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Education, Physical Activity, and Reproductive Health in Women: Understanding the Impact of the Vaginal Microbiome

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ABSTRACT

Background. The vaginal microbiome is essential for women's reproductive health, affecting fertility, implantation, pregnancy outcomes, and vulnerability to gynecological conditions. It is increasingly recognized within the broader context of women's health literacy and lifestyle, including physical activity, which may influence microbial balance.

Aim. To summarize current evidence on the composition and clinical importance of the vaginal microbiome while integrating insights from public health, health education, and sports science.

Material and methods. A review of open access studies published between 2021 and 2025 identified 23 eligible articles. Additional literature on women's health education and physical activity was included to highlight interdisciplinary links.

Results. Lactobacillus-dominant communities, especially those enriched with *Lactobacillus crispatus*, support mucosal stability and favorable reproductive outcomes. Dysbiosis, characterized by low Lactobacillus levels and high microbial diversity (CST IV), is linked to bacterial vaginosis, subfertility, implantation failure, and preterm birth. Education and lifestyle-focused interventions may help mitigate dysbiosis, while early evidence suggests physical activity supports systemic regulation relevant to microbial stability.

Conclusions. The vaginal microbiome significantly influences reproductive and overall health. Integrating microbiome knowledge into health education and lifestyle promotion may improve preventive strategies and clinical outcomes.

Keywords: vaginal microbiome, reproductive health, dysbiosis, health education, physical activity, fertility

1. Introduction

The vaginal microbiome is a dynamic, hormonally regulated ecosystem essential for women's reproductive health across the lifespan (Cheng et al., 2025). Stability maintained by Lactobacillus-dominated communities supports mucosal protection, immune regulation and a low pH crucial for reproductive well-being (Günther et al., 2022; Holdcroft et al., 2023). Dysbiosis is linked to bacterial vaginosis (BV), infertility, implantation failure and adverse pregnancy outcomes (Gerede et al., 2024; Zhai et al., 2025). Advances in sequencing technologies have improved understanding of microbial variability across reproductive stages and treatment contexts (Parraga-Leo et al., 2024).

Microbiome composition is shaped by hormonal changes, sexual practices, hygiene behaviors, antibiotic use and population-level factors (Holdcroft et al., 2023). Certain community state types (CSTs) correlate with fertility disorders, while vaginal and endometrial microbial profiles can affect assisted reproductive technology (ART) outcomes (Samama et al., 2025; Xiao et al., 2024). Pregnancy studies further show the microbiome's involvement in inflammation-related complications, preterm birth and neonatal colonization (Gerede et al., 2024; Mendz, 2023).

In addition to biological determinants, educational and lifestyle factors may contribute to microbial stability. Women's health literacy regarding intimate hygiene, antibiotic stewardship, sexual health and early recognition of dysbiosis can help prevent harmful behaviors (Günther et al., 2022). Physical activity may indirectly support favorable microbial conditions through effects on metabolism, endocrine function and immunity, although mechanistic data remain limited (Cheng et al., 2025).

Given these multidimensional influences, this review integrates biological, educational and lifestyle perspectives to summarize current knowledge on the vaginal microbiome's role in reproductive health. Based on 23 recent open-access studies, it provides an updated interdisciplinary overview and highlights priorities for future research (Da Silva et al., 2025; Vinitha et al., 2025). The aim of this narrative review is to summarize current evidence on the role of the vaginal microbiome in women's reproductive health, with particular attention to health education and physical activity as modifiable determinants.

2. Material and methods

This narrative review was conducted using a structured search strategy to identify recent open access publications examining the vaginal microbiome and its relationship with women's reproductive health. A comprehensive search of PubMed, PubMed Central, Google Scholar, Frontiers, MDPI, PLoS, Nature Portfolio, Elsevier, Wiley Open Access and institutional repositories were performed for studies published between January 2021 and December 2025. Search terms combined keywords related to the vaginal microbiome, dysbiosis, fertility, pregnancy outcomes, assisted reproduction and women's health, using Boolean operators to refine results.

Inclusion criteria required: (i) open access availability, (ii) peer reviewed status, (iii) English language publication, and (iv) relevance to vaginal or endometrial microbiota in the context of fertility, pregnancy, ART or host-microbe interactions. Both original studies and reviews were eligible. Exclusion criteria included non-English papers, inaccessible full texts and studies unrelated to microbial composition or reproductive outcomes.

The search initially identified 178 records. After removing duplicates and screening titles, abstracts and full texts, 23 publications met all criteria and were included in the final synthesis. These encompassed studies on microbiome physiology, pregnancy related microbial dynamics, infertility and ART, dysbiosis and BV, as well as emerging diagnostic and therapeutic approaches. All data were extracted manually without automation to ensure methodological rigor and adherence to publication ethics.

3. Results

3.1. Physiology of the vaginal microbiome

The vaginal microbiome is a hormonally responsive ecosystem shaped by interactions between host immunity, epithelial physiology and microbial metabolism (Cheng et al., 2025). In women of reproductive age, Lactobacillus species typically dominate, maintaining a low pH through lactic acid production and providing colonization resistance against pathogens (Günther et al., 2022; Holdcroft et al., 2023). Stable, health associated communities are most often enriched with Lactobacillus crispatus or L. jensenii, whereas L. iners is frequently observed in transitional or less stable microbial states (Dong et al., 2024; Vinitha et al., 2025). Community state types (CSTs) offer a structured classification of these patterns and help explain interindividual and hormonally driven variability (Zhai et al., 2025).

Physiological stability is strongly influenced by estrogen, which promotes glycogen accumulation in the vaginal epithelium and supports Lactobacillus proliferation (Gerede et al., 2024; Mendz, 2023). Pregnancy further exemplifies this hormonal regulation, with increased Lactobacillus dominance and reduced microbial diversity contributing to an anti-inflammatory environment (Parraga-Leo et al., 2024; Ng et al., 2021). Immune factors such as defensins, mucosal antibodies and cytokine signaling also interact with the microbiota to maintain homeostasis and regulate responses to microbial disturbances, including those triggered by antimicrobial treatment (Williams et al., 2025; Sadeghpour Heravi, 2024).

Overall, current evidence demonstrates that the vaginal microbiome is an active, adaptable component of reproductive physiology with important implications for fertility, pregnancy and gynecologic health (Xiao et al., 2024; Da Silva et al., 2025).

3.2. The Role of *Lactobacillus* species

Lactobacillus species are central to maintaining a healthy vaginal ecosystem, supporting reproductive function through biochemical and immunological mechanisms (Günther et al., 2022; Cheng et al., 2025). Dominant species such as L. crispatus, L. jensenii and L. gasseri help preserve low pH and inhibit pathogenic anaerobes through lactic acid, hydrogen peroxide and other antimicrobial metabolites (Holdcroft et al., 2023). Their presence reinforces epithelial barrier integrity and regulates local immune responses, contributing to reduced inflammation and enhanced mucosal stability (Sadeghpour Heravi, 2024; Williams et al., 2025).

In contrast, L. iners, although common in women of reproductive age, often represents a transitional or less stable microbial state and shows greater susceptibility to shifts toward dysbiosis (Vinitha et al., 2025).

Across fertility and pregnancy contexts, L. crispatus dominated communities are associated with improved implantation, higher ART success rates and lower risks of inflammation related complications, including preterm birth (Samama et al., 2025; Parraga-Leo et al., 2024). Overall, Lactobacillus species function as key ecological protectors and clinically relevant biomarkers of reproductive health (Da Silva et al., 2025; Gullo et al., 2025).

3.3. Factors modulating the vaginal microbiome

The composition and stability of the vaginal microbiome are shaped by hormonal, behavioral, therapeutic and environmental factors throughout a woman’s life (Cheng et al., 2025; Condori-Catachura et al., 2025). Estrogen driven glycogen accumulation supports Lactobacillus dominance and low pH homeostasis, explaining predictable microbial shifts during puberty, pregnancy and menopause (Gerede et al., 2024; Mendz, 2023; Parraga-Leo et al., 2024).

Beyond hormonal influences, hygiene practices, intimate products and sexual behaviors can alter microbial balance, with some cleansing habits linked to reduced Lactobacillus abundance and increased risk of dysbiosis (Holdcroft et al., 2023). Antibiotics, including metronidazole, may cause substantial short-term perturbations and inconsistent recovery, especially in communities dominated by L. iners or CST IV profiles (Williams et al., 2025; Sadeghpour Heravi, 2024). Fertility related interventions, such as ovarian stimulation or prophylactic antibiotics during ART, may also transiently disrupt microbial stability (Samama et al., 2025; Tong et al., 2023).

Geographic, dietary and population level factors contribute further to interindividual variability, as demonstrated in large global cohorts (Condori-Catachura et al., 2025; Vinitha et al., 2025). The vaginal microbiome is a dynamic system responsive to multiple internal and external influences, with significant implications for reproductive health, diagnostics and personalized therapeutic approaches (Xiao et al., 2024; Da Silva et al., 2025).

3.4. Dysbiosis of the vaginal microbiome

Vaginal dysbiosis refers to a shift from a Lactobacillus dominant, low diversity microbiome to a heterogeneous community enriched with anaerobic or opportunistic species, often accompanied by inflammation and weakened mucosal defense (Dong et al., 2024; Cheng et al., 2025). This transition typically involves reductions in L. crispatus or L. jensenii and increased abundance of organisms such as Gardnerella, Atopobium, Prevotella or Mobiluncus, which are characteristic of bacterial vaginosis (Günther et al., 2022). Dysbiosis disrupts lactic acid production, epithelial barrier integrity and cytokine regulation, thereby increasing susceptibility to infections and amplifying inflammatory signaling (Williams et al., 2025; Holdcroft et al., 2023).

Microbial profiles associated with CST IV have been linked to subfertility, recurrent BV and adverse pregnancy outcomes through their influence on inflammatory pathways and host immunity (Gerede et al., 2024; Mendz, 2023). Dysbiosis is often recurrent and influenced by hormonal fluctuations, antibiotic exposure, sexual behaviors and individual treatment responses (Parraga-Leo et al., 2024; Condori-Catachura et al., 2025). Recovery after antimicrobial therapy varies, particularly among women with BV associated communities or L. iners dominated profiles (Williams et al., 2025). Women undergoing fertility treatment may be especially vulnerable to dysbiosis due to medical or hormonal interventions (Samama et al., 2025; Tong et al., 2023).

Dysbiosis represents a clinically significant condition with mechanistic links to inflammation, reproductive dysfunction and negative obstetric outcomes (Da Silva et al., 2025; Gullo et al., 2025).

3.5. Dysbiosis and the immune response

Dysbiosis significantly alters immune regulation within the vaginal mucosa, shifting the environment from a protective, anti-inflammatory state toward heightened innate immune activation and epithelial stress (Cheng et al., 2025; Holdcroft et al., 2023). In healthy Lactobacillus dominant conditions, lactic acid and antimicrobial peptides maintain barrier integrity and suppress pro-inflammatory pathways. When anaerobes such as Gardnerella, Atopobium or Prevotella proliferate, Toll-like receptor activation and increased cytokine and chemokine production promote inflammation and weaken epithelial defenses (Sadeghpour Heravi, 2024; Williams et al., 2025).

Pregnancy studies show that these immune disturbances are associated with increased sialidase activity, cytokine imbalance and higher risks of preterm birth and infection related complications (Gerede et al., 2024; Ng et al., 2021). Dysbiosis related inflammation also impairs endometrial receptivity and embryo implantation, impacting natural and assisted conception (Balla et al., 2024; Samama et al., 2025). Evidence from microbial atlases such as VMAP highlights that even minor deviations from Lactobacillus dominant states may influence reproductive risk (Parraga-Leo et al., 2024). Collectively, dysbiosis represents an immune and biological disturbance with significant consequences for reproductive and obstetric outcomes (Da Silva et al., 2025; Vinitha et al., 2025).

3.6. Vaginal microbiome and fertility

Growing evidence demonstrates that the composition of the vaginal and genital tract microbiome is closely linked to female fertility, influencing natural conception and outcomes of assisted reproductive technologies (Günther et al., 2022; Gullo et al., 2025). Lactobacillus dominated communities, particularly those enriched with Lactobacillus crispatus, support optimal reproductive conditions by maintaining low pH, reducing inflammation and strengthening mucosal integrity, all of which promote sperm survival and early embryo development (Cheng et al., 2025; Vinitha et al., 2025). In contrast, diverse CST IV type communities are associated with subfertility, implantation failure and gynecologic inflammation (Balla et al., 2024; Zhao et al., 2023).

Studies in women undergoing infertility evaluation and ART show that Lactobacillus rich vaginal or endometrial profiles correlate with higher implantation and clinical pregnancy rates, whereas dysbiotic or BV like communities are more frequent in recurrent implantation failure or unexplained infertility (Xiao et al., 2024; Balla et al., 2024). Microbial profiling is increasingly proposed as an adjunct in fertility diagnostics, with potential for identifying at risk patients and informing preconception optimization (Samama et al., 2025; Gullo et al., 2025).

Medical interventions such as ovarian stimulation or surgical procedures may temporarily disrupt microbial stability, further highlighting the need to consider microbiome status as both a determinant and modifiable factor in reproductive care (van den Tweel et al., 2024; Tong et al., 2023). The vaginal microbiome acts as a key biological interface influencing fertility through its interaction with hormonal, immunologic and epithelial pathways (Condori-Catachura et al., 2025; Da Silva et al., 2025).

3.7. Vaginal microbiome and assisted reproductive technologies (ART)

The vaginal microbiome is increasingly recognized as an important factor influencing ART outcomes, particularly embryo implantation, endometrial receptivity and early pregnancy development (Xiao et al., 2024; Balla et al., 2024). Lactobacillus dominant profiles, especially those enriched with Lactobacillus crispatus, are associated with higher implantation rates, better embryo quality, and improved chances of clinical pregnancy (Samama et al., 2025; Tong et al., 2023). In contrast, CST IV type or BV associated communities correlate with reduced ART success, heightened inflammatory signaling and impaired conditions around implantation (Günther et al., 2022; Gullo et al., 2025).

Evidence also shows that ART related procedures, including ovarian stimulation and prophylactic antibiotics, can transiently disrupt microbial composition and reduce microbial stability (van den Tweel et al., 2024; Samama et al., 2025). As a result, integrating microbiome assessment into evaluation before ART is increasingly proposed to identify dysbiosis, guide targeted interventions and potentially optimize endometrial receptivity (Gullo et al., 2025; Da Silva et al., 2025).

The vaginal microbiome represents a clinically relevant but often overlooked determinant of ART outcomes, offering opportunities for more personalized reproductive treatment strategies (Condori-Catachura et al., 2025; Vinitha et al., 2025).

3.8. Vaginal microbiome and pregnancy outcomes

The vaginal microbiome undergoes characteristic stabilization during pregnancy, typically shifting toward low diversity, Lactobacillus dominant communities that protect against infection and support maternal-fetal health (Gerede et al., 2024; Parraga-Leo et al., 2024). Increased abundance of L. crispatus and L. jensenii helps maintain acidic pH, strengthen epithelial barriers and suppress pathogenic anaerobes (Mendz, 2023; Ng et al., 2021).

When pregnancy is accompanied by dysbiosis, especially CST IV or elevated Gardnerella or Atopobium abundance, studies consistently report higher risks of preterm birth, premature rupture of membranes, intra-amniotic infection and heightened inflammatory activity (Gerede et al., 2024; Mendz, 2023). Large scale mapping efforts such as VMAP further show that deviations from Lactobacillus dominance correlate with increased sialidase activity, immune imbalance and indicators of reproductive risk (Parraga-Leo et al., 2024).

Dysbiosis related inflammation may disrupt cytokine networks, weaken epithelial integrity and promote ascending infection, contributing to obstetric complications (Cheng et al., 2025; Williams et al., 2025). Additionally, the maternal vaginal microbiome seeds neonatal microbial colonization during vaginal delivery, influencing early immune development (Mendz, 2023; Da Silva et al., 2025).

Current evidence positions the vaginal microbiome as a significant determinant of pregnancy health, with implications for prevention, risk stratification and personalized obstetric management (Gullo et al., 2025; Xiao et al., 2024).

3.9. Microbiome across the female lifespan

The vaginal microbiome shifts markedly across the female lifespan in response to hormonal changes, immune maturation and epithelial physiology (Cheng et al., 2025; Condori-Catachura et al., 2025). During puberty, rising estrogen levels increase epithelial glycogen, promoting the establishment of Lactobacillus-dominant, low-diversity communities typical of reproductive-age women (Gerede et al., 2024; Mendz, 2023). Across adulthood, menstruation, sexual activity, pregnancy and postpartum changes contribute to periodic fluctuations, occasionally leading to transient microbial instability (Parraga-Leo et al., 2024; Ng et al., 2021). Pregnancy is characterized by enhanced stability and strong Lactobacillus dominance, supporting low pH and reduced infection risk (Gerede et al., 2024; Vinitha et al., 2025).

With perimenopause and menopause, declining estrogen and reduced glycogen lead to a loss of Lactobacillus dominance and increased microbial diversity, often accompanied by inflammation-related symptoms (Günther et al., 2022; Holdcroft et al., 2023). Population-based research shows that these life-stage patterns are further shaped by ethnicity, geography, lifestyle and environmental exposures (Condori-Catachura et al., 2025; Vinitha et al., 2025). Medical interventions such as fertility treatments and antibiotic use may also alter microbial composition during the reproductive years (Samama et al., 2025; Tong et al., 2023).

The vaginal microbiome is a dynamic, hormonally responsive ecosystem that evolves across the lifespan and influences reproductive health at every stage (Da Silva et al., 2025; Xiao et al., 2024).

3.10. Health education and awareness across the female lifespan

Health education and awareness of the vaginal microbiome are important but often underestimated determinants of women's reproductive health (Cheng et al., 2025; Holdcroft et al., 2023). Adolescence and early adulthood are key periods for building literacy about intimate hygiene, sexual behavior and symptoms of dysbiosis or sexually transmitted infections, with school programs, primary care and gynecological visits offering opportunities to promote evidence based practices such as avoiding intravaginal douching, limiting unnecessary antibiotics and seeking timely evaluation of abnormal discharge or odor (Gerede et al., 2024; Günther et al., 2022; Mendz, 2023).

In women of reproductive age, counseling within contraceptive care, infertility consultations and preconception visits can address the impact of the vaginal microbiome on fertility, implantation and pregnancy outcomes, while clear communication about hormonal changes, intimate products, sexual practices and medical interventions may improve adherence to preventive recommendations (Balla et al., 2024; Xiao et al., 2024; Da Silva et al., 2025; Gullo et al., 2025). For pregnant individuals, targeted education about links between dysbiosis, BV and preterm birth supports earlier screening and more active engagement in proposed treatment (Gerede et al., 2024; Parraga-Leo et al., 2024).

In perimenopause and menopause, informing patients about the effects of declining estrogen, hormone therapy, lubricants, local estrogen preparations and lifestyle factors on vaginal health can guide individualized management and potentially reduce infection risk (Günther et al., 2022; Holdcroft et al., 2023; Condori-Catachura et al., 2025; Vinitha et al., 2025). Integrating microbiome related education into clinical care and public health initiatives may help modify behaviors that influence the vaginal microbiome and improve reproductive outcomes across the female lifespan (Cheng et al., 2025; Da Silva et al., 2025).

3.11. Physical activity, systemic health, and the vaginal microbiome

Physical activity is a key component of women's overall health and affects metabolic, endocrine and immune pathways that may indirectly influence the vaginal microbiome and reproductive function (Cheng et al., 2025; Gullo et al., 2025). Regular moderate exercise improves insulin sensitivity, lowers systemic inflammation and supports hormonal stability, which may help maintain mucosal immunity and reduce susceptibility to dysbiosis, although direct mechanistic evidence remains limited (Condori-Catachura et al., 2025; Da Silva et al., 2025; Vinitha et al., 2025).

In fertility care and ART settings, lifestyle optimization, including weight management and physical activity, is increasingly viewed as part of preconception preparation, as obesity and sedentary behavior contribute to inflammation and endocrine disruption that may affect genital tract conditions and endometrial receptivity (Balla et al., 2024; Tong et al., 2023). Findings from broader microbiome research also suggest that combined diet and exercise interventions can modify microbial communities at other body sites, supporting the need for targeted studies on the vaginal niche (Ng et al., 2021; Parraga-Leo et al., 2024).

During pregnancy, appropriately tailored physical activity supports metabolic health and lowers the risk of complications such as gestational diabetes and hypertensive disorders, which may interact with immune and microbial homeostasis (Gerede et al., 2024; Mendz, 2023). Later in life, maintaining an active lifestyle may help sustain immune function and reduce chronic inflammation, indirectly supporting vaginal microbial stability (Holdcroft et al., 2023; Xiao et al., 2024).

Physical activity should be considered part of a holistic approach to women's health that complements microbiome-focused prevention and care, although further longitudinal and interventional studies are needed to clarify direct effects on the vaginal microbiome (Da Silva et al., 2025; Gullo et al., 2025).

4. Discussion

Current evidence underscores the vaginal microbiome as a key determinant of reproductive health, influencing fertility, pregnancy outcomes and gynecologic stability across the lifespan (Cheng et al., 2025; Gullo et al., 2025). Lactobacillus dominated communities, especially those enriched with L. crispatus, are consistently linked with reproductive resilience through pH regulation, epithelial protection and immune modulation (Günther et al., 2022; Xiao et al., 2024). In contrast, CST IV communities with anaerobic overgrowth are strongly associated with subfertility, implantation failure, preterm birth and heightened inflammation, highlighting the clinical relevance of dysbiosis (Gerede et al., 2024; Mendz, 2023).

Despite advances in sequencing technologies, translation of microbiome research into routine clinical practice remains limited due to variability in diagnostic methods, lack of standardized thresholds and inconsistent interpretation across studies (Condori-Catachura et al., 2025; Holdcroft et al., 2023). High BV recurrence rates further demonstrate that conventional antibiotic therapy may suppress pathogenic taxa without restoring stable Lactobacillus dominance, emphasizing the need for more comprehensive approaches, including probiotics, microbiome guided strategies and emerging interventions such as vaginal microbiota transplantation (Williams et al., 2025; Da Silva et al., 2025).

This review also highlights the importance of health education as a modifiable determinant of microbial stability. Improved literacy related to intimate hygiene, antibiotic stewardship, sexual health and early recognition of dysbiosis can reduce behaviors that disrupt vaginal ecosystems (Holdcroft et al., 2023; Günther et al., 2022). Integrating educational interventions into contraceptive counseling, infertility care and prenatal programs may support early detection, adherence to treatment and improved reproductive outcomes (Da Silva et al., 2025; Gullo et al., 2025).

Similarly, physical activity, through effects on metabolic, inflammatory and endocrine pathways, may indirectly support microbiome stability and fertility, although mechanistic data are still emerging (Condori-Catachura et al., 2025; Cheng et al., 2025). Lifestyle optimization, including exercise and weight management, is increasingly recognized as part of preconception and fertility care, and research specific to pregnancy suggests that physical activity may mitigate inflammation related complications relevant to microbiome balance (Gerede et al., 2024; Mendz, 2023).

Current research supports a multidimensional understanding of the vaginal microbiome, shaped not only by physiological and clinical factors but also by education, behavior and lifestyle. Integrating microbiome science with health literacy initiatives, physical activity promotion and personalized clinical care may enhance prevention and improve reproductive outcomes. Continued longitudinal and multiomics research is essential to clarify mechanisms, refine diagnostics and validate new therapeutics, enabling clinical guidelines that encompass both biological and behavioral determinants of reproductive well-being.

This narrative review is limited by the restriction to open access studies published between 2021 and 2025 and by methodological heterogeneity across the included articles, which may affect the generalizability of the synthesized findings.

5. Conclusions

Current evidence confirms that the vaginal microbiome is a key determinant of women's reproductive health, influencing fertility, pregnancy outcomes and gynecologic stability through interactions with mucosal immunity, hormonal regulation and epithelial homeostasis (Cheng et al., 2025; Günther et al., 2022). Lactobacillus dominated communities, especially those enriched with Lactobacillus crispatus, consistently correlate with lower inflammation and more favorable reproductive outcomes, whereas dysbiosis and CST IV type communities are strongly linked to subfertility, implantation failure and adverse obstetric events (Xiao et al., 2024; Gerede et al., 2024).

Despite growing diagnostic precision, the clinical translation of microbiome research remains limited by methodological variability, recurrence of dysbiosis after antibiotics and gaps in mechanistic understanding. These challenges highlight the need for standardized diagnostics and longitudinal multiomics studies (Williams et al., 2025; Sadeghpour Heravi, 2024). Emerging therapeutic approaches, including probiotics, microbiome guided interventions and vaginal microbiota transplantation, show promise but require further clinical validation (Da Silva et al., 2025; Vinitha et al., 2025).

Importantly, evidence suggests that health education and lifestyle behaviors, including physical activity, may support microbial stability and improve reproductive outcomes by reducing harmful practices and promoting overall metabolic and immune health. Integrating educational strategies and lifestyle promotion with microbiome-based diagnostics and therapies may enhance prevention and contribute to a more holistic, personalized approach to women's reproductive care (Parraga-Leo et al., 2024; Tong et al., 2023).

Disclosure:

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