

A COMPREHENSIVE STUDY - VAGINAL MICROBIOTA AND IT'S LINK TO PREGNANCY OUTCOMES

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ABSTRACT

Pregnancy outcomes are highly associated with the vaginal microbiome, which is essential for preserving reproductive health. This microbial community, which is primarily made up of Lactobacillus species in healthy people, produces lactic acid, hydrogen peroxide, and other antimicrobial substances that prevent the formation of harmful microbes and help to maintain an acidic vaginal environment. Negative pregnancy outcomes, such as preterm birth, miscarriage, and infections like bacterial vaginosis (BV), have been linked to dysbiosis, or an imbalance in the vaginal microbiota. New research emphasizes how important particular microbial patterns, immunological reactions, and metabolic interactions are in determining the course of pregnancy. Our understanding of these intricate interactions is being improved by developments in metabolomic profiling and sequencing technology, opening the door to new preventative, therapeutic, and diagnostic approaches that will maximize the health of mothers and newborns. To improve pregnancy outcomes globally, more research is needed to identify causal relationships and create therapies that target the microbiome.

This article highlights the concept of vaginal microbiota and its association with prevalence of microbial dysbiosis in pregnancy, preterm birth and gestational diabetes complications, screening methods for VMF, strategies for monitoring and restoring vaginal microbial balance and the need for standardized approaches for better understanding the relationship between the vaginal microbiota and pregnancy outcome.



Fig1 (a and b) -Vaginal microbiota and its associated risk of causing dysbiosis

Keywords: - *Vaginal Microbiota, Microorganisms, Lactobacillus species, Dysbiosis, Preterm Birth, Miscarriage, Metagenomics, Probiotics*

Introduction to Vaginal Microflora and Its Species Community being Related to Pregnancy

The microbes that live in the vagina are referred to as the vaginal microbiota. These microbes have a major impact on a woman's overall and reproductive health. *Lactobacillus* species that produce lactic acid predominate in a low-diversity environment that is indicative of a healthy vaginal microbiome. Conditions like bacterial vaginosis can result from factors that upset the equilibrium of the vaginal microbiota, including the use of antibiotics, sexual activity, obesity, maternal age and hormonal changes. The vaginal microbiota's makeup shifts and becomes more significant during pregnancy, acting as a barrier to prevent infection for

both the mother and the foetus. Although the microbes that inhabit the vagina are significant, little is known about how variations in their diversity and composition may affect the course of pregnancy. This is particularly true for women who have a high *Gardnerellavaginalis* prevalence.

The approximately 1011 microorganisms, mostly bacteria, that reside on and within each person make up the human microbiota as a whole. (1) The vaginal microbial community (VMC), which is made up of all the bacteria that live in the vagina, is unique to women in terms of both composition and function. The digestive tract in humans has the greatest diversity and quantity of microorganisms, whereas the VMC is different in composition and typically exhibits a significantly lower diversity of microorganisms. (2) The health of women in general and women of reproductive age in particular is greatly influenced by the VMC. Beginning soon after birth and continuing until menopause, the vaginal consortium's makeup goes through several different stages. (3) Ovarian steroid hormone cycle causes changes in the vaginal environment of women of reproductive age, with estrogen being associated with higher glycogen availability (4,5). Because estrogen levels rise during gestation, these effects are exacerbated during pregnancy, and it has been demonstrated that the VMC during pregnancy differs markedly from that of women of childbearing age who are not pregnant. (6) The VMC community works with the host during pregnancy to give the growing foetus a barrier of defence against any infections. The pH of the environment can be lowered by converting the rich energy source from the breakdown of free glycogen by α -amylase into lactic acid. (7-9) Almost all of the species that produce lactic acid are members of the *Lactobacillus* genus. Culturing, microscopy, and molecular biology were initially explained by Döderlein (10) and then further developed by Rogosa et al. (11)

Techniques have revealed that members of the *Lactobacillus* genus (12) dominate the VMC. *Lactobacillus* species prevent colonization by other taxa, especially possible pathogens, by keeping their pH acidic below 4.5. High-throughput sequencing and other contemporary molecular approaches

revealed a clear structure in the VMC that was centred on *Lactobacillus* species. Using 16 s rDNA sequencing and analysis, Ravel et al. identified four main community sequence types (CSTs), with *Lactobacillus crispatus* (CST I), *Lactobacillus gasseri* (CST II), *Lactobacillus iners* (CST III), and *Lactobacillus jensenii* (CST V) predominating. A fifth CST was characterized by a comparatively higher proportion of anaerobic organisms, such as the species *Gardnerella vaginalis* (CST IV), and a lower proportion of bacteria that produce lactic acid. (13).

The frequency of *Gardnerella vaginalis* has long been thought to be a dysbiotic CST that is frequently linked to bacterial vaginosis (BV) and increased health concerns. One prevalent type of dysbiosis that affects women in their reproductive years is bacterial vaginosis. Reduced *Lactobacillus* abundance in the VMC, which raises pH > 4.5 and causes a corresponding rise in diversity (14), is a characteristic of BV. Most frequently, BV is linked to a high concentration of *Gardnerella vaginalis* in CST IV, which is frequently accompanied by an increase in anaerobes, *Bacteroides*, and *Prevotella* as well as a variety of other possible pathogens, such as *Ureaplasma* and Gram-positive *Mobiluncus* and *Megasphaera*. (15–17)

A baby born before 37 weeks of pregnancy is referred to as a preterm birth. Preterm births account for 11.1% of live births worldwide and are a major contributor to infant mortality and morbidity (18). Preterm birth problems are directly responsible for around one million fatalities among children under the age of five (19). Preterm infants may experience respiratory issues, feeding issues, and developmental delays, and they frequently need specialized medical care in neonatal intensive care units. Our knowledge of the cause of preterm delivery is still incomplete, with the exception of the 20% of preterm deliveries that are medically induced. A number of characteristics, such as numerous pregnancies, age, smoking, racial origin, high or low maternal BMI, and others, make it challenging to determine risk, but infections seem to be responsible for 30–40% of spontaneous preterm births (19). As previously mentioned, the vaginal microbiota's defence against infection is strengthened during pregnancy as

hormonal shifts lead to *Lactobacilli*'s increased dominance (20). Along with its protective function, the VMC is probably also in charge of the newborn's first significant microbe colonization event, which happens during vaginal delivery; some of the initial components of the newborn's oral and intestinal microbiota are transferred through the birth canal (21,22). Contrary to the gut microbiota's strong diversity, it has long been believed that the ideal condition during pregnancy is one of low diversity and dominance by a single *Lactobacillus* species. However, it has recently been documented that the vaginal microbiota's structure changes and becomes more diverse in late-term pregnancy, which may help with this first colonization step (23).

In a mouse model, another study showed that the human VMC's composition had a discernible impact on the health and microbiota of the offspring (24). More focus has been placed on this community, its makeup during pregnancy, and its correlation with perinatal illnesses and premature birth because a number of VMC species are early colonizers of the neonatal microbiota at delivery. There is great interest in learning how changes in the composition of the VMC (25) are associated with the risk of adverse pregnancy outcomes, regardless of whether this is because of BV or another kind of disturbance to the normal vaginal microbiota. Certain organisms have been linked to an increased risk of preterm delivery, early amniotic membrane rupture prior to delivery and gestational diabetes.

Here, we delve deeply into how the vaginal microbiota, its diversity, and the frequency of various community types relate to the outcome of pregnancy.

Role of *Lactobacillus* in maintaining Vaginal Health

Because of their protective properties and dominance in the vaginal microbiome, *Lactobacillus* species are essential for maintaining vaginal health:

1. **Lactic Acid Production:** *Lactobacilli* produce lactic acid, which prevents the growth of harmful bacteria and fungi and keeps the vaginal pH acidic (between 3.8 and 4.5).

2. **Antimicrobial Compounds:** They generate bacteriocins and hydrogen peroxide (H_2O_2), which further inhibit pathogenic microorganisms and ward against illnesses including yeast infections and bacterial vaginosis (BV).
3. **Attachment to Vaginal Epithelium:** By vying for attachment sites, Lactobacilli prevent harmful microorganisms from colonizing the vaginal environment.
4. **Immunological Modulation:** By influencing the generation of cytokines, lowering inflammation, and encouraging a well-rounded immunological response, they control the vaginal immune system.
5. **Preserving Microbial Balance:** Lactobacillus contributes to the stability and health of the vaginal microbiota by outcompeting other bacteria for resources and space.
6. **Support During Pregnancy:** A microbiota dominated by Lactobacillus is linked to improved pregnancy outcomes, such as a lower risk of infections and preterm birth.

Factors influencing composition of Vaginal Microbiota during Pregnancy

1. **Hormonal Changes:** Increased levels of estrogen and progesterone during pregnancy promote the growth of Lactobacillus species. These bacteria maintain a low vaginal pH (around 3.5–4.5), creating an environment unfavourable for pathogenic microbes.
2. **pH Alteration:** The acidic environment during pregnancy supports Lactobacillus dominance while inhibiting anaerobic and pathogenic bacteria, such as Gardnerella vaginalis and Prevotella.
3. **Immune Modulation:** Pregnancy involves changes in the immune system to prevent fetal rejection. This can influence microbial balance by reducing inflammation and allowing beneficial microbes to thrive.
4. **Nutrient Availability:** Increased glycogen levels in vaginal epithelial cells, driven by oestrogen, provide a food source for Lactobacillus, fostering their growth and metabolic activity.

5. **Antimicrobial Peptides:** The production of antimicrobial peptides, such as defensins, helps regulate the microbial community by limiting overgrowth of harmful bacteria.
6. **Genetic Factors:** Individual genetic predisposition can affect immune responses, vaginal epithelial function, and microbial composition.
7. **Sexual Activity:** Exposure to semen and other external factors during sexual activity can introduce new microbes, potentially influencing the vaginal microbiome.
8. **Hygiene Practices:** Use of vaginal douches or other hygiene products can disrupt the microbial balance by altering pH or removing beneficial microbes.
9. **Antibiotic Use:** Antibiotics prescribed during pregnancy can unintentionally reduce beneficial microbes, leading to dysbiosis.
10. **Health Conditions:** Conditions like gestational diabetes or bacterial vaginosis can significantly impact the composition and stability of the vaginal microbiota.

Pregnancy outcomes influenced by Vaginal Microbiota

1. **Preterm Birth:** - PTB is a leading cause of neonatal morbidity and mortality worldwide. While there are many factors that contribute to preterm birth, an emerging area of research has focused on the role of vaginal microbiota. The undermentioned mechanisms influence the dysbiosis phenomenon during pregnancy influencing the risk of preterm birth.

Mechanisms involved:

1. **Inflammation and Vaginal Microbiota:** Dysbiosis of the vaginal microbiota, such as reduced *Lactobacillus* dominance and increased anaerobic bacteria (*Gardnerella vaginalis*, *Prevotella*), triggers inflammation. These microbes produce metabolites and stimulate the release of pro-inflammatory cytokines (e.g., IL-6, TNF- α), leading to uterine contractions and preterm labour.
2. **Infection Ascension:** Pathogens from the vagina, facilitated

by a disrupted microbiota, ascend into the uterus and infect the amniotic fluid or placenta. This intrauterine infection activates inflammatory pathways, increasing the risk of fatal injury and preterm delivery.

3. **Cervical Remodelling:** Altered microbiota induces the production of matrix metalloproteinases (MMPs) through inflammation, which degrade cervical collagen. This premature cervical softening and dilation contribute to preterm labour.

4. **Fetal Membrane Weakening:** Bacterial byproducts and inflammation weaken the foetal membranes by degrading extracellular matrix proteins. Increased oxidative stress from dysbiosis further compromises membrane integrity, leading to preterm rupture of membranes (PROM).

5. **Integrated Risk:** The interplay between microbiota imbalance, immune activation, and tissue damage creates a cascade that culminates in preterm birth. Addressing vaginal dysbiosis may reduce these risks.

2. Gestational Diabetes: - It is a condition characterised by elevated blood sugar levels that develop during pregnancy in women who did not previously have diabetes, also influenced by the variation in composition of vaginal microbiota. It typically occurs in the second or third trimester and results from hormonal changes that impair the body's ability to effectively use insulin.

Mechanisms involved: -

1. **Altered Microbial Composition:** Pregnancy-induced changes in gut and vaginal microbiota, such as reduced diversity and increased pathogenic bacteria, disrupt glucose metabolism. Dysbiosis can impair gut barrier integrity, allowing microbial endotoxins (e.g., lipopolysaccharides, LPS) to enter the bloodstream and trigger systemic inflammation, promoting insulin resistance.

2. **Inflammation:** Dysbiosis-induced inflammation activates immune pathways, releasing cytokines like TNF- α , IL-6, and CRP. These cytokines interfere with insulin signalling in skeletal muscle, liver, and adipose tissues, exacerbating

glucose intolerance and insulin resistance.

3. **Insulin Resistance:** Elevated pregnancy hormones (e.g., human placental lactogen) already increase insulin resistance to ensure fetal glucose supply. Inflammation and altered microbial metabolites further impair insulin sensitivity, leading to hyperglycaemia.

4. **Metabolic Changes:** Changes in short-chain fatty acids (SCFAs) produced by gut microbes affect energy balance and insulin secretion. Dysbiosis reduces beneficial SCFAs, worsening insulin dysregulation and contributing to gestational diabetes.

5. **Integrated Risk:** The combined effects of microbial imbalance, inflammation, and metabolic disruption create a vicious cycle, increasing susceptibility to gestational diabetes. Addressing these factors can help mitigate risks.

3. Miscarriage: - The vaginal microbiota plays a significant role in pregnancy outcomes, including the risk of miscarriage; the spontaneous loss before 20 weeks of gestation. Several mechanisms influence this risk of miscarriage which is discussed under forth.

Mechanisms involved: -

1. **Inflammation and Immune Dysregulation:** - Dysbiosis reduces protective *Lactobacillus* dominance and promotes the overgrowth of pathogenic bacteria (e.g., *Gardnerella vaginalis*, *Prevotella* species). These pathogens trigger the release of pro-inflammatory cytokines (e.g., IL-6, TNF- α) and chemokines, leading to local inflammation in the uterus. Disruption of maternal-fetal tolerance, causing rejection of the embryo or fetus.

2. **Infection and Ascension of Pathogens:** - Pathogens from the vagina can ascend into the uterus, causing: a) Chorioamnionitis: Infection of the fetal membranes; b) Endometritis: Uterine lining infection.

These infections damage the uterine environment and trigger miscarriage through premature rupture of membranes or fetal compromise.

3. **Cervical Remodelling and Weakening:** - Vaginal dysbiosis increases the production of matrix metalloproteinases (MMPs), which degrade collagen in the cervix. Premature cervical softening or dilation leads to cervical insufficiency, increasing the risk of miscarriage.

4. **Hormonal Disruption:** - Dysbiosis alters vaginal pH and produces harmful metabolites, disrupting hormonal signalling critical for pregnancy maintenance, such as progesterone.

5. **Oxidative Stress:** - Pathogens from dysbiosis produce reactive oxygen species (ROS), causing oxidative stress in the uterine environment. This damages the placenta and fetal membranes, leading to pregnancy loss.

The disruption of vaginal microbiota influences miscarriage through a cascade of infection, inflammation, immune activation and tissue damage.

4. Pre-eclampsia: - It is a hypertensive disorder that occurs during pregnancy, typically after 20 weeks of gestation, characterised by high blood pressure and signs of damage to organs such as the kidneys and liver. This is also a result of the altered vaginal microbiota composition being influenced by various mechanisms.

Mechanisms involved: -

1. **Systemic Inflammation:** Dysbiosis, particularly the reduction of *Lactobacillus* species and overgrowth of pathogenic bacteria (e.g., *Gardnerella vaginalis*, *Prevotella*), triggers systemic inflammation. This results in the release of pro-inflammatory cytokines like IL-6, TNF- α , and CRP, which impair endothelial function and increase vascular permeability, key components in the pathogenesis of eclampsia.

2. **Endothelial Dysfunction:** Altered vaginal microbiota can contribute to endothelial dysfunction by stimulating the production of anti-angiogenic factors (e.g., soluble FM's-like tyrosine kinase-1 or sFlt-1). This disrupts normal placental development and blood vessel formation, causing poor placental perfusion and leading to the hypertension seen in

pre-eclampsia and eclampsia.

3. **Oxidative Stress:** Dysbiosis increases the production of reactive oxygen species (ROS) from pathogenic bacteria, which causes oxidative stress in the maternal circulation. Oxidative stress is a key mediator in vascular damage, endothelial dysfunction, and the development of hypertension, contributing to the onset of eclampsia.

4. **Immune Activation and Pregnancy Complications:** An imbalanced vaginal microbiota affects immune regulation, leading to an exaggerated immune response during pregnancy. This dysregulated immune response can result in heightened inflammation, placental damage, and increased risk of pregnancy complications like eclampsia.

5. **Altered Hormonal Signalling:** Vaginal dysbiosis affects the local immune environment and can disrupt the balance of hormones such as progesterone and estrogen, which are critical for maintaining vascular health.

Hormonal imbalances may exacerbate blood pressure dysregulation, contributing to the development of severe complications such as eclampsia. These mechanisms show how vaginal dysbiosis can increase the risk of eclampsia through inflammation, immune dysfunction, oxidative stress, endothelial damage, and hormonal disruption.

Analysing The Vaginal Dysbiosis During Pregnancy

The phenomenon of vaginal dysbiosis can be analysed mainly by carrying out Metagenomics study: -

Metagenomics in the context of analysing vaginal microbiota, refers to the study of the collective genetic material of all microorganism present in the vaginal environment. This approach provides a comprehensive understanding of the composition, diversity and functional potential of the vaginal microbial community without the need for culturing individual species.

Mechanism involved

The metagenomics process for analysing vaginal microbiota during pregnancy involves several systematic steps. Here's

an overview:

1. Sample Collection; Purpose: Obtain microbiota samples from the vaginal environment.

Method: Sterile swabs are used to collect vaginal secretions.

Samples are stored in appropriate media to preserve microbial DNA.

2. DNA Extraction; Purpose: Isolate microbial DNA from the collected samples.

Steps: Lysis of cells to release DNA.

Removal of proteins, lipids, and other contaminants.

Purification of DNA for further analysis.

3. Library Preparation; Purpose: Prepare DNA for sequencing.

Steps: Fragmentation of DNA into manageable sizes.

Addition of adapters or barcodes to each DNA fragment.

Amplification using PCR to ensure sufficient DNA quantities.

4. Sequencing; Purpose: Determine the genetic sequences of the DNA.

Technologies: 16S rRNA Sequencing: Targets bacterial ribosomal RNA genes to identify bacterial species.

Whole Genome Sequencing (WGS): Analyses the entire genetic content of all organisms present.

Platforms: Illumina, Oxford Nanopore, PacBio, etc.

5. Bioinformatics Analysis; Purpose: Analyse the sequencing data to identify microbial composition.

Steps: Quality control to filter out low-quality reads.

Alignment of sequences against reference databases (e.g., SILVA, Green genes).

Taxonomic classification and identification of microbial species.

Functional analysis to determine microbial roles.

6. Data Interpretation; Purpose: Relate microbial profiles to pregnancy health outcomes.

Aspects: Identification of beneficial and pathogenic microbes.

Correlation with gestational age, infections, or pregnancy complications.

7. Reporting; Purpose: Summarize findings for clinical or research purposes.

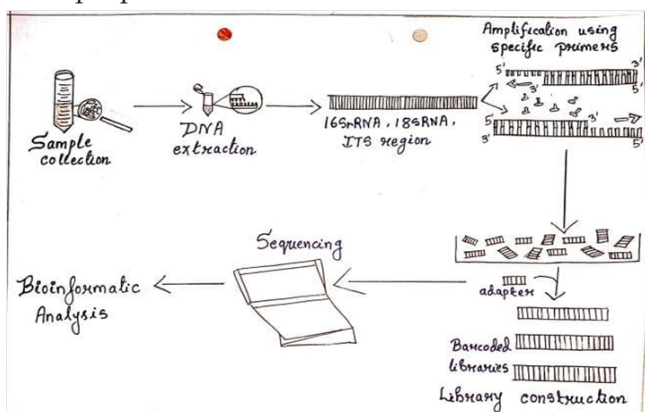


Fig 2 - The basic metagenomic process for analysing vaginal microbiota is carried out in the above outlined process

Application of Metagenomics on Vaginal Health during Pregnancy

1. Monitoring Vaginal Microbial Dynamics Role of Lactobacillus:

During pregnancy, a healthy vaginal microbiota is often dominated by Lactobacillus species, which maintain a low vaginal pH by producing lactic acid. Metagenomics can monitor the abundance of these beneficial bacteria.

Detecting Dysbiosis: Metagenomic sequencing can identify imbalances (dysbiosis) in the vaginal microbiota, such as overgrowth of pathogenic bacteria linked to bacterial vaginosis (BV) or yeast infections. These conditions may increase the risk of preterm birth or other complications.

2. Early Detection of Infection Risks

Preventing Preterm Birth: Dysbiosis has been associated with an increased risk of preterm labour. Metagenomics can identify specific microbial patterns or biomarkers linked to infection or inflammation, allowing for timely interventions.

Pathogen Identification: Metagenomics can detect and characterize pathogens such as *Gardnerella vaginalis* or *Candida* species, even if they are non-culturable, ensuring accurate diagnosis and treatment.

3. Personalized Probiotic and Prebiotic Strategies

Probiotic Development: By understanding the composition of a healthy vaginal microbiota, metagenomics can guide the development of targeted probiotics to restore or maintain a beneficial microbial balance during pregnancy.

Prebiotic Interventions: Insights from metagenomics can help identify dietary or supplemental strategies to promote the growth of beneficial bacteria like *Lactobacillus*.

4. Tailored Antimicrobial Treatments

Reducing Antibiotic Misuse: Metagenomics provides a detailed understanding of the microbial community, reducing the unnecessary use of broad-spectrum antibiotics, which can disrupt the vaginal microbiota and harm beneficial bacteria.

Specific Pathogen Targeting: Enables precise treatment of specific infections while preserving overall microbial diversity.

5. Supporting Maternal and Neonatal Outcomes

Foetal Development: A healthy vaginal microbiota during pregnancy reduces the risk of infections ascending into the uterus, protecting foetal development.

Birth Canal Microbiota: During vaginal delivery, the newborn is exposed to the mother's vaginal microbiota, which shapes their initial microbiome. Maintaining a healthy vaginal microbiota ensures optimal microbial seeding.

6. Research on Pregnancy-Associated Conditions

Preeclampsia and Inflammation: Metagenomics can explore potential links between vaginal microbiota and systemic conditions like preeclampsia, enabling new diagnostic and therapeutic approaches.

Gestational Diabetes: Emerging evidence suggests that vaginal and gut microbiota interact; metagenomics can uncover connections and offer insights into metabolic health during pregnancy.

By providing a detailed understanding of vaginal microbial ecosystems, metagenomics can revolutionize the management of vaginal health during pregnancy, ensuring better outcomes for both the mother and baby.

Therapeutic Interventions for maintaining Vaginal Health during Pregnancy

Maintaining optimal vaginal health during pregnancy is essential for reducing the risk of complications such as preterm birth, infections, and adverse neonatal outcomes. Therapeutic interventions focus on restoring and preserving a healthy vaginal microbiota dominated by *Lactobacillus* species. Here are key therapeutic approaches:

1. Probiotics

Purpose: Replenish beneficial *Lactobacillus* species that maintain a low vaginal pH and inhibit pathogenic microorganisms.

Examples: *Lactobacillus crispatus*, *Lactobacillus rhamnosus*, *Lactobacillus reuteri*

Delivery Methods:

Oral probiotics: Provide systemic support and gut-to-vagina microbial transfer.

Vaginal suppositories: Directly introduce probiotics to the vaginal environment.

Evidence: Probiotics have shown promise in reducing the recurrence of bacterial vaginosis (BV) and improving vaginal

microbial balance during pregnancy.

2. Prebiotics

Purpose: Stimulate the growth of beneficial bacteria by providing nutrients (e.g., inulin, fructooligosaccharides).

Mechanism: Prebiotics create a favourable environment for *Lactobacillus* species while inhibiting harmful pathogens.

Use in Combination: Often paired with probiotics for enhanced effectiveness (sybiotic therapy).

3. Antibiotic Therapy

Targeted Use: For treating bacterial vaginosis (BV) or sexually transmitted infections (STIs) like chlamydia and gonorrhoea.

Common antibiotics include metronidazole and clindamycin.

Precautions: Must be prescribed carefully during pregnancy to avoid disrupting the vaginal microbiota and causing antibiotic resistance. Probiotic co-administration is often recommended to restore microbiota post-treatment.

5. Antifungal Therapy

Purpose: Treat vaginal yeast infections (e.g., caused by *Candida albicans*).

Medications: Topical antifungals (e.g., clotrimazole or miconazole) are preferred during pregnancy.

Oral antifungals are usually avoided due to potential risks to the fetus.

Complementary Strategies: Probiotic use can help prevent recurrence.

5. Hormonal Regulation

Role of Oestrogen: Oestrogen levels during pregnancy promote the growth of *Lactobacillus* by increasing glycogen production in vaginal epithelial cells.

Hormonal therapies are generally avoided during pregnancy but may play a role postpartum.

6. Dietary and Lifestyle Modifications

Healthy Diet: Include fermented foods (e.g., yogurt, kefir) that naturally contain probiotics. High-fibre foods support overall gut and vaginal health.

Hygiene Practices: Avoid douching or using harsh chemicals that can disrupt the vaginal microbiota. Wear breathable, cotton-based undergarments.

Stress Reduction: Chronic stress can alter the immune response and microbiota balance.

7. Vaginal pH Modulation

Purpose: Maintain an acidic vaginal environment to deter pathogen growth.

Methods: Lactic acid gels or suppositories. Regular monitoring of pH during prenatal care.

8. Immunotherapy and Microbiota Transplantation (Emerging Therapies)

Vaginal Microbiota Transplantation (VMT): Involves transferring microbiota from a healthy donor to restore a balanced vaginal ecosystem. Still experimental but promising for women with recurrent dysbiosis.

Immune-Modulating Therapies: Focus on enhancing maternal immunity to support a healthy microbiota.

9. Regular Prenatal Care

Frequent monitoring; of vaginal health during prenatal visits ensures early detection and management of imbalances or infections.

Therapeutic interventions should always be tailored to individual needs, and all treatments must be prescribed under medical supervision to ensure safety for both the mother and foetus.

Conclusion

In conclusion, maintaining vaginal health during pregnancy is essential for ensuring maternal and foetal well-being,

as the vaginal microbiota plays a pivotal role in protecting against infections and maintaining reproductive health. The intricate interaction between host factors, such as hormonal changes, and microbial communities, particularly *Lactobacillus* species, highlights the importance of a balanced vaginal environment. Disruptions to this balance can lead to infections and complications, including preterm birth. The metagenomic study can be carried out on a proficient level for understanding the causal relationship of host-microbe interaction in the vaginal microbiota and implementing its analysed data for therapeutic development and decreasing the risk of vaginal dysbiosis to occur. By adopting healthy practices, such as proper hygiene, a balanced diet rich in probiotics, and regular prenatal care, women can support the stability of their vaginal microbiota. Understanding the symbiotic relationship between the host and microbial communities emphasizes the need for proactive measures to preserve vaginal health and promote a safe pregnancy outcome.

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