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# Improving Pregnancy Tactics at Risk of Premature Birth

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**Abstract:** There is no clear understanding of which microbes are normal for the human microbiome [1]. The Human Microbiome Project (IMP) has done a lot of research to define the concept of a microbiome that is considered normal for humans, and the concept of "Normal Microbiome" is every concluded that it is individual for one organism [2]. Sub-Saharan Africa faces serious challenges in maternal and infant health. In 2017, 66% of all maternal deaths worldwide occurred in sub-Saharan Africa [33], and in 2020 there were 50 infant deaths per 1,000 live births [34]. Many of these adverse birth outcomes are caused by preventable or treatable infectious diseases. HIV accounts for 24–50% of pregnancy-related deaths in high-prevalence areas and is the leading cause of death among cisgender women of reproductive age [3, 4]. The risk of HIV infection increases during pregnancy and the postpartum period, which increases the risk of vertical transmission [5]. Pregnancy is a normal physiological state that affects the composition of the vaginal microbiome. During pregnancy, there is a gradual increase in lactobacillus species (including L. iners) and a decrease in microbial diversity, followed by a rapid increase in the diversity and anaerobic species in the postpartum period [6, 7, 8, 9, 10,11]. This is mediated by estrogen, which promotes the accumulation of glycogen in the vaginal epithelium and supports the growth of lactobacilli [11, 12]. Given the relationship between Lactobacillus abundance and an optimal microbiome, studies have shown that pregnancy induces favorable changes in the microbiome to prevent maternal genital infections and adverse birth outcomes [7]. In contrast, there is a rapid increase in bacterial diversity during the postpartum period [10, 11]. Premature birth is more than 10% worldwide. There are significant disparities in the frequency of preterm birth between countries' populations. Worldwide, approximately 15 million pregnancies occur at less than 37 weeks of gestation each year [13]. Preterm birth (PB) remains the second most common cause of neonatal death worldwide and the most common cause of infant mortality in middle- and high-income countries [14]. The consequences of PB persist from early childhood through adolescence and adulthood [15,16].

**Keywords:** The Human Microbiome Project (IMP), HIV-human immunodeficiency virus, NM-Normal Microbiome, Preterm birth (PB).

**Introduction.** Preterm birth is a leading cause of neonatal morbidity and mortality worldwide [80]. Recently, the vaginal microbiome has been considered as one of the causes of preterm birth, linking the pathological changes of VF with the risk of spontaneous preterm birth. Preterm birth (< 37 completed weeks of gestation) accounts for more than 10% of births worldwide [17]. It is one of the leading causes of neonatal mortality and morbidity [18]. Many factors can trigger preterm labor, including premature rupture of membranes (PEM), infections (eg, Trichomonas

vaginalis and Chlamydia trachomatis), and the introduction of microbes into the amniotic cavity. [19]. The vaginal microbiome protects against such infections. A low-diversity microbiome is dominated by Lactobacillus species, which are considered "healthy". In contrast, a diverse microbiome with low numbers of Lactobacilli and high numbers of anaerobic bacteria may result in a dysbiosis that overlaps with the clinical diagnosis of bacterial vaginosis (BV) [20,21]. BV is often asymptomatic, but is associated with genital infections and complications, including human papillomavirus (HPV) infections [22,23] and pelvic inflammatory disease. Furthermore, it has been suggested that different Lactobacillus species may present different risk factors for different diseases [24,27]. Because vaginal dysbiosis affects millions of women, it is important to understand the role of the vaginal microbiome in preterm birth [25,28]. Currently, there are few studies evaluating the relationship between the vaginal microbiome and preterm birth, with conflicting findings as to whether the vaginal microbiome may influence the risk of preterm birth [26,29].

**The purpose of the study.** The main goal of this study is to determine the possibility of improving pregnancy and childbirth outcomes by reducing the incidence of vaginal and cervical dysbiosis as one of the factors that increase the risk of preterm birth by conducting a retrospective analysis of 90 women.

**Research tasks:** Study of the cervix and vaginal microbiome in the risk group of fertile age.

1. Studying the microbiome of the cervix and vagina in women against the background of the risk of premature birth.
2. Improvement of treatment for the risk of premature birth.
3. Development of a predgavidar preparation plan

**Research object**. 60 women at risk of premature birth and 30 women of childbearing age.

1. General clinical and laboratory tests.
2. instrumental investigations: CTG, UTT Dopplerography.
3. Bacteriological smear from cervix and vagina.
4. Analysis of smear results obtained from 3 points (cervix, urethra, vagina).

**Result of study:** The pH test results showed a higher mean pH value for the preterm group (5.6) compared to the full-term group (4.4), with a highly significant p-value of less than 0.001. A general assessment of vaginal microbiota based on the Nugent Score indicating normal, intermediate or bacterial vaginosis showed significant differences between the two groups ($p = 0.001$). In the preterm group, 39.3% had a normal microbiota compared to 64.2% in the full-term group, indicating a higher prevalence of normal microbiota in full-term births. Intermediate microbiota was found in 31.5% of the preterm group and 23.6% of the full-term group. Notably, the preterm group (29.2%) had a higher rate of bacterial vaginosis than the full-term group (12.3%), suggesting that bacterial vaginosis is more common among preterm women. shows. In the study of specific microbiota species, the coccal microbiota was more prevalent in the preterm group (19.1%) compared to the full-term group (8.5%), with a p-value of 0.029, indicating that preterm indicates a possible connection with ilish. Staphoid vaginitis was also more common in the preterm group (13.5% vs. 6.6%); however, the difference was not statistically significant ($p = 0.106$). Fungal infection, as indicated by the presence of fungi, was significantly more frequent in the MOTX group (23.6% vs. 9.4%, $p = 0.007$). The combination of bacterial vaginosis and fungi was also more frequent in the preterm group (10.1% vs. 3.8%), although this result was not significant ($p = 0.077$). The presence of Candida spp. The PB group (24.7%) was significantly higher than the full-term group (9.4%), with a p-value of 0.004. Similarly, the prevalence of Gardnerella vaginalis was significantly higher in the preterm group (25.8%) compared to the full-term group (12.3%), with a p-value of 0.015. Significant reduction of Lactobacillus spp. was noted among the preterm group (73.0%) compared to the full-term group (87.7%), p-value 0.009.

Mycoplasma hominis was also significantly more common in the preterm group (16.9%) compared to the full-term group (5.7%), with a p-value of 0.012. Ureaplasma urealyticum was found more frequently in the preterm group (14.6%) than in the full-term group (3.8%), with a significant p-value of 0.007. Less significant flora, including Actinomyces spp., Bacillus spp., Corynebacterium spp., Enterococcus spp., Escherichia coli, Haemophilus influenzae, Klebsiella spp., Peptostreptococcus anaerobius, Staphylococcuscuscus spp, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus mitis and Streptococcus salivarius did not show a strong association with preterm or full-term birth. A significant negative correlation was found between the period of pregnancy and the number of white blood cells (leukocytes) (rho = -0.307 *), which indicates an early birth with a decrease in the period of pregnancy, indicating an increase in the number of leukocytes. Vaginal pH showed a strong negative correlation with gestational age (rho = -0.452*), indicating that lower gestational age was associated with higher vaginal pH. Lactobacillus spp. had a positive correlation with gestational age (rho = 0.406*) and a strong negative correlation with vaginal pH (rho = -0.559*). Candida spp. showed a positive correlation with vaginal pH (rho = 0.308 *), which means that yeast infections are associated with high pH levels, which can lead to negative pregnancy outcomes. In addition, there was a negative correlation between Candida spp. and Lactobacillus spp. (rho = -0.256 *), which emphasizes the competitive relationship between microorganisms. Mycoplasma hominis showed a negative correlation with gestational age (rho = -0.217*) and Lactobacillus spp. (rho = -0.312 *) and positive correlations with vaginal pH (rho = 0.357 *) and Ureaplasma urealyticum (rho = 0.504 *), indicating that it is associated with conditions that lead to premature birth. Ureaplasma urealyticum is negatively correlated with gestational age (rho = -0.259*) and Lactobacillus spp. (rho = -0.359 *) and positive with vaginal pH (rho = 0.418 *), which indicates its role in the microbial imbalance associated with premature birth. The Nugent score used to diagnose bacterial vaginosis showed the strongest negative correlation with gestational age (rho = -0.551*), suggesting that a higher score (and therefore more severe bacterial vaginosis) was strongly associated with preterm birth**.**

**Conclusion.** Taken together, the results suggest that differences in the microbiota of women with PB, such as microbiota richness and diversity and a greater prevalence of other bacteria, may play a role in PB. Other differences between cohorts may have been masked by the presence of highly dominant bacteria such as Lactobacillus. At a general level, we did not identify a specific vaginal microbial community structure that predicted spontaneous PB at 11–16 weeks' gestation. Also, differences in relative abundance of bacterial species between term and preterm groups were significant only for a few less abundant species. Although causal relationships remain to be elucidated, our results confirm previous reports of associations between the microbiome and preterm birth and further suggest that different bacterial communities may contribute to the role of the microbiome in spontaneous PB. Alternatively, the richer and more diverse microbiota of the preterm group may reflect physiological differences between the groups affecting bacterial selection. This study provides valuable evidence of subtle changes in the microbiome associated with preterm birth, which warrants further study using sequencing methodology. Furthermore, future research should include assessment of microbial metabolite production and specific response to further elucidate factors leading to spontaneous PB and identify women at risk early in pregnancy. Vaginal microbiota composition is associated with spontaneous preterm birth (sPB) by ethnicity. Host-microbiota interactions play an important role in the association between ethnicity, vaginal microbiota and sPB plays We aimed to further elucidate the relationship between vaginal microbiota, specific microbiota interactions, and sPB. We studied populations with different risk stratifications for sPB to explore the role of population characteristics and to explore the uncharted territory by examining the association between vaginal microbiota and local immunoglobulins (Igs). We found a correlation between microbial IgA and IgG coverage and microbiota composition, with Lactobacillus dominant microbiota having higher microbial immunoglobulin coverage. However, we found no evidence that

immunoglobulin coverage is associated with preterm birth. Also, in a systematic review and meta-analysis, we found that asymptomatic vaginal colonization was not associated with sPB.

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