes, tingling in the scalp, numbness in the extremities, blurry vision, dizziness, headaches, itchy skin, extreme fatigue, bone and muscle pain in the hips, thighs, and arms, and left upper quadrant pain. It is difficult to know which occurred first, which disease led to the others, if any causation, although it is likely that the shingles occurred in response to untreated CD. It is difficult to understand how long the CD was present or if EBV from the past, or recent past, played a role. Over the next year, the patient adhered to a strict certified gluten free diet and the tTG IgA level decreased over time to 73 U/mL 4 mo later, 18 U/mL 8 mo later, and 12 U/mL 15 mo later.

MULTIDISCIPLINARY EXPERT CONSULTATION

The PA referred the patient to an infectious disease physician to discuss the symptoms of EBV and shingles as well as leukopenia. The infectious disease specialist suggested to continue resting adequately, have a CBC repeated in 4 wk if lymph node swelling persists, and to reassess the size of the spleen if necessary.

FINAL DIAGNOSIS

An endoscopy was performed and impressions from the test were: Duodenal mucosal changes seen, suspicious for CD. Biopsies were taken and results from the biopsies indicated celiac disease.

TREATMENT

The patient should be placed on a gluten free diet indefinitely and recommended to have gluten antibody levels checked periodically.

Table 1 Results from Epstein-Barr virus antibody profile

Name	Value	Reference range
EBV Ab VCA, IgM	81.6 H	0.0-35.9 (U/mL), Negative ≤ 36.0 U/mL, Equivocal = 36.0-43.9 U/mL, Positive ≥ 43.9 U/mL
EBV Ab VCA, IgG	225.0 H	0.0-17.9 (U/mL), Negative = 18.0 U/mL, Equivocal = 18.0-21.9 U/mL, Positive ≥ 21.9 U/mL
EBV Nuclear Antigen Ab, IgG	66.7 H	0.0-17.9 (U/mL), Negative ≤ 18.0 U/mL, Equivocal = 18.0-21.9 U/mL, Positive ≥ 21.9 U/mL

EBV: Epstein-Barr virus.

Table 2 Results from celiac disease panel

Name	Value	Reference range
Endomysial antibody IgA	Positive	Negative
t-Transglutaminase (tTG[1]) IgA	> 100 H	0-3 (U/mL), Negative = 0-3 U/mL, Weak Positive = 4-10 U/mL, Positive ≥ 10 U/mL
Immunoglobulin A, Qn, serum	137 H	87-32 (mg/dL)

[1]t-Transglutaminase has been identified as the endomysial antigen. Studies have demonstrated that endomysial IgA antibodies have over 99% specificity for gluten sensitive enteropathy.

OUTCOME AND FOLLOW-UP

Over the next year, the patient adhered to a strict certified gluten free diet and the tTG IgA level decreased over time to 73 U/mL 4 mo later, 18 U/mL 8 mo later, and 12 U/mL 15 mo later.

DISCUSSION

Celiac disease description, symptoms, and causes

The National Institute of Diabetes and Digestive and Kidney Diseases estimates that about 2 million people in the United States have CD, many of which have not been diagnosed[2]. CD is described as a chronic digestive immune disorder that damages the villi of the small intestine and other tissues and is triggered by ingesting foods with gluten. Foods that are high in gluten are wheat, rye, and barley and these are common in breads, pasta, and baked goods. In addition, gluten contaminates many other foods and is also present in cosmetics, vitamins, and medicines.

Patients with celiac disease are unable to obtain all of the nutrients the body needs because of damage to the intestine[3]. In addition to pale, fatty, and loose stools, bloating, nausea, vomiting, constipation, and abdominal pain, patients also have many other symptoms since CD is an autoimmune disease and not just an allergy. Patients have malabsorption, weight loss, fatigue, headaches, tingling of the extremities, cognitive impairment, joint pain, nervous system problems, reduced spleen function, itchy skin rashes, anemia, bone loss, and more. Rare complications of celiac disease include cancer of the small intestine, liver damage, and non-Hodgkin's lymphoma[2]. People with CD are more likely to have other immune-related diseases such as thyroid diseases, Sjogren's Syndrome, rheumatic diseases, type 1 diabetes, and others.

Advancements have been made to determine prevalence of celiac among various combinations of HLA genes. Individuals with DQ2.5/DQ2.5 genotype are in the highest risk gradient with a risk of 1:7 [4]. Those with DQ2.5/DQ2.2 are in a 1:10 risk gradient while DQ2.5/DQ8 are in the 1:19 risk gradient. The patient in this case study has a DQ2.2/DQ2.5 genotype, placing her in the 1:10 risk gradient. Individuals with genotypes HLA-DQ are more at risk for celiac disease because these molecules present gluten proteins to T cells[5].

Whereas genotype is one factor that contributes to celiac disease, there are environmental risks as well. It has been suggested that formula feeding in infants, timing of gluten introduction, infectious agents, and gut microbiota may relate to onset of celiac disease[6]. It is generally understood that the pathogenesis of autoimmune diseases is due to an imbalance between T helper 1 and 2 cell responses [7]. The recipe that fuels celiac disease appears to be a mix of genetic predisposition, gluten exposure, reduction of intestinal barrier function, an innate inflammatory response to gluten, an imbalanced gut microbiome, and a faulty adaptive immune response.

Relationship of celiac disease to shingles and infectious mononucleosis

There are a few studies that link CD with shingles and that link CD with EBV. A nationwide cohort study performed in Sweden indicated that CD leads to a 1.62-fold increased risk of VZ over time, even in patients who are less than 60 years of age[8]. There are also cases available for discussion in celiac patient forums that indicate a correlation between the 2 diseases, even in patients who are less than age 50[9]. More studies are needed in other global regions to further determine any correlation between CD and VZ. Delayed treatment of shingles, such as that of the patient in this case, risks further complications such as post-herpetic herpes and blindness[10,11].

It has been shown that a protein known as EBNA2 that is produced by EBV binds to locations along the human genome[12]. The virus is closely associated with celiac disease as well as several other autoimmune diseases, including multiple sclerosis, type 1 diabetes, rheumatoid arthritis, inflammatory bowel disease, and systemic lupus erythematosus. These findings are highly suggestive that EBV plays a role in auto-immunity. There are also numerous cases that specifically link EBV with CD, some of which show the virus actively present within inflammatory cells and enterocytes of those with CD[13,14]. Much more research on the effects of EBV on CD and other autoimmune diseases is certainly warranted.

CONCLUSION

More studies are needed that correlate infectious agents such as EBV and VZV to CD. In addition, further in-depth studies on this particular patient, as well as others, may yield more information on immune status of patients with CD. This case and others demonstrate that more health care practitioners should understand that shingles can occur in patients outside of those recommended for vaccination; delaying treatment places patients more at risk. Practitioners also need to better understand CD, its wide range of symptoms, and its relationship to other infectious agents.

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SYSTEMATIC REVIEWS

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SYSTEMATIC REVIEWS

Epigenetics in the etiology and management of infertility

Tajudeen Olanrewaju Yahaya, Danlami M Bashar, Esther O Oladele, Ja'afar Umar, Daniel Anyebe, Abdulrazaq Izuafa

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Abstract

BACKGROUND

Epigenetic disruptions have been implicated in some cases of infertility and can serve as therapeutic targets. However, the involvement of epigenetics in infertility has not received adequate attention.

AIM

This study aimed to determine the epigenetic basis of infertility in order to enhance public knowledge.

METHODS

Relevant articles on the subject were collected from PubMed, RCA, Google Scholar, SpringerLink, and Scopus. The articles were pooled together and duplicates were removed using Endnote software.

RESULTS

Available information shows that epigenetic mechanisms, mainly DNA methylation, histone modification, and microRNA interference are necessary for normal gametogenesis and embryogenesis. As a result, epigenetic disruptions in genes that control gametogenesis and embryogenesis, such as *DDX3X*, *ADH4*, *AZF*, *PLAG1*, *D1RAS3*, *CYGB*, *MEST*, *JMJD1A*, *KCNQ1*, *IGF2*, *H19*, and *MTHFR* may result in infertility. Aberrant DNA methylation during genomic imprinting and parental epigenetic mark erasures, in particular, may affect the DNA epigenomes of sperm and oocytes, resulting in reproductive abnormalities.

Histone epigenetic dysregulation during oocyte development and histone-protamine replacement in the sperm may also cause reproductive abnormalities. Furthermore, overexpression or repression of certain microRNAs embedded in the ovary, testis, embryo, as well as granulosa cells and oocytes may impair reproduction. Male infertility is characterized by spermatogenesis failure, which includes oligozoospermia, asthenozoospermia, and teratozoospermia, while female infertility is characterized by polycystic ovary syndrome. Some epigenetic modifications can be reversed by deactivating the regulatory enzymes, implying that epigenetic reprogramming could help treat infertility in some cases. For some disorders, epigenetic drugs are available, but none have been formulated for infertility.

CONCLUSION

Some cases of infertility have an epigenetic etiology and can be treated by reversing the same epigenetic mechanism that caused it. As a result, medical practitioners are urged to come up with epigenetic treatments for infertility that have an epigenetic cause.

Key Words: DNA methylation; Gametogenesis; Infertility; Polycystic ovary syndrome; Oligozoospermia; Teratozoospermia

Core Tip: This article reviews the role of epigenetics in the etiology of infertility, which can be used as a therapeutic target. Some cases of infertility are due to epigenetic disruptions, and this is probably the cause of unknown etiology in some cases of infertility. However, there is little awareness on this subject, hindering its application in mainstream medicine.

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INTRODUCTION

Infertility is defined as a couple's inability to conceive after a year of consistent copulation without the use of contraception[1]. Infertility is becoming more prevalent worldwide and is now a serious public health concern[2,3]. At the very least, roughly 15% of couples are infertile[4], with males accounting for 40%, females also account for 40%; and both jointly contributing to the remaining 20%[5]. The most common feature of male infertility is spermatogenesis failure, which is responsible for half of all human infertility[6]. Spermatogenesis failure is characterized by an abnormal sperm count (oligozoospermia), weak sperm motility (asthenozoospermia), and abnormal sperm morphology (teratozoospermia)[6,7]. The most common features of female infertility are amenorrhea and irregular menstruation[8].

Infertility is often devastating and affects all aspects of life, including physical, mental, and social health[9,10]. Infertility causes enormous psychological problems, poor sexual satisfaction, and a low quality of life[10]. Women are often more affected by the effects of infertility than men, as they are deprived of financial support and basic needs by their husbands, families, and communities[11]. In cultures that prioritize child-bearing, childless couples are stigmatized and mocked[1]. In some cases, childlessness causes infidelity, polygamy, and divorce or separation. Infertility treatment can also be expensive, especially in developing countries like Nigeria where people with this problem often have to pay for their own medical care[3].

The pathophysiology of infertility is complex. It may be caused by specific or multiple physical and physiological factors, including hormonal and homeostatic disruptions, environmental and genetic alterations[3]. Recently, epigenetic alterations have been implicated in some cases of infertility[3]. "Epigenetics" refers to biological processes that regulate gene expression without altering the genetic material[12]. The most common epigenetic mechanisms are DNA methylation, histone modification, and microRNA (miRNA) interference[12]. Biological processes, including gametogenesis and embryogenesis, require epigenetic modifications[13]. However, epigenetic modifications, apart from normal cellular functions or responses to external factors, can cause heritable epigenetic mutations and thus, diseases, including infertility[7,12]. By inhibiting the enzymes that modulate epigenetic mechanisms, epigenetic changes and normal functions of the affected genes can be restored[12]. This suggests that epigenetic reprogramming can be used to treat infertility with an epigenetic origin in some cases. This

study, therefore, provides an update on the role of epigenetics in the etiology and management of infertility.

MATERIALS AND METHODS

Reputable academic repositories, namely PubMed, Google Scholar, RCA, SpringerLink, and Scopus, were searched separately for peer-reviewed articles on the subject. The keywords used for the search were: "epigenetics," "infertility," "male infertility," "female infertility," "DNA methylation," "histone modifications," "microRNAs," "epigenetic tests for infertility," and "epigenetic drugs for infertility." Other keywords used include "epigenetic mechanisms," "role of DNA methylation in infertility," "role of histone modification in infertility," and "role of microRNAs in infertility." The articles retrieved were sorted using EndNote software, and double citations were removed.

Article inclusion/exclusion criteria

Included articles were those that were available in the English language, those that focused on the epigenetic basis of infertility and management, and those that were published between the years 2000 and 2021, this was to obtain up-to-date information.

Excluded articles were those that were not available in the English language, articles written before the year 2000, and articles for which only abstracts were available.

In all, 702 articles were retrieved from the databases searched (Figure 1), but 220 articles were retained after removing duplicates. The retained articles were subjected to the eligibility test, and 155 passed. Of the 155 eligible articles, 99 fitted the study objectives and thus made the final selection.

RESULTS

Epigenetic mechanisms

The word "epigenetics" was previously employed to describe the relationship between the genome and the environment that takes part in the development of mammals and some other organisms[14]. However, it is currently defined as heritable alterations in DNA accessibility and chromatin structure, affecting gene expression without changing the DNA sequence[14,15]. Epigenetics plays an important role in normal development, cell differentiation, and disease pathologies[14,15]. There are several epigenetic mechanisms. However, the most common epigenetic mechanisms are DNA methylation, histone modifications, and microRNA (miRNA) interference[12,16]. These mechanisms may alter gene expressions individually or interact to control gene expressions[12]. Figure 2 depicts interactions among epigenetic mechanisms, and Table 1 summarizes the mechanistic links between epigenetic disruptions and infertility.

DISCUSSION

DNA methylation in the etiology of infertility

DNA methylation is the most researched epigenetic mechanism and often results in gene silencing[17,18]. DNA methylation involves the binding of a methyl group to the DNA, resulting in a change of the expression and functions of the embedded genes (Figure 3).

In somatic cells, the binding occurs mainly close to the CpG sites, while in gamete cells occurs near the non-CpG sites[15,19]. CpG sites are DNA sections where a cytosine nucleotide is adjacent to a guanine nucleotide. During DNA methylation, S-adenosyl-L-methionine releases a methyl group and binds to the 5-carbon of the cytosine ring, resulting in 5-methylcytosine (5-mC)[15,20]. The methyl group is then thrusted into the DNA and alters gene transcription. DNA methylation is mediated by a family of enzymes known as the DNA methyltransferases (DNMTs), and members of these enzymes include: DNMT1, DNMT2, DNMT3a, DNMT3b, and DNMT3L[15,21]. DNMT1 regulates established methylated DNA, while DNMT3a and DNMT3b regulate new DNA methylation processes (Figure 4). However, in diseased cells, DNMT1, DNMT3a, and DNMT3b combine to cause DNA over-methylation. Furthermore, during epigenetic reprogramming, DNMT1 prevents the methylation of new DNA, while a group of enzymes called the ten-eleven translocation (TET) modulates the de-methylation of already methylated DNA. DNMT2 inhibits the mutation of small RNA molecules[22]. DNMT3L is similar to DNMT3A and 3B, but does not catalyze epigenetic changes[23]. Instead, DNMT3L enhances the functions of DNMT3A and B[23]. DNMT3L also identifies un-methylated histone H3-lysine 4 (H3K4) nucleosomes and stimulates cells to produce more DNMT3A and DNMT3B to methylate them[24].

DNA methylation is important in reproduction, particularly during genomic imprinting[12,17]. Genomic imprinting is an epigenetic phenomenon in which only one parental allele is expressed while

Table 1 Mechanistic links between epigenetic disruptions and infertility

Epigenetic mechanisms	Links (Pathophysiology)	Ref.
DNA methylation	Hypermethylation or hypomethylation disrupts genomic imprinting and parental epigenetic mark erasure, resulting in abnormal expression of some genes and imprinted genes involved in gametogenesis and embryogenesis	[3,4,12,13,17,20,25,29-42,44-49]
Histone post-translational modification	Abnormal histone modification alters the expression of certain genes important in gametogenesis and embryogenesis. Also, it disrupts sperm DNA protamination, causing sperm abnormalities	[7,43,56-63]
miRNA	Up-regulation or down-regulation alters the expression of certain genes important in gametogenesis and embryogenesis	[15,68-75]

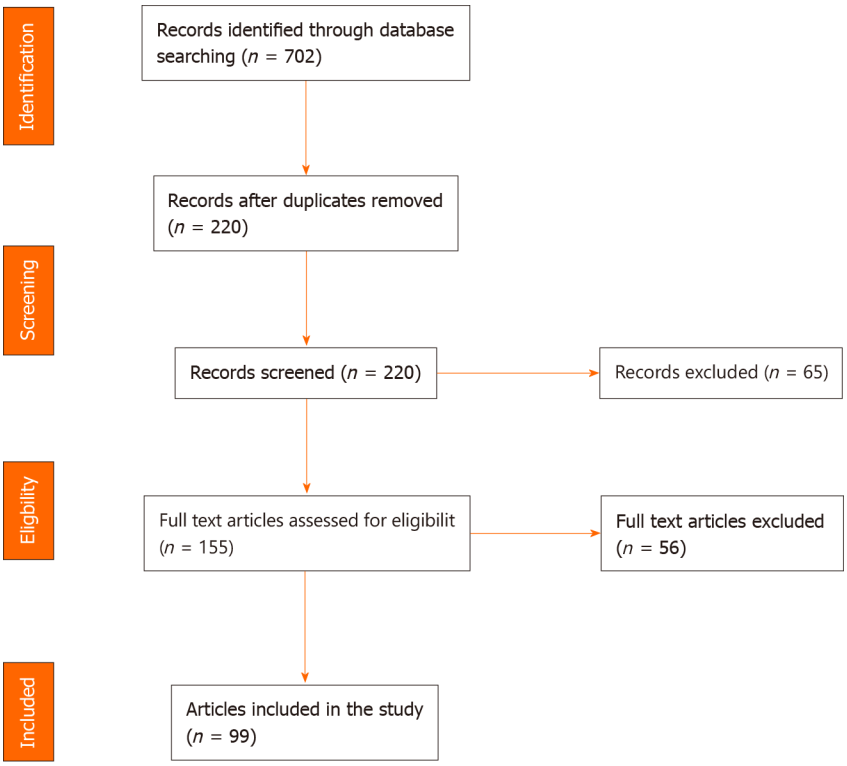

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Figure 1 Flow chart of article selection.

the other allele is imprinted or silenced[25]. Thus, genomic imprinting maintains the parent-of-origin expression of genes. However, some genes may not be fully imprinted; instead of one allele being completely expressed and the other repressed, the two alleles show varied expressions[26]. As of 2019, 228 imprinted genes have been reported in the human genome[27]. Normal imprinting of some genes is necessary for healthy development as it protects the genome's integrity[25,28]. Abnormal imprinting, often caused by alterations in DNA methylation, is associated with many diseases, including impaired spermatogenesis and infertility[3,29]. In a study that analyzed the DNA methylation patterns of seven differently methylated regions (DMRs), in the sperm of 97 infertile men, 14 showed abnormal paternal DNA methylation at H19 and GTL2, and 20 had abnormal maternal DNA methylation at PEG1, LIT1, ZAC, PEG3, and SNRPN[30]. These DMRs contain imprinted genes that regulate spermatogenesis, and at least half of the genes show maternal and paternal imprint abnormalities in infertile men[30]. In another study, methylation and imprinting errors were observed in the IGF2/H19 imprinting control region 1 (ICR1) and MEST DMRs in the spermatozoa of 148 idiopathic infertile men compared with 33 normozoospermic controls[31]. The idiopathic infertile men (sperm motility below 40% and normal sperm morphology below 5%) displayed hypermethylation of the MEST DMRs and hypomethylation of the IGF2/H19 ICR1, while the control showed the opposite. Thus, in the study, infertility was clearly linked with IGF2/H19 ICR1 hypomethylation and MEST hypermethylation[32,33]. In another study, seven out of 15 (46.7%) individuals with low sperm count (below 10×10^6/mL) showed defective methylation of H19 and/or MEST imprinted genes[34]. Of the seven patients that expressed imprinting errors, two had both H19 hypomethylation and MEST hypermethylation, while five had only one of the impaired imprinted genes[34]. This again proved that imprinted genes in H19 and MEST play an

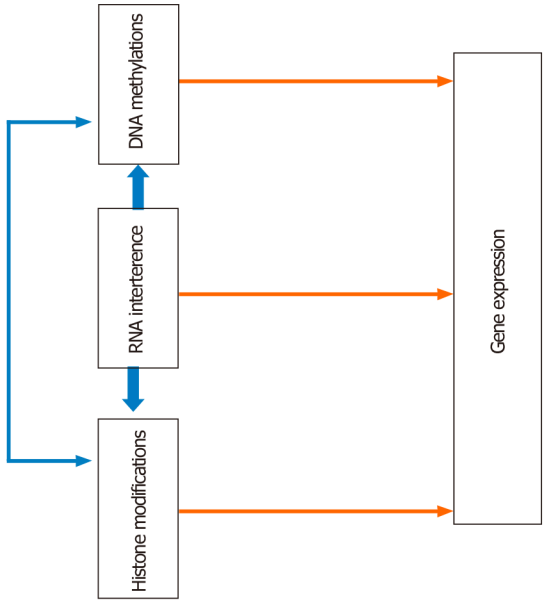

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Figure 2 Epigenetic mechanisms.

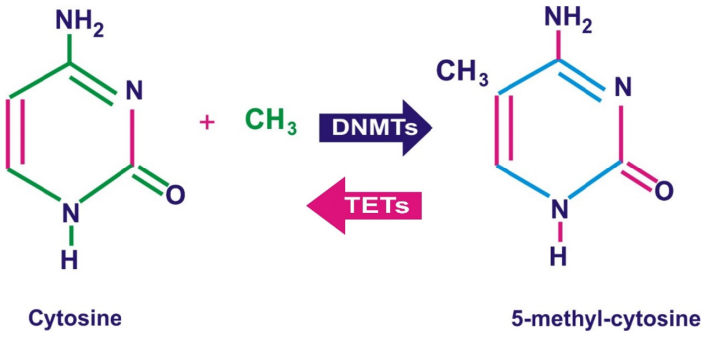

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Figure 3 DNA methylation (arrow pointing right) and de-methylation (arrow pointing left) *via* DNA methyltransferase and ten-eleven translocation, respectively. DNMTs: DNA methyltransferase; TETs: Ten-eleven translocation.

important role in spermatogenesis, fetal growth and development, and placental function[35,36]. Similarly, in a study that compared the DNA methylation at DMRs of maternally imprinted genes extracted from stillborn pups and control embryos, hypermethylations were observed at Zac1 imprinting genes in the stillborn pups[37]. Zac1 regulates an imprinted gene network that is important in the regulation of embryonic growth[38]. Aberrant DNA methylation has also been implicated in some genomic imprinting disorders, which, in severe cases, can cause recurrent molar pregnancy, miscarriage, or infertility[39]. These disorders include Prader-Willi syndrome and Angelman syndrome, which are caused by loss of function of imprinted genes on chromosome 15 in females and males, respectively[40]. Beckwith-Wiedemann syndrome and Russell-Silver syndrome are two others. Both are caused by the loss of function of imprinted genes on chromosomes 7 or 11[41,42].

Aside from genomic imprinting, DNA methylation is also involved in parental epigenetic mark erasures in which DNA methylation undertakes two rounds of epigenetic reprogramming during gametogenesis and embryogenesis[13]. One reprogramming occurs immediately after fertilization, in which sperm and oocyte DNA are stripped of the parental methylation marks (DNA demethylation)[4]. Some DNA demethylation occurs specifically in paternally inherited imprinted genes[43]. The erasure of DNA methylation continues until new imprints are formed[43]. The stripping allows the totipotent zygote to start new gene transcription and new cell methylation[4]. Because of this, most epigenetic modifications that occur in sperm and egg cells when the two merge to form a fertilized egg are removed[3]. Thus, epigenetic reprogramming enables the fetus's cells to start afresh and determine their own epigenome[3]. However, some of the epigenetic modifications in parents' sperm and egg cells may escape the reprogramming and be transmitted to the next generation[3]. Another genome-wide stripping of DNA methylation and subsequent new DNA methylation occurs in the primordial germ

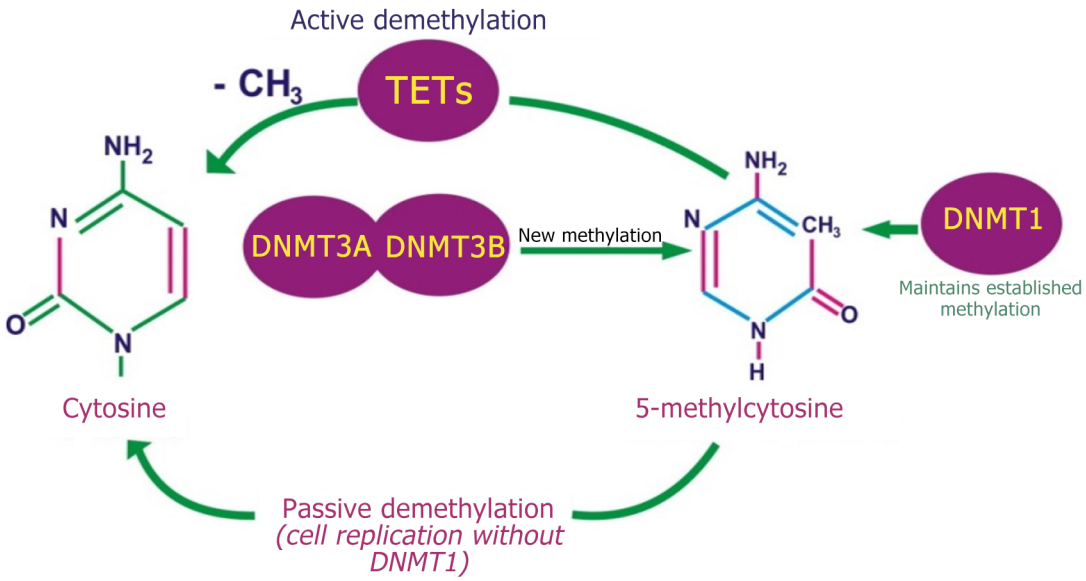

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Figure 4 DNA methylation and de-methylation processes, showing the roles of each modulating enzyme; DNMT1, DNMT3A, and DNMT3B stand for DNA methyltransferases 1, 3A, and 3B, respectively; TET2 is short for ten-eleven translocation. DNMTs: DNA methyltransferase; TETs: Ten-eleven translocation.

cells (gamete precursors), which subsequently differentiate into the gametes (sperm and eggs)[17,44]. Overall, this showed the importance of DNA methylation in gametogenesis and embryogenesis and, hence, fertility. In fact, DNMT1, DNMT3a, and DNMT3b have been shown to be highly expressed in the early embryonic stage[20]. Furthermore, it has been shown that more than 150 genes are associated with mammalian spermatogenesis, and if the normal expression of any of these genes is altered, the reproductive success of males could be compromised[25]. Thus, aberrant DNA methylation may cause dysfunctional gametogenesis and embryogenesis, resulting in infertility[4,25]. In a study, 696 differentially methylated CpGs, comprising 184 (26%) hypomethylations and 512 (74%) hypermethylations associated with 501 genes, were identified between the spermatozoa of 19 fertile men and 42 infertile men[45]. The CpGs are home to 13 processes related to spermatogenesis. Moreover, 17 differentially methylated genes related to spermatogenesis were observed between the fertile and infertile groups [45]. In another study that compared 46 sperm samples obtained from 17 normospermic fertile men and 29 normospermic infertile men, 2752 CpGs showing aberrant DNA methylation patterns were observed in the sperm of infertile men[46]. Importantly, these differentially methylated CpGs were significantly associated with CpG sites that are involved in spermatogenesis[46]. Additionally, 48 imprinted genes were abnormally methylated in the altered CpGs of the infertile patients. In a related study that compared the sperm of 12 fertile and 45 infertile men, reactive oxygen species were found to cause DNA fragmentation and abnormal methylation in the infertile group's sperm[47]. Similar to infertile men, abnormal DNA methylation has also been reported in the germ cells or reproductive tract of infertile women. For instance, in a genome-wide methylation study of the endometrium of women expressing endometriosis, compared with a matched control, 59 genes were hypermethylated and 61 genes were hypomethylated[48]. It was observed in the study that aberrant methylation and expression of these genes contributed to abnormal endometrial cell proliferation and function in women[48]. In another genome-wide study involving 85 women expressing polycystic ovary syndrome, the CpG sites of luteinizing hormone/choriogonadotropin receptor promoter regions were hypomethylated compared with the control[49]. The hypomethylation of the luteinizing hormone/choriogonadotropin receptor caused its overexpression in women with polycystic ovary syndrome compared with that in control women.

Histone post-translational modifications in the etiology of infertility

Histones are the 'cylindrical' protein building-blocks of chromatin around which DNA winds and shortens the DNA[50]. Thus, post-translational modifications of histones restructure the chromatin (condensed or non-condensed), which determines the transcriptional status of the associated DNA and genes[15,51]. Non-condensed or loose chromatin (euchromatin) is active and transcribes DNA, while condensed chromatin (heterochromatin) is inactive and thus lacks the ability to transcribe genes[15,52]. The genes in the condensed chromatin are tightly bonded to the DNA and are thus silenced due to the inability of the transcription factors to gain access to the promoters of the genes[15,52]. There are five main classes of histones, which are: H1/H5, H2A, H2B, H3, and H4[53,54]. The core histones are histones H2A, H2B, H3, and H4, while the linker histone is histone H1/H5[53]. Histones can be

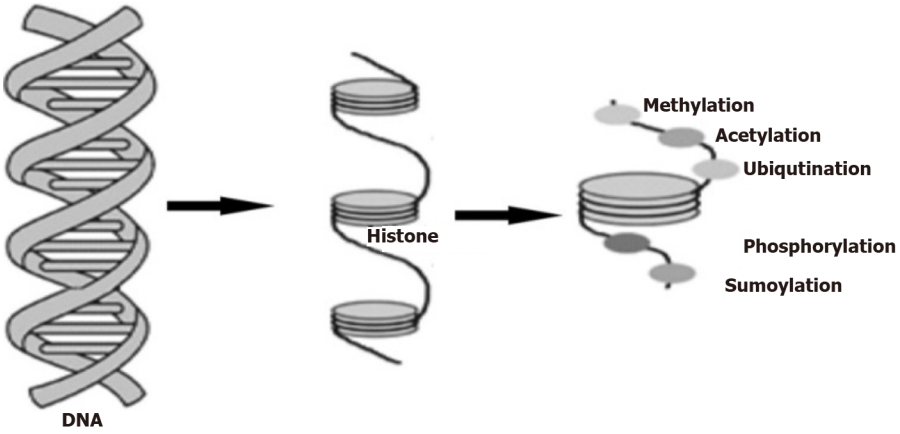

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Figure 5 Histone post-translational modification processes, showing mechanisms.

modified through several mechanisms, such as methylation, acetylation, phosphorylation, sumoylation, and ubiquitylation (Figure 5). However, methylation and acetylation are the most common mechanisms [15,55]. Acetylation binds an acetyl group to the amino acid lysine in the histone, while methylation binds a methyl group to the amino acids of histone proteins, primarily lysine and arginine residues[15, 55]. As lysine and arginine are the most abundant amino acids in histones, they are frequently acetylated and methylated[50]. Acetylation ideally takes place in non-condensed chromatin, while deacetylation usually takes place in condensed chromatin[15]. Histone methylation can take place in both forms of chromatin. Histone acetyltransferases and histone methyltransferases catalyze histone acetylation and methylation, respectively[12], whereas histone deacetylases (HDACs) and histone demethylases catalyze deacetylation and demethylation[12]. Aside from the structural state of chromatin mentioned earlier, the effects of histone post-translational modifications on gene expression also depend on the mechanisms and degree of methylation or acetylation, which could be mono-, di-, or tri-methylated[12]. Sometimes, both DNA methylation and histone post-translational modification combine to cause epigenetic changes[12]. DNA methylation plays a part in ensuring high levels of chromatin structure[45].

Histone modifications play an important role in gametogenesis and embryogenesis, as well as in fertility[56]. To successfully transfer a sperm's genetic and epigenetic materials to an egg, the chromatin must be very condensed for proper motility and protection of the paternal DNA and epigenome from external stimuli[56,57]. This is guaranteed by the replacement of histones with protamines (a unique, sperm-specific protein) by sperm DNA protamination[56,57]. Despite this, some regions, particularly the sperm head, retain histones, which are prone to modifications[56,57]. Protamination and some other biological events during spermatogenesis are controlled by epigenetic mechanisms in which abnormal histone modifications may cause the sperm to lose its oocyte fertilizing capacity[7]. Defects in either the replacement or the modification of histones might cause male infertility, characterized by azoospermia, oligozoospermia, or teratozoospermia[58]. In females, during oocyte development, histone methylation and acetylation increase significantly, resulting in the global restructuring of chromatin and the silencing of many embedded genes[43]. This global change is mediated by the increased production of methyltransferases and acetyltransferases[43]. Thus, histone epigenetic dysregulation can disrupt oogenesis, leading to aneuploidy in fertilized oocytes, culminating in embryonic death[7]. In a study that compared the sperm transcriptomes of 3 oligozoospermic infertile men with 8 fertile men, the former showed a 17-fold down-regulation in genes involved in histone modifications[59]. In the study, 157 transcripts were either overexpressed or repressed in the sperm of oligozoospermic infertile men as compared to normozoospermic fertile individuals[59]. Importantly, the histone dysregulation in infertile men caused up to a 43-fold reduction in the expression of some genes involved in spermatogenesis and sperm motility, such as DDX3X and JMJD1A[59]. Furthermore, a 17-fold increase was observed in the expression of some genes that prevent oxidative stress and abortive spermatogenesis[59]. These genes include: ADH4, HSD17B7, CYGB, and NXNL1[59]. It is noteworthy that at the start of the mentioned study, the patients were screened and confirmed negative for known causes of infertility, including chromosome anomalies and Y chromosome AZF deletions[59]. This suggests that the observed epigenetic changes were responsible for the reproductive abnormalities in the infertile men. In a transgenic mouse study, overexpression of KDM1A (a histone demethylase) during spermatogenesis reduces histone H3 Lysine 4 dimethylation (H3K4me2) in sperm at more than 2300 genes[60]. Some of these genes regulate development, and the reduction of H3K4 dimethylation in the mice sperm severely impaired the fertility, development, and survivability of the offspring[60]. The defects were observed across multiple generations in the absence of KDM1A germline expression and were linked to altered RNA profiles in sperm and offspring[60]. In a study that determined the cause of idiopathic early

miscarriage in 3 pregnant women, 81 genes were overexpressed in the chorionic villous of the affected compared with controls[61]. These genes take part in several important physiological processes, such as cell proliferation, nuclear division, chromatic assembly, DNA packing, and modification[61]. Furthermore, 231 genes that are functionally involved in histone modifications and cell cycle control were down-regulated in the chorionic villous of the affected women compared with controls[61]. In a study of histone locations and modifications, in the semen of seven infertile patients, unlike fertile men, five infertile men had non-programmatic (randomly distributed) histone retention genome-wide[62]. Although the methylation patterns of H3K4me and H3K27me in infertile men were similar to those in the control group, the amounts of histones retained by developmental transcription factors and certain imprinted genes were decreased[62]. In a study that monitored the effects of chlordecone exposure on the epigenome of the ovaries of mice, compared with the control, reduced H3K4me3 and H4ac in fully grown oocytes were observed. This reduction caused repression of genes associated with estrogen signaling and oocyte maturation in adult ovaries[63]. Furthermore, gene expression analysis revealed that RCBTB2 and RBPMS genes were not expressed in the embryonic gonads[63]. Reproductive abnormalities observed in the exposed mice included compromised meiotic double-strand break repair in female embryos, puberty delay, decreased primordials, and increased atretic follicles[63]. The study showed that exposure to a low dose of chlordecone during pregnancy impaired female reproductive functions, which are mediated by abnormal histone modifications[63].

MicroRNAs in the etiology of infertility

MicroRNAs (miRNAs) are small, single-stranded non-coding RNA molecules of between 19 and 25 nucleotides[15,64]. MicroRNAs interact with transcriptional and epigenetic regulators in cells to maintain lineage-specific gene expression[15,65]. Specifically, miRNAs control the expression of genes during transcription by disrupting the translation of target messenger RNA. However, in diseased cells, miRNA expression is changed, leading to altered expression, mostly overexpression of the target genes [15,66]. Approximately 1% of the human genome is made up of genes that contain miRNAs[67], which shows how important they are.

MicroRNAs play an active role in many cellular functions, including cell cycle control, cell differentiation, intra and intercellular communication (cell-to-cell communication), and apoptosis[15,68]. In mammalian reproduction, miRNAs are embedded in the tissues of the ovary, testis, and embryo, as well as granulosa cells and oocytes[68]. MicroRNAs are actively involved in mammalian sex differentiation, gametogenesis, fertilization, zygotic genome activation and early development, implantation, germ layer specification, and pregnancy[69,70]. These mentioned reproductive functions and others show that impairing miRNAs may result in reproductive anomalies such as infertility and pregnancy failure[15]. It has been demonstrated that the loss of one or both components of the miRNA processing machinery (Dicer and Drosha) severely impairs gametogenesis, resulting in male and female infertility[70]. In an experiment, deletion of Dicer1 at the early stage of male gamete cell development in six transgenic mice caused infertility compared with matched controls[71]. The infertility was caused by several cumulative defects at the meiotic and post-meiotic stages, culminating in the absence of functional spermatozoa [71]. Increased apoptosis in spermatocytes, fewer spermatids, and spermatozoa with abnormal morphology were also observed in the tested rats, unlike the controls[71]. Furthermore, the expression of transposable elements of the SINE family was overexpressed in the Dicer1-deficient spermatocytes [71]. In another study that examined the expression of 736 miRNAs in the spermatozoa of 10 fertile men, 221 miRNAs were frequently present in all the participants[72]. Additionally, 452 miRNAs were present in some participants, and 63 were absent in all the participants[72]. Further analysis showed that these miRNAs take part in processes related to cell differentiation, development, morphogenesis, and embryogenesis[72]. This shows that human sperm contains many miRNAs, which functionally promote embryogenesis and spermatogenesis[72]. In a study of human spermatozoa from 27 patients with various spermatogenic abnormalities, 50 miRNAs were up-regulated and 27 miRNAs were down-regulated in asthenozoospermic males compared with controls (Table 2). In the oligoasthenozoospermic participants, 42 miRNAs were up-regulated and 44 miRNAs were down-regulated when compared with normozoospermic males[73]. The most overexpressed miRNAs in asthenozoospermic men were miR-34b, miR-122, and miR-1973, whereas in oligoasthenozoospermic men were miR-34b, miR-34b*, miR-15b, miR-34c-5p, miR-122, miR-449a, miR-1973, miR-16, and miR-19a[73]. These miRNAs play an essential role in male germ cell development and spermatogenesis, and, hence, their imbalances may cause male infertility[73]. The regulatory role of miRNAs in oogenesis has also been demonstrated in several studies. In a female mouse study, the removal of the miR-17-92 cluster in the ovaries caused overexpression of several genes involved in apoptotic pathways compared with controls[74]. These genes include pro-apoptotic BH3-only genes (Noxa, Bmf, Bid, Bik, Bad, and Bim) and the pro-apoptotic effector protein genes (Bax and Bak)[74]. Other genes are initiator caspases (Caspase 8 and Caspase 9), executioner caspase (Caspase 3), and some follicular atresia-related genes (Cyp1a1 and Egr-1)[74]. This suggests that apoptosis is the major mechanism involved in the reproductive anomalies observed in the miR-17-92 deficient mice[74]. The reproductive anomalies caused by these epigenetic alterations include increased oocyte degradation and follicular atresia, decreased ovulation, perturbed oogenesis, and ultimately culminate in subfertility and reduced fecundity[74]. Overall, the study showed that the miR-17-92 cluster is an important regulator of oogenesis[74]. Similarly, in a study that compared the

Table 2 Status of some microRNAs in infertile men and women

miRNAs	Status	Effect	Ref.
miR-34b	Up-regulated	Asthenozoospermia	[73]
miR-122	Up-regulated	Asthenozoospermia	[73]
miR-1973	Up-regulated	Asthenozoospermia	[73]
miR-15b	Up-regulated	Asthenozoospermia	[73]
miR-34c-5p	Up-regulated	Oligoasthenozoospermia	[73]
miR-449a	Up-regulated	Oligoasthenozoospermia	[73]
miR-16	Up-regulated	Oligoasthenozoospermia	[73]
miR-19a	Up-regulated	Oligoasthenozoospermia	[73]
miR-17-92	Deficient	Abnormal oogenesis	[74]
miR-145	Up-regulated	Implantation failure	[75]
miR-23b	Up-regulated	Implantation failure	[75]
miR-99a	Up-regulated	Implantation failure	[75]
hsa-miR-32	Down-regulated	Implantation failure	[75]
hsa-miR-628-5p	Down-regulated	Implantation failure	[75]
hsa-miR-874	Down-regulated	Implantation failure	[75]

miRNAs: MicroRNAs.

endometrium of patients with repeated implantation failure with controls, 13 differentially expressed miRNAs that regulate 3800 genes were identified in the affected patients[75]. Ten of the miRNAs were overexpressed (including miR 145, 23b, and 99a), and three were repressed (Table 2). These miRNAs target genes are involved in important implantation processes, such as adherens junctions, cell adhesion molecules, Wnt-signaling, p53 signaling, and cell cycle pathways[75].

EPIGENETIC-BASED TESTS FOR INFERTILITY

Currently, there is no standard epigenetic-based test for infertility. This could be due to the relative newness of the field, thus, the field is not yet fully understood. However, as of the time of writing this review, only one commercially available epigenetic-based infertility test called "Seed" has been announced. The epigenetic test is a male infertility test that was developed in 2016 by reputable reproductive scientists and computational biologists at Episona Incorporation, California, United States [76]. Seed identifies alterations in the sperm's DNA that provide an insight into why some pregnancies fail[76]. Seed focuses mainly on DNA methylation and examines at least 480000 regions of sperm DNA for unusual methylation at certain gene sites important to fertility[76]. Each abnormal region detected is scored as a risk for either male factor infertility or poor embryo development[76]. The results of the test determine the type of reproductive assistance the person needs, which could be either intrauterine insemination or *in vitro* fertilization (IVF)[76].

The manufacturers of Seed believe the test is more effective than the available infertility tests, including traditional semen analysis. According to them, while semen analysis gives useful information on sperm counts, motility, and morphology, Seed goes further to identify problems related to sperm function and embryo development[76]. Seed combines modern discoveries in science and technology to provide patients with previously unknown information about their fertility[76]. Seed increases the chances of pregnancy; it is more cost-effective and can be used to personalize fertility treatment for the affected persons[76]. The precision of Seed has been validated in two clinical studies; one was a retrospective study involving 127 IVF patients and 36 fertile controls[76], the second was a prospective study involving over 200 patients from several clinics and 96 fertile controls[76].

EPIGENETIC-BASED INFERTILITY DRUGS

As epigenetic changes are dynamic and reversible, they can thus be used as therapeutic targets in

Table 3 Selected epigenetic drugs and their activities

Epigenetic drug	Target	Effect	Ref.
Choline	HDAC3	Increases DNA methylation	[15]
Betaine	HDAC3	Increases DNA methylation	[15]
Bobcat339	TETs and TET2	Increases DNA methylation	[15]
C35	TET	Increases DNA methylation	[91]
Zebularine	DNMTs	Reduces hypermethylation	[92]
Disulfiran	DNMTs	Reduces hypermethylation	[92]
Decitabine	DNMTs	Reduces hypermethylation	[92]
Azacitidine	DNMTs	Reduces hypermethylation	[92]
Chaeton	DNMTs	Reduces hypermethylation	[92]
RGFP966	HDAC3	Inhibits histone modification	[95,96]
RG108	Anti-miRNA	Reduces gene expression	[98,99]

DNMTs: DNA methyltransferase; HDAC: Histone deacetylases; TETs: Ten-eleven translocation; miRNA: MicroRNA.

diseases that have an epigenetic etiology[77-81]. This can be achieved by blocking or deleting the enzymes that modulate the epigenetic alterations in the affected individuals, thereby preventing or reversing the associated disease[82-84]. Complementary single-stranded oligonucleotides (otherwise called anti-miRNAs) can also be used to silence overexpressed genes or boost repressed genes[85-87].

Currently, there is no particular epigenetic drug for treating infertility. However, epigenetic drugs have been developed for some diseases, such as cancer and diabetes mellitus (Table 3). Notably, a HDAC3 inhibitor known as RGFP966 has been shown to reverse Type 1 diabetes and its complications in transgenic mice fed for three months[88]. The DNA methylation inhibitor known as 5-Azacytidine destroys cancer cells[89]. As epigenetic mechanisms are the same in all biological processes, including disease pathologies, it can be hypothesized that some available epigenetic drugs may also be helpful in the treatment of infertility. Alternatively, infertility epigenetic drugs can be formulated from the bioactive components of existing epigenetic drugs or from entirely different bioactive substances. Thus, infertility caused by DNA hypomethylation in both males and females can potentially be reversed or reduced by methyl-donating compounds and epigenetic drugs such as folate, methionine, choline, betaine, and vitamin B-12[15]. Hypomethylation in infertile persons can also be corrected by epigenetic drugs that block DNA-demethylating enzymes (TETs)[15]. These drugs include a cytosine-based lead compound known as Bobcat339 (though not approved yet), which has been shown to inhibit TET1 and TET2[90]. A small molecule known as C35 is another inhibitor that has been demonstrated to target the TET catalytic domain and decrease the 5hmC concentration in the genome[91]. Similarly, infertility caused by DNA hypermethylation can potentially be treated by DNA methylation inhibitors, which include zebularine, disulfiram, decitabine, azacitidine, and chaetocin[92]. The mentioned epigenetic drugs work by inhibiting the catalyzing enzymes of DNA methylation and inducing activation of genes silenced by methylation[93,94]. Moreover, infertility caused by histone post-translational modification can potentially be treated by histone modification inhibitors such as RGFP966, vorinostat, romidepsin, garcinol, and belinostat[95,96]. Infertility caused by abnormal expression of miRNAs can be corrected by anti-miRNA oligonucleotides such as locked nucleic acid, antagomirs, morpholinos, byetta, victoza, trulicity, janu-via, onglyza, and tradjenta[15,97]. RG108 and MG98, for example, bind to the 3′ untranslated region of DNMT1, preventing gene transcription[98,99].

CONCLUSION

Abnormal epigenetic modifications in genes that control gametogenesis and embryogenesis such as *DDX3X*, *ADH4*, *AZF*, *PLAG1*, *D1RAS3*, *CYGB*, *MEST*, *JMJD1A*, *KCNQ1*, *IGF2*, *H19*, and *MTHFR* can cause infertility. This suggests that some cases of infertility have epigenetic etiologies. The most common epigenetic mechanisms regarding infertility are DNA methylation, histone post-translational modification, and microRNA interference. Dysregulation of these mechanisms in reproductive tissues and cells can disrupt genomic imprinting as well as oocyte and sperm epigenomes. Fortunately, epigenetic changes are reversible by blocking the mediating enzymes such as HDAC3, TET, TET2, and DNMTs. This indicates that infertility induced by epigenetic alterations can be treated by reversing the same mechanisms that caused them. There are some certified epigenetic drugs currently in use,

including Choline, Betaine, Zebularine, Disulfiran, Decitabine, Azacitidine, Chaeton, RGFP966, and RG108, but none have been formulated specifically for infertility. It is theorized that some of the available epigenetic drugs could be helpful in infertility as epigenetic mechanisms are the same in all disease pathologies. Epigenetic drugs for infertility can also be formulated from the bioactive compounds of existing epigenetic drugs or from entirely different bioactive substances.

ARTICLE HIGHLIGHTS

Research background

Medical practitioners are advised to formulate treatment procedures and epigenetic drugs for infertility having an epigenetic etiology.

Research motivation

Epigenetic disruption is involved in some cases of infertility.

Research objectives

Epigenetic disruptions in genes that control gametogenesis and embryogenesis, such as *DDX3X*, *ADH4*, *AZF*, *PLAG1*, *D1RAS3*, *CYGB*, *MEST*, *JMJD1A*, *KCNQ1*, *IGF2*, *H19*, and *MTHFR* may result in infertility.

Research methods

Relevant information was collected from notable academic repositories and the articles collected were sorted using Endnote software.

Research results

The study was aimed at articulating and disseminating the epigenetic basis of infertility to raise public awareness.

Research conclusions

The study was motivated by the desire to reduce the incidence and burden of infertility.

Research perspectives

Abnormal epigenetic modifications have been implicated in some cases of infertility and can be used as therapeutic targets. However, the role of epigenetics in infertility has not been given adequate attention.

FOOTNOTES

Author contributions: Yahaya TO conceptualized, performed the literature search, article writing and correspondence; Bashar DM performed the literature search and article writing; Oladele EO and Umar J performed article writing and proofreading; Anyebe D and Izuafa I performed article sorting; all authors proofread, and approved the final manuscript.

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