Review Article

Exploring the Vaginal Microbiome: Implications for Reproductive Health in Indian Women

Abstract: The vaginal microbiome plays a crucial role in women's reproductive health. It consists of a variety of bacteria that help maintain a healthy environment in the vagina. A balanced microbiome can prevent infections and support overall reproductive health. However, many women in India face challenges such as poor hygiene practices, dietary habits and lack of access to medical care which can disrupt this balance. One significant conclusion is that the diversity of the vaginal microbiome is closely linked to reproductive health outcomes, with a balanced microbiome associated with lower risks of infections and complications. The review emphasizes the role of specific hygiene practices and management, which can significantly impact the composition of the vaginal microbiome. Additionally, dietary habits were found to influence microbial diversity, suggesting that a diet rich in probiotics may promote a healthier vaginal environment. The article advocates for increased awareness and education regarding these factors among women, as they can play a crucial role in enhancing reproductive health and preventing diseases. Overall, this review provides valuable understanding of microbiome and emphasizes that promoting a healthy vaginal microbiome is essential for improving women's health and how lifestyle choices can affect women's health at a microbiological level, particularly in the context of Indian demographics.

Keywords: vaginal microbiome, women's health, reproductive health.

1. Introduction

The human vagina is not a sterile organ; it harbors complex microbial communities that play a significant role in women’s reproductive health. This consortium of bacteria, fungi, viruses, and archaea residing within the lower reproductive tract is termed the vaginal microbiome. The structure and composition of the vaginal microbiome determine the type of environment in which it is inherited. In healthy conditions, Lactobacilli are the predominant bacterial species in the vaginal microbiome and maintain an acidic environment to suppress the colonization of pathogens. The diversity in the community of microbial members, known as dysbiosis, is directly linked to reproductive complications such as preterm birth, sexually transmitted infections, and human immunodeficiency virus infection.

Strongly powered catalog and microbiome studies in many populations have established substantial differences in the types and subtypes of the vaginal microbiome across geographical sites and between women. Several studies have also demonstrated changes in the numeric proportion of members of different genera in the microbiome during pregnancy as well as parturition. As a result, an increasing number of data linking the vaginal microbiome with a variety of gynecological and reproductive processes are providing the tools to unravel the complexities of women’s health. The importance of the vaginal microbiome lies in the association with reproductive tract phenotypes that are confined to women, and the roles it plays in the wide range of outcomes concerning gynecological as well as general health of women.

The intricate relationship between the vaginal microbiome and women's reproductive health has garnered significant attention in recent years, as emerging research reveals the critical role of microbial communities in various aspects of reproductive physiology. The literature presents a compelling narrative that underscores the importance of understanding this interplay, particularly in the context of reproductive health and disease.

In 2020, (Al-Nasiry *et al*., 2020) explored the interplay between reproductive tract microbiota and the immunological system, positing that cesarean delivery deprives infants of essential exposure to vaginal microbiota, potentially leading to neonatal dysbiosis. Their pilot study indicated that vaginal seeding could partially restore microbiome composition in cesareanborn infants, although the small sample size raised concerns about the reliability of the findings. This study highlights the necessity for larger, methodologically sound investigations to assess the long-term health implications of microbiome restoration practices and the complex relationship between maternal microbiota and fetal development. Building on this foundation, (Kaur *et al*., 2020) examined the crosstalk between female gonadal hormones and vaginal microbiota throughout various phases of a woman's gynecological lifecycle. They identified how hormonal fluctuations can lead to dysbiosis, emphasizing that increased microbial diversity during pregnancy does not equate to infection. Their findings suggest a need for a comprehensive study that captures the structural variations of the vaginal microbiome across different life stages, particularly during menopause. This research contributes to the understanding of how hormonal changes influence microbial communities and, consequently, women's gynecological health. Further expanding this dialogue, (Tomaiuolo *et al*., 2020) focused on the implications of female reproductive microbiota on infertility. Their review highlighted the role of vaginal and uterine microbiota in maintaining reproductive health and the success of assisted reproductive technologies. They noted that while the vaginal microbiota is relatively well-characterized, the uterine microbiota remains underexplored, indicating a gap in current research. The authors emphasized that dysbiosis within these microbial communities could be a contributing factor to infertility, thereby reinforcing the need for further investigation into the composition and function of the female reproductive microbiome.

Together, these articles paint a comprehensive picture of the vaginal microbiome’s role in women's reproductive health, illustrating the multifaceted interactions between microbial communities, hormonal changes, and reproductive outcomes. The collective insights from these studies underscore the necessity of ongoing research to elucidate the complexities of the vaginal microbiome and its implications for women's health across their reproductive lifespan.

1.1. Definition and Composition of the Vaginal Microbiome

The vaginal microbiome consists of the combined genetic material of the microorganisms in the vagina. The vagina hosts a wide variety of microbial agents such as bacteria, yeast, and viruses, and bacterial species differ among different women (Chopra C *et al*., 2022). The healthy vagina is generally dominated by one or two Lactobacillus species. Lactobacilli produce lactic acid, the main source of energy in vaginal cells, as well as other substances that are toxic and protective for the vagina. This is the reason why a healthy vagina has a low pH that can impede the growth of pathogens and infections. In general, vaginal communities are complex and maintain a dynamic balance by influencing each other, rather than having a specific bacterium that causes a disease.

Several factors can change the microbial community in the vagina at different times in a woman's life, such as puberty, pregnancy, menopause, hormonal contraceptives, menstrual cycles, vaginal douching, and sexual activity. An optimal microbiome optimizes oocyte quality, embryo health and development, and uterine receptivity in terms of normal pregnancy (Punzón-Jiménez P *et al*., 2021). The prevalence of dysfunctional vaginal communities is common, affecting different populations on different continents. Disturbances in vaginal communities can have adverse health effects, including resulting in a poor obstetric outcome characterized by early rupture of the membranes, preterm premature birth, low birth weight, and neonatal morbidity. Their impact on the reproductive health of women is also significant. In general, such infections have a high incidence in women of childbearing age.

1.2 Related work

The article titled "The Interplay Between Reproductive Tract Microbiota and Immunological System in Human Reproduction" by (Al-Nasiry *et al*., 2020) provides a comprehensive examination of the relationship between the vaginal microbiome and reproductive health, particularly in the context of cesarean delivery and its implications for neonatal health. The authors highlight the emerging concern that cesarean delivery may deprive infants of essential exposure to maternal vaginal microbiota, potentially leading to a state of neonatal dysbiosis. This concept has given rise to the practice of "vaginal seeding," which aims to mitigate the effects of this microbiome deprivation. However, the article critically evaluates the current evidence surrounding vaginal seeding, noting significant limitations in the existing research, such as small sample sizes and the presence of confounding variables that may bias outcomes. As a result, the authors reference the stance of the American College of Gynecology and Obstetrics, which does not endorse perinatal seeding as a standard practice, emphasizing the need for larger, rigorously designed studies to ascertain any long-term health benefits for offspring. Furthermore, the authors delve into the intricate dynamics between the female reproductive tract microbiome and the host's immunological system, suggesting that the stability of the reproductive tract microbiota is crucial for both maternal and fetal health during gestation. This stability is posited to influence not only the physiological aspects of pregnancy but also the overall maternal-fetal status, indicating a complex interplay that warrants further investigation. The article "Crosstalk Between Female Gonadal Hormones and Vaginal Microbiota Across Various Phases of Women's Gynecological Lifecycle" by (Kaur *et al*., 2020) presents a comprehensive examination of the interplay between hormonal fluctuations and the vaginal microbiome throughout different stages of a woman's reproductive life. The authors propose a hormone-level driven microbiome diversity hypothesis, which posits that variations in hormone levels significantly impact the composition and diversity of the vaginal microbiota. The findings of this study emphasize the critical role that hormonal perturbations play in creating imbalances within the vaginal microbiome. This is particularly relevant during key phases such as menstruation, pregnancy, and menopause, where hormonal levels fluctuate dramatically. The authors highlight that understanding these dynamics is crucial for elucidating the mechanisms behind the maintenance of gynecological health and the prevention of conditions such as bacterial vaginosis, which is characterized by a disruption in the normal microbial community.

One of the notable strengths of this article is its holistic approach to studying the vaginal microbiome across the entire gynecological lifecycle. By focusing on the structural variations of the microbiome in relation to hormonal changes, the authors provide valuable insights into how these factors contribute to the overall health of women. However, the article also acknowledges a significant gap in the existing literature, specifically the lack of comprehensive studies that contextualize the structural variations of the vaginal microbiome throughout various stages of the reproductive cycle and menopause. This limitation suggests a need for further research to validate the proposed hypotheses and to explore the implications of microbiome diversity on reproductive health more thoroughly. The study's methodology, which includes analyzing correlations between female sex hormone levels and vaginal microbial diversity, is a significant contribution to the field. The authors also make a compelling case for the importance of understanding the patterns of community diversity in both healthy states and conditions like bacterial vaginosis. This knowledge could lead to improved diagnostic and therapeutic strategies for maintaining vaginal health. The article "Microbiota and Human Reproduction: The Case of Female Infertility" by (Tomaiuolo *et al*., 2020) provides a comprehensive overview of the significant role that the female reproductive microbiota plays in women's reproductive health, particularly in the context of infertility. The authors highlight the advancements made in understanding microbial communities within the human body through next-generation sequencing technologies, which have revealed the intricate presence of these communities in the reproductive tract. One of the key insights presented is the concept of microbial dysbiosis, which refers to an imbalance in the microbial communities that can result from various internal and external factors. This dysbiosis has been implicated in several pathologies, including infertility. The article emphasizes that while the vaginal microbiota has been extensively studied, the uterine microbiota remains relatively underexplored. This gap in research is critical, as the uterine microbiota could play a pivotal role in reproductive processes, including embryo implantation and pregnancy maintenance.

The authors note that Lactobacilli are the predominant bacteria in the vaginal microbiota, constituting about 9% of the entire human microbiota. These bacteria are essential not only for maintaining a healthy vaginal environment but also for supporting various reproductive phases, from gamete formation to influencing the microbial colonization of the fetus. The review effectively summarizes the current understanding of the 'healthy' female reproductive microbiome and elaborates on how dysbiosis may adversely affect fertility. Furthermore, the authors provide a critical evaluation of the existing literature, indicating that while there is growing evidence linking dysbiosis to infertility, more research is needed to fully elucidate the mechanisms at play and the potential therapeutic implications. The article serves as a valuable resource for understanding the complex interactions between the vaginal microbiome and reproductive health, underscoring the necessity for further exploration into the uterine microbiota and its contributions to fertility and reproductive outcomes.

2. Importance of the Vaginal Microbiome in Women's Reproductive Health

The mammalian reproductive tract lies open to the exterior environment and has significantly more elements of microbial life. In human women, the vaginal canal is a mucosal organ comprising microbiota-specific communities, especially Lactobacillus spp. The composition of vaginal bacterial communities can change to form a structure like other parts that lack Lactobacilli, as determined by the micro-bio types of the human vaginal microbiome. During this time, women's menstruation and the administration of contraceptives can both stimulate hormonal changes that can influence some features of the microbiome.

Given that, in different reproductive activities, vaginal bacterial communities might influence and/or occur, it is not out of the question that microbiomes have an impact. For many women in India, reproductive experiences need to be studied. Once infection is present, the role of the pelvic reactions set up for an optimal microbiome can prevent the advancement of reproductive structures that could complicate or lower fertility or cause ectopic pregnancy. As we have described, the vaginal bacterial communities can discharge items related to immunity and interfere directly with immunity by presenting low-efficacy antigens, linking to and transferring or communicating with other local systems of the body. Recent work with human fluids has discovered bacteria and their DNA not within the lumens but in the blood and other areas.

2.1. Impact on Reproductive Outcomes

The most studied association between the vaginal microbiota and reproduction is fertility and pregnancy. The vaginal microbiota has been correlated with various fertility outcomes, including physiological implantation and decidualization, early embryo development, endometrial receptivity, and spontaneous pregnancy rates. In assisted fertility, first trimester pregnancy success has been associated with intermediate Lactobacillus dominance. The evidence is that there are specific microbial profiles that may support fertility and that implantation of the early embryo following natural or assisted implantation most commonly occurs in a Lactobacillus-dominated vaginal microbiome. (Chopra *et al.*2022) Other evidence associates bacterial vaginosis equivalence to preimplantation failure (Al-Nasiry *et al.*2020) (Diaz-Martínez *et al.*2021). The microbiome can also contribute to pregnancy complications. Some of the most extensive data for this relates to the association between bacterial vaginosis and preterm birth. Consistent findings include that bacterial vaginosis is one of the few biomarkers strongly associated with a 30% increase in preterm birth, and this holds true even for women of low socioeconomic status, smokers, or those trying to access healthcare (Juliana *et al.*2020) (Bayar *et al.*2020) (Coudray and Madhivanan2020) (Gudnadottir *et al.*2022) (Bhakta *et al.*, 2021) (Feehily *et al.*2020).

Women with bacterial vaginosis have an altered cervico-vaginal or local immune landscape that can present as endocervical-decidual activation or inflammation during pregnancy. The reason for this could be that both pathogenic bacteria and their toxic metabolites can ascend or cause a systemic infection at the site of placental implantation. This is supported by animal models. A leading theory is that on entry to the uterus, bacteria can also elicit a preterm activation response by entering the uterine blood circulation and by increasing immune cells and cytokines at the decidual maternofetal interface, leading to activated maternal decidual matrix metalloproteinases that can compromise the placental bed. However, it is likely that even in populations with low rates of preterm birth, a small amount of alpha diversity exists. It has been documented that Lactobacillus diversity and diversity of species such as L. iners are associated with resilience or protection against preterm birth. Thus, a general conclusion is that the more alpha diversity, that is, the more species present in any woman, especially during the second to third trimester of pregnancy, the more resilient the vagina may be to influence preterm birth, particularly spontaneous preterm birth due to ascent infection.

Microbial interactions inside the lower genital tract are able to produce chemicals, and for example, gases such as nitric oxide and hydrogen sulfide. It is hypothesized that the microbiota may be able to produce gases that could affect reproductive dynamics. Choline is a semi-essential nutrient, from which the gut microbiome is able to produce trimethylamine, which is then transformed to trimethylamine-N-oxide. Decreased levels of vaginal choline are thought to be a result of low levels of the two main choline-utilizing Lactobacilli. Nevertheless, it has been stated that decreased levels of choline in the blood serum are correlated with increased rates of tubal factor infertility or intrauterine growth restriction (Mauchart *et al.*2023) (Owen *et al.*2021) (Wang *et al.*, 2022). Currently, researchers need to gain deeper and more specific knowledge about the still unknown consequences of whether and how fecal-produced choline and serum choline may influence vaginal choline and then influence fertility. Fertility is increased by dietary carnitine and is directly correlated to greater levels of carnitine, at least in part due to its metabolic conversion to the metabolite trimethylamine-N-oxide.

3. Factors Influencing the Vaginal Microbiome in Indian Women

Microbiomes exist not only between individuals but also within the same host for different body sites. This is mostly due to different host evolutionary pressures shaping unique body habitats. The study of the interplay between the surrounding environment and the vaginal microbiota of diverse women can offer different views on the functioning of microbial communities. Indeed, many factors have been recently identified that could shape the vaginal ecosystem, including hygiene practices and diet, which in turn have a long and completely different history in European and American women compared to Asian women, and particularly women living in low- and middle-income countries, profoundly modifying the microbial community. It is thus anticipated that the vaginal microbiomes of different groups of Indian women can result from the collective influence of factors spanning from the sociocultural to the individual level (Borgogna *et al.*2021) (Das *et al.*2023) (Chopra *et al.*, 2024) (Gupta *et al.*, 2020).

The vaginal ecosystem in India is affected by lifestyle, hygiene practices, diet, socio-economic status, culture, and women's reproductive status. These factors can be linked to a geographical area, ethnicity, or religion, giving each woman a unique microbiome. Several recent studies conducted on various groups of Indian women have shown that there are several factors contributing to lower levels of Lactobacillus compared to women in the United States (Das *et al.*2023) (Garg *et al.*2023) (Vasundhara *et al.*2021) (Chopra *et al.*2022). These factors include diet, personal hygiene, increased incidence of urinary and reproductive tract infections, and the use of intrauterine devices. The studies have highlighted specific issues such as a high proportion of meat-eating women in certain communities, inadequate hygiene facilities in urban slums, and low levels of gender equality, women's education, good hygiene practices, and water treatment in women from higher caste groups (Vogel *et al.*, 2022) (Yadav *et al.*2020) (Vishwakarma *et al.*2021). All these factors, which certainly have a long and complex historical evolution and potentially reflect different body metabolic statuses, are to be taken into consideration in the design of specific health promotion strategies at the level of rural and urban women in India (Anjana *et al.*2023) (Biswas *et al.*2022) (Chopra *et al.*2020).

4. Diversity of Vaginal Microbiome Across Different Regions of India

India is known for its rich cultural diversity, structural inequality, and wide variation in dietary intakes, lifestyle-related factors, occupational hazards, and reproductive health practices. Lifestyle choices have an effect on the vaginal microbiome that further influences women's reproductive health. Based on the presence of bacterial species, the vaginal microbiome of North Indian and South Indian women shows interesting regional variations. Certain locations are geographically isolated and unexplored, and hence, culture-specific health, including reproductive health, is not well known. Very few studies have described the vaginal microbiomes of Indian women akin to their geographic locations. In addition to geographical and climatic differences, this note describes the differences in the vaginal ecological composition of women based on changing lifestyle, hygienic practices, nutrition, etc., thereby influencing their reproductive health in a very diverse country such as India.

In India's scope and linguistic dimensions, the dietary habits not only differ but also reflect cultural uniqueness in relation to a geographical area or city from one place to another. Within various Indian geographical regions, the analysis of the vaginal microbiome reflects regional differences in bacterial community structure. Many studies have profiled healthy women as a control group, and pathogenic associations with bacterial species were also reported in these women. There is a gap in knowing the variation in vaginal microbial communities among the healthy population within the cities with comparable environmental factors. In an earlier investigation, it was inferred that multiple facets of human reproductive health bring into play a potential influence—the vaginal microbiota. Research primarily contemplated from the

Western sphere cannot essentially serve the purpose of replicating the health maintenance advantages of vaginal lactobacilli in other populations, especially in India, because of divergences in food and dietary habits, mating patterns, etc. Thus, it is interesting to investigate the indigenous Indian vaginal microbiome, primarily representative of a specific South Asian regional and ethnographic group, for its potential in managing women's reproductive health, particularly in Indian women.

5. Methods for Studying the Vaginal Microbiome

Traditionally, the working horse in microbiology, microbial culture, is a valuable method for tracking vaginal microbiota communities of healthy and diseased women in the 19th and early 20th centuries in Europe, as well as for investigating the vaginal microbiota of non-Western women (France *et al.*, 2022). In the past 60 years, significant methodological advances have been made in molecular techniques, particularly 16S rRNA gene-based techniques, for vaginal microbiota community characterization. Although many early studies of the H_2O_2-producing Lactobacillus species have been based on DNA sequencing or real-time PCR at the species or genus level, no studies have adopted the NGS approach (Berman *et al.*2020) (France *et al.*, 2022) (Molina *et al.*2021) (Hugerth *et al.*2020). From the few studies adopting the NGS approach, we know that the *Lactobacillus spp.* H_2O_2 producers typically inhabit only 30% to 80% of non-Western women's vaginal microbiotas (De *et al.*2021). Future metagenomic or metatranscriptomic studies will greatly enhance our understanding of the function of the vaginal microbiota. It is important for the impact of these findings in clinical medicine and public health that sample-processing procedures be both uniform and appropriate for the investigations of interest. The simpler methods, such as microscopy, microbial culture, and species-specific PCR, are more readily interpretable for use in clinical settings and in anthropological research where H2O2-producing and non-H_2O_2 vaginal microbiota types are most commonly reported (Calderaro *et al.*2022) (Muzny *et al.*2023) (Yang *et al.*, 2023). Certainly, molecular methods are less affected by sample collection procedures. Each method used in the study of the vaginal microbiota has distinct strengths and limitations which, combined with the population question of interest, should guide method selection. The aim of a given study, along with the expected nature of vaginal microbiota profiles to be encountered in a study population, should be used as guidelines for method selection.

6. Common Vaginal Microbiome Profiles in Indian Women

Lactobacillus species, predominantly Lactobacillus crispatus, Lactobacillus iners, and *Lactobacillus jensenii*, are known to colonize the lower reproductive mucosa in healthy women of reproductive age around the world. Similar to other studies on the vaginal microbiome, multiple studies have reported five specific vaginal microbiome profiles in Indian women, with microbiomes dominated by the presence of *L. crispatus*, *L. iners*, *L. jensenii*, *and L. gasseri*, as well as mixed-community variations in which only some proportions of Lactobacillus species are present, typically with an abundance of either *L. crispatus* or *L. iners* (Mehta *et al.*2020)(Vasundhara *et al.*2021)(Kamble *et al.*2024)(Kumar *et al.*2021)(Gupta *et al.*, 2020). Functional investigations have found that Indian women reveal specific metabolic pathways in the vagina, such as lactic acid metabolism and the metabolism of other amino acids and proteins. Profiling the translational importance of these specific vaginal microbiomes and metabolic pathways, recent work has revealed that the chance of acquiring HIV infection in Indian women is linked with the relative abundance of the vaginal microbiomes (Gupta *et al.*, 2020) (Deka *et al.*2021) (Chopra *et al.*, 2024).

Studies indicate that the ethnicity and age of different Indian women, from adult to infant stages, affect the vaginal microbiome composition. A recent study conducted in Indian women attending an infertility clinic reported higher vaginal pH accompanied by lower abundance of *Lactobacilli*, as well as BVAB-1 and *Clostridiales spp*., which correlate with a clinical diagnosis of vaginitis (Mehta *et al.*2020) (Kulshrestha *et al.*2024). Other vaginal infections, such as vulvodynia and urinary tract infections, have been described in Indian women, and the abundance of Lactobacillus in the vagina is associated with a lower occurrence of UTI. Understanding the presence of these variations in healthy women and knowing how such variations change during specific disorders will help improve clinical management and inform strategies for targeted intervention. The clinical implications of these variabilities in vaginal microbiology are important for female healthcare clinicians in dealing with reproductive and sexual health and the risk of reproductive failure in Indian women.

7. Association Between Vaginal Microbiome and Gynecological Conditions in Indian Women

Studies around the world have shown that the vaginal microbiome plays a role in maintaining reproductive health by preventing infections. The role of the vaginal microbiota in bacterial vaginosis and adverse reproductive health outcomes has been detailed in numerous studies. The vaginal microbiome could facilitate the overgrowth of harmful pathogens and their subsequent invasion into the upper reproductive tract, leading to pelvic inflammatory diseases and infertility. Growing evidence also indicates that the vaginal microbiota may play a key role in susceptibility to reproductive tract infections, such as chlamydia and gonorrhea. It has been suggested that correction of the vaginal microbiome may reduce the susceptibility to these sexually transmitted infections. Dysbiosis may also contribute to the increased risk of human immunodeficiency virus infection among women in lower-income settings through similar biological changes. Such infections are of particular concern, where control programs need to consider a wider range of potential pathogens leading to increased morbidity.

According to available evidence from the field of microbiome research, we observed that the vaginal microbiome is shaped by several factors such as age at menarche, early age at first sex, hormonal contraception use, and presence of reproductive tract infection, especially concerning *Trichomonas vaginalis*. Findings also confirm a role of the vaginal microbiota in the prevalence of bacterial vaginosis and/or vaginal yeast infection. One study showed a significant protective effect of a Lactobacillus-dominant vaginal microbiome that promoted acidic pH to suppress the Candida species. *Lactobacillus crispatus* has been associated with a reduced risk of bacterial vaginosis, which could be due to the ability of this species to produce a more stable protective biofilm. Given these potential associations of the vaginal microbiome with these clinical conditions, there is potential scope for the use of specific Lactobacillus probiotics as an adjunct microbiome-based treatment or diagnostic tool.

8. Impact of Diet and Lifestyle on the Vaginal Microbiome in Indian Women

Indian women's dietary choices, variant across the length and breadth of the country, have the potential to impact the vaginal microbiome in unique ways. Traditional diets are rich in prebiotics and constitute a variety of fermented foods that can provide a rich repertoire of probiotics. Despite regional heterogeneities, traditional diets are primarily plant- and fiber-based, such as salads, pickles, raw chutneys, and sauces. In light of the evidence linking the same to health, studies need to garner evidence of vaginal health. The Western diet, on the other hand, has an association with a reduction in vaginal Lactobacillus species. However, the opportunistic pathogens, especially *Atopobium vaginae*, can easily scavenge dietary glycogen, indicating the contribution of diet-induced host-derived substrate for the overgrowth of *A. vaginae.* The relationship of physical activity with the microbiome is limited, and only one study has previously been reported. Chronic stress can lead to the Rashomon effect, assigning diversity both in positive and negative ways in different circumstances. Substances such as alcohol, tobacco, gutkha, areca nut, and smokeless tobacco also can influence the vaginal microbiome.

Considering the close relationship and the far-reaching effects on reproductive outcomes, it is important to explore studies implicating how diet and nutrition can act as key players in regulating vaginal health. Nutritional status can alter the flux through numerous associated pathways that impact all stages of reproduction. The gut microbial community and metabolic pathways are indeed a host-microbiome signature. Furthermore, people consume different nutrients, and therefore the food components can have critical effects on natal origin. Based on countable evidence, a vaginal health improvement program involving a dietary intervention approach can be developed. Such an intervention needs to be culturally and regionally specific in order to be successful. The results of ongoing clinical trials about the potential roles of probiotics, prebiotics, and synbiotics might be directed to answer the hypothesis. It is unclear if diet can be directly linked to the vaginal microbiome, but a healthy diet can have systemic benefits that extend to reproductive health. Knowledge of how dietary choices can influence the vaginal microbiota is limited, especially in the Indian women population.

9. Therapeutic Interventions Targeting the Vaginal Microbiome in Indian Women

An increasing body of literature suggests that a healthy, diverse, and resilient vaginal microbiome is an important part of the path towards reproductive health in women. Therapeutic interventions focused on restoring and maintaining a lactobacillus-dominant vaginal microbiome are widely used across the world. Specific approaches to achieve this include using probiotics, including lactobacillus species; consuming prebiotics, such as oligosaccharides, to foster the growth of lactobacilli; and promoting dietary modifications—rich in plant-based and nutritious foods—capable of enhancing microbial health. In addition to these approaches, there is limited research that supports the use of pharmacological treatments aimed at addressing dysbiosis. However, there are currently no guidelines of best practice related to these therapies, especially when it comes to the Indian context. We hypothesize the need for interventional studies investigating the potential of using all the above strategies to optimize the reproductive health of women and potentially improve pregnancy outcomes. Despite the absence of clinical trials focused on therapeutic intervention, we have identified that the research community is currently collecting evidence towards this approach in low-middle-income countries. In India, where the use of intravaginal products is linked with sexual behavior, therapeutic interventions are likely to also be acceptable only if they are culturally sensitive and compatible with the Hindu and Islamic practices of the majority of the population. Given the importance of the vaginal microbiome in women's reproductive health, incorporating interventions based on this organ could well be the way of the future of public health. In this review, we have reviewed attempted therapeutic interventions that could restore and optimize the vaginal microbiome of Indian women. We found that the available treatment options encompass dietary approaches, as well as efforts to replenish the lactobacilli by administering probiotics. These interventions are effective in restoring a lactobacillus-dominant microbiota, but specific trials to evaluate a possible effect on improving reproductive health outcomes in Indian women have yet to be conducted.

10. Conclusion

The investigation into the role of the vaginal microbiome in women's reproductive health has revealed significant insights into how microbial communities interact with various physiological processes. The studies reviewed illuminate the multifaceted relationship between the vaginal microbiome and reproductive outcomes, emphasizing the need for further research to fully understand this complex interplay. The article by (Al-Nasiry *et al.*, 2020) highlights the implications of cesarean delivery on neonatal microbiota, suggesting that the lack of exposure to maternal vaginal microbiota can lead to dysbiosis in infants. This research underscores the potential benefits of vaginal seeding, although it also points to the need for larger studies to validate these findings and assess long-term health outcomes. The authors emphasize the importance of a stable microbiome for both maternal and fetal health, suggesting that the dynamics of the vaginal microbiome can significantly influence reproductive physiology (Al-Nasiry *et al.*, 2020). In examining the relationship between female gonadal hormones and vaginal microbiota, (Kaur *et al.*, 2020) presents a compelling argument for the influence of hormonal fluctuations on microbial diversity throughout a woman's life. Their findings indicate that variations in hormone levels can lead to dysbiosis, particularly during critical life stages such as menstruation, pregnancy, and menopause. This article highlights a substantial gap in the literature regarding the comprehensive study of the vaginal microbiome across the gynecological lifecycle, suggesting that further research is necessary to understand how these dynamics contribute to gynecological health and disease (Kaur *et al.*, 2020). The review by (Tomaiuolo *et al.*, 2020) focuses on the implications of the female reproductive microbiota for infertility, emphasizing the need for a deeper understanding of both vaginal and uterine microbiota. The authors point out that while the vaginal microbiota has been extensively characterized, the uterine microbiota remains largely unexplored, creating a significant gap in knowledge. They highlight the role of microbial dysbiosis in infertility, suggesting that a balanced microbiome is crucial for reproductive health and successful assisted reproductive technologies (Tomaiuolo *et al.*, 2020).

In conclusion, the literature indicates that the vaginal microbiome plays a critical role in women's reproductive health, influencing various physiological processes and outcomes. The studies reviewed collectively emphasize the need for further research to explore the complexities of the vaginal and uterine microbiota, particularly regarding hormonal influences and their implications for reproductive health and infertility. Continued investigation in this area is essential for developing effective diagnostic and therapeutic strategies that could enhance women's reproductive health across their lifespan.

Data availability statement: Data sharing is not applicable to this article, as no new data were created or analyzed in this study.

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