Pecheriaha Svitlana, Candidate of Medical Sciences, assistant Department of Obstetrics, Gynecology and Perinatology, Bukovinian State Medical University, Chernivtsi, Ukraine, https://orcid.org/0000-0003-3884-9109

Balan Anastasiia, student of higher medical education, Bukovinian State Medical University, Chernivtsi, Ukraine

THE MICROBIOME IN THE DEVELOPMENT OF PRETERM BIRTH: MODERN DIAGNOSTIC AND THERAPEUTIC PERSPECTIVES

Abstract

Preterm birth (PTB) remains one of the most pressing problems in modern obstetrics and neonatology, being a leading cause of perinatal morbidity, neonatal mortality, and long-term neurological and metabolic complications in children. Despite significant advances in perinatal medicine, the incidence of PTB in most countries worldwide has not shown a substantial decline, highlighting the need to identify new pathogenetic mechanisms underlying its development. In recent years, increasing attention has been focused on the role of the microbiome in maintaining physiological pregnancy and in the development of obstetric complications.

This review summarizes current scientific data regarding the role of the vaginal, gut, oral, and intra-amniotic microbiome in the pathogenesis of preterm birth. The characteristics of the normal vaginal microbiome during pregnancy, the significance of Lactobacillus spp. dominance, as well as the role of vaginal dysbiosis, anaerobic flora, and microbe-induced inflammation in the premature activation of labor are discussed. Particular attention is paid to the molecular mechanisms involving Toll-like receptor activation, NF-κB signaling pathways, and the production of proinflammatory cytokines, prostaglandins, and matrix

metalloproteinases involved in cervical remodeling, premature rupture of membranes, and stimulation of myometrial contractility.

Current approaches to microbiome diagnostics, including 16S rRNA sequencing, shotgun metagenomics, and metabolomic analysis, are analyzed as promising tools for developing personalized models for PTB risk prediction. Modern strategies for the correction of microbiome disturbances during pregnancy are also reviewed, including the use of probiotics, dietary modification, targeted antimicrobial therapy, and experimental vaginal microbiome transplantation. The перспективність integration of microbiome analysis into prenatal monitoring systems and the need for further large-scale studies to implement personalized preventive strategies into clinical practice are emphasized.

Keywords: preterm birth, microbiome, vaginal dysbiosis, pregnancy, Lactobacillus spp., bacterial vaginosis, probiotics.

Problem Statement. Preterm birth remains one of the leading causes of perinatal morbidity and mortality worldwide. According to the World Health Organization, approximately 15 million preterm infants are born annually, and the rate of preterm birth in most countries ranges from 8% to 12% of all deliveries [1, 2]. Prematurity is associated with a high risk of neonatal mortality, respiratory disorders, central nervous system injury, metabolic disturbances, and long-term disability in children [3]. Despite significant advances in modern obstetrics, the effectiveness of preterm birth prevention remains insufficient, and its incidence has not demonstrated a stable downward trend.

The etiology of preterm birth is multifactorial and includes infectious and inflammatory processes, placentation disorders, cervical insufficiency, multiple pregnancy, as well as genetic and socio-economic factors. However, in a substantial proportion of women, the exact pathogenetic mechanisms underlying spontaneous preterm labor remain unclear [4]. Over the past decade, increasing

attention has been focused on the role of the reproductive tract, gut, and oral microbiome in the development of local and systemic inflammatory responses capable of prematurely activating labor mechanisms. The development of next-generation sequencing (NGS) technologies has enabled detailed characterization of microbial communities and identification of associations between vaginal dysbiosis, reduced dominance of *Lactobacillus spp.*, and an increased risk of preterm birth [5]. Therefore, summarizing current evidence regarding the role of the microbiome in the pathogenesis of preterm birth and evaluating the prospects for novel approaches to prediction, prevention, and therapeutic correction of microbiome disturbances remain highly relevant.

Analysis of recent research and publications. Current studies confirm that the vaginal microbiome plays an essential role in maintaining normal pregnancy. Healthy pregnant women are typically characterized by the dominance of *Lactobacillus spp.*, particularly *L. crispatus*, which maintain a low vaginal pH, produce lactic acid, and inhibit the growth of anaerobic pathogens. Reduced lactobacilli dominance and the formation of CST IV-type vaginal microbiota have been associated with an increased risk of spontaneous preterm birth [6, 7]. Particular attention has been paid to *Gardnerella vaginalis, Sneathia spp., Prevotella spp., Ureaplasma spp.*, and *Mycoplasma hominis*, which are capable of inducing local inflammation and activating Toll-like receptors.

The role of microbe-induced inflammation in the premature activation of labor is widely discussed in the current literature. Activation of NF-κB signaling pathways is accompanied by increased production of IL-1β, IL-6, TNF-α, prostaglandins, and matrix metalloproteinases, contributing to cervical ripening, myometrial contractility, and premature rupture of membranes [14]. Recent studies have also demonstrated the importance of the gut and oral microbiome in the development of systemic inflammatory responses and the possible hematogenous translocation of bacteria to the feto-placental complex [19].

A promising area of current research is the implementation of microbiome technologies into clinical practice. Metagenomic sequencing, shotgun metagenomics, and metabolomic analysis make it possible to identify a "microbiome signature" associated with the risk of preterm birth already during the first and second trimesters of pregnancy [10]. At the same time, considerable attention is being paid to personalized approaches for correcting dysbiosis, including the use of probiotics, dietary modification, targeted antimicrobial therapy, and vaginal microbiome transplantation. However, the results of clinical studies remain heterogeneous, highlighting the need for further large-scale randomized trials.

Purpose of the article. The aim of this study was to summarize current scientific data regarding the role of the microbiome in the pathogenesis of preterm birth, analyze the mechanisms of microbe-induced inflammation, and evaluate promising approaches to early diagnosis, prevention, and therapeutic correction of microbiome disturbances during pregnancy.

Presentation of the main material of the study. During pregnancy, the vaginal microbiome undergoes further stabilization characterized by an increased relative abundance of *L. crispatus* and *L. iners* and reduced microbial diversity, which is considered a protective maternal adaptation [5,7]. Lactobacilli play a key protective role by producing lactic acid, thereby maintaining the vaginal pH at 3.8–4.5, as well as synthesizing bacteriocins and hydrogen peroxide that inhibit the growth of opportunistic microorganisms [8,9].

Importantly, not all lactobacilli exhibit the same protective potential. According to the study by Fettweis J.M. et al. (2019), dominance of *Lactobacillus crispatus* is associated with the lowest risk of preterm birth, whereas predominance of *L. iners* or the formation of CST IV (characterized by reduced lactobacilli content and dominance of anaerobic flora) is associated with an increased risk of spontaneous preterm birth. *L. iners* is considered an unstable

transitional species capable of coexisting with opportunistic anaerobes and contributing to the development of vaginal dysbiosis [5].

The association between vaginal microbiome dysbiosis and preterm birth is supported by extensive epidemiological evidence. Bacterial vaginosis (BV), the most common manifestation of vaginal dysbiosis, is considered one of the most significant independent risk factors for preterm birth. A meta-analysis by Leitich et al., which included more than 20,000 pregnant women, demonstrated that BV approximately doubles the risk of preterm birth [10].

However, conventional clinical diagnostic methods for BV (Amsel criteria and Nugent scoring system) are unable to fully identify microbiome variations associated with an increased risk of preterm birth. Studies using next-generation sequencing (NGS) have shown that some women without clinical signs of BV exhibit subclinical dysbiosis characterized by increased levels of *Gardnerella vaginalis, Prevotella bivia, Sneathia amnionii*, and other anaerobes, which is associated with a similarly elevated risk of preterm birth [11].

An important finding was the identification of a direct correlation between the composition of the cervicovaginal microbiome in early pregnancy and subsequent obstetric outcomes. In the prospective study by Kindinger et al. (2017), women with *L. crispatus* dominance during the first trimester had a significantly lower risk of preterm birth compared with women with an *L. iners*-dominant microbiome or polymicrobial communities ($p<0.001$) [12].

Disruption of the vaginal microbiome and ascending microbial invasion are considered among the key mechanisms underlying spontaneous preterm birth. Vaginal dysbiosis is characterized by a reduction in protective lactobacilli, particularly *Lactobacillus crispatus*, accompanied by excessive colonization by anaerobic microorganisms (*Gardnerella vaginalis, Ureaplasma spp., Mycoplasma hominis, Prevotella spp., Sneathia spp.*). Microorganisms and their structural components are capable of penetrating through the cervical canal into the decidual

tissue, fetal membranes, and amniotic fluid, thereby activating a local immune response. Toll-like receptors (TLRs) of innate immune cells play a crucial role in this process by recognizing pathogen-associated molecular patterns (PAMPs). In particular, lipopolysaccharide from Gram-negative bacteria activates TLR4, bacterial peptidoglycan activates TLR2, and bacterial DNA activates TLR9. Activation of TLRs initiates an intracellular signaling cascade via the adaptor protein MyD88, followed by activation of the transcription factor NF-κB, which regulates the synthesis of proinflammatory mediators [13].

Activation of NF-κB results in increased production of proinflammatory cytokines (IL-1β, IL-6, TNF-α), chemokines, prostaglandins, and matrix metalloproteinases, forming the so-called “inflammatory cascade of labor.” Prostaglandins stimulate myometrial contractility, whereas metalloproteinases promote degradation of cervical and fetal membrane collagen, accelerating cervical ripening and premature rupture of membranes. Simultaneously, infiltration of neutrophils and macrophages into the decidual tissue and chorioamnion contributes to the maintenance of chronic inflammation. Thus, microbe-induced inflammation represents a central pathogenetic mechanism of preterm birth, integrating immune, biochemical, and tissue processes that prematurely activate the physiological program of labor. This process is characterized by multifactorial interactions among microbial, immune, and genetically determined factors [14].

Although amniotic fluid was long considered sterile, the application of molecular genetic techniques, particularly next-generation sequencing (NGS), has enabled the detection of microbial sequences in the amniotic fluid of some women with preterm birth. The presence of intra-amniotic microorganisms is associated with activation of the intrauterine inflammatory response, chorioamnionitis, and adverse neonatal outcomes even in the absence of classical clinical signs of infection [15].

The primary mechanism of intra-amniotic infection is believed to be the ascending spread of microorganisms from the lower genital tract through the cervical canal. However, hematogenous dissemination of bacteria from distant sites, including the oral cavity and gastrointestinal tract, has also been described. Evidence supporting this pathway includes the detection of microorganisms such as *Fusobacterium nucleatum* and *Streptococcus mutans* in amniotic fluid and placental tissues, both of which are traditionally associated with the oral microbiota [16].

Recent evidence suggests the existence of a complex interaction between the maternal gut microbiome and pregnancy outcomes. The gut microbiome modulates systemic levels of inflammatory cytokines and short-chain fatty acids (SCFAs), which influence immune tolerance within the fetoplacental complex. Reduced butyrate production — the primary energy substrate for enterocytes and a potent inhibitor of NF-κB — in cases of intestinal dysbiosis may enhance the maternal systemic inflammatory response and increase myometrial excitability [17].

Notably, in the study by Vinturache et al. (2016), the gut microbiome of women with preterm birth differed significantly from that of women with term pregnancies: a reduced relative abundance of *Akkermansia muciniphila* and *Bifidobacterium spp.* was observed alongside an increased abundance of *Clostridiales* and *Enterobacteriaceae* [18]. These alterations correlated with elevated serum levels of C-reactive protein and IL-6.

Current studies confirm that oral microbiome dysbiosis and periodontitis may be associated with an increased risk of preterm birth through systemic inflammatory responses and the possible translocation of bacteria to the fetoplacental complex. Particular attention has been focused on *Fusobacterium nucleatum*, a member of the oral microbiota associated with chorioamnionitis, premature rupture of membranes, and preterm birth [19]. In addition to direct

bacterial invasion, periodontal pathogens are capable of stimulating the production of proinflammatory cytokines (IL-1β, TNF-α, IL-6) and prostaglandins, which may prematurely activate the mechanisms of labor [20].

At the same time, recent systematic reviews suggest that the relationship between periodontitis and preterm birth is complex and depends on microbiome composition, the severity of systemic inflammation, and the timing of dental intervention. Early microbiome diagnostics and personalized prevention of inflammatory pregnancy complications are currently considered promising approaches [16]. A meta-analysis demonstrated that treatment of periodontitis may be associated with approximately a 15% reduction in the risk of preterm birth (RR 0.85), although the level of evidence was assessed as moderate due to study heterogeneity and the risk of systematic bias. The authors emphasized that the findings are not yet conclusive but support the concept linking oral inflammation, systemic production of proinflammatory cytokines, and activation of the mechanisms underlying preterm labor [21].

Traditional diagnostic methods for vaginal dysbiosis (Amsel criteria and the Nugent scoring system) have limited predictive value for preterm birth because they fail to detect a substantial proportion of uncultivable microorganisms within the vaginal microbiome. The use of 16S rRNA metagenomic sequencing has significantly expanded our understanding of microbial community composition, although this method still has certain limitations, including amplification bias and insufficient assessment of bacterial functional activity [22].

A promising approach is whole-genome shotgun metagenomics, which enables evaluation not only of the taxonomic composition of the microbiome but also of its functional characteristics, including virulence genes, antimicrobial resistance genes, and metabolic activity. Combining these technologies with metabolomic analysis of vaginal secretions makes it possible to identify a

“microbiome signature” associated with the risk of preterm birth already during the first and second trimesters of pregnancy [23].

Among microbiome markers associated with an increased risk of preterm birth, the most significant include reduced dominance of *Lactobacillus crispatus*, increased vaginal microbial diversity with predominance of anaerobic flora, detection of *Sneathia spp.* and *Ureaplasma parvum/urealyticum*, as well as increased bacterial sialidase activity and vaginal pH >4.5 [24].

Lactobacillus-based probiotics remain one of the most promising and safest approaches for correcting vaginal dysbiosis during pregnancy. Recent systematic reviews indicate that the use of vaginal and oral probiotics contributes to restoration of a *Lactobacillus*-dominant microbiome, reduction in the incidence of bacterial vaginosis, and attenuation of local inflammatory responses. However, convincing evidence regarding a significant reduction in the rate of preterm birth is still insufficient due to study heterogeneity and differences in probiotic strains used [25]. Particular interest has been focused on preparations containing *Lactobacillus crispatus, L. rhamnosus* GR-1, and *L. reuteri*, which have demonstrated the ability to stabilize the vaginal microbiome and suppress the growth of anaerobic pathogens.

Another promising strategy is the combined vaginal and oral administration of probiotics aimed at simultaneous correction of both vaginal and gut microbiota and reduction of systemic inflammation. Current studies are also exploring the possibility of personalized selection of probiotic strains according to the vaginal microbiome community state type (CST) and the individual risk of preterm birth [16,20].

Analogous to fecal microbiota transplantation (FMT), which has demonstrated effectiveness in recurrent *Clostridioides difficile* infection, the concept of vaginal microbiota transplantation (VMT) has been actively investigated in recent years. Initial studies demonstrated the possibility of partial

restoration of a *Lactobacillus*-dominant vaginal microbiome following transfer of vaginal secretions from healthy donors. Particular interest has been generated by the studies of Dominguez-Bello et al. on “vaginal seeding” in newborns delivered by cesarean section, which confirmed the possibility of modifying early microbial colonization [26, 27]. Currently, vaginal microbiota transplantation is considered an experimental approach for the correction of persistent vaginal dysbiosis, and clinical studies evaluating its safety and efficacy are ongoing.

Traditional treatment of bacterial vaginosis with metronidazole or clindamycin is associated with a high recurrence rate, which is related to the nonspecific effects of antibiotics on the vaginal microbiome and insufficient restoration of *Lactobacillus*-dominant flora. Modern approaches involve personalized correction of vaginal dysbiosis based on the individual microbiome profile, including targeted antimicrobial therapy followed by restoration of lactobacillary flora using probiotics. A promising strategy is the use of dequalinium chloride, which demonstrates antimicrobial activity against anaerobic pathogens while exerting a relatively lower impact on *Lactobacillus spp.* [28].

Maternal nutrition during pregnancy significantly influences the composition of the gut microbiome and indirectly affects the vaginal microbiome. The Mediterranean diet, rich in fiber, polyphenols, and omega-3 fatty acids, is associated with increased production of short-chain fatty acids, particularly butyrate, and reduced systemic inflammatory responses. Recent cohort studies indicate that greater adherence to a Mediterranean dietary pattern during pregnancy is associated with a lower risk of preterm birth and improved perinatal outcomes [29].

Conclusions. Current evidence suggests that the microbiome is an important factor in the regulation of pregnancy and the pathogenesis of preterm birth. Alterations in the vaginal, gut, and oral microbiome are associated with activation of local and systemic inflammatory responses, increased production of

proinflammatory cytokines, and premature activation of labor mechanisms. The most unfavorable conditions are characterized by reduced dominance of *Lactobacillus crispatus* and predominance of anaerobic flora (*Gardnerella, Sneathia, Prevotella, Ureaplasma*).

The use of modern molecular genetic technologies, including 16S rRNA sequencing, shotgun metagenomics, and metabolomic analysis, has significantly expanded our understanding of the role of the microbiome in the development of preterm birth and created the basis for personalized approaches to prediction and prevention. Promising directions include early microbiome diagnostics, individualized correction of vaginal dysbiosis, probiotic therapy, and further investigation of vaginal microbiota transplantation. However, further large-scale studies are required for the implementation of microbiome technologies into routine obstetric practice.

References

1. WHO. Born Too Soon: Decade of Action on Preterm Birth. Geneva: World Health Organization; 2023. Available at: https://www.who.int/publications/i/item/9789240073890

2. Purisch, S. E., & Gyamfi-Bannerman, C. (2017). Epidemiology of preterm birth. *Seminars in perinatology*, *41*(7), 387–391. https://doi.org/10.1053/j.semperi.2017.07.009

3. Blencowe, H., Cousens, S., Chou, D., Oestergaard, M., Say, L., Moller, A. B., Kinney, M., Lawn, J., & Born Too Soon Preterm Birth Action Group (2013). Born too soon: the global epidemiology of 15 million preterm births. *Reproductive health*, *10 Suppl 1*(Suppl 1), S2. https://doi.org/10.1186/1742-4755-10-S1-S2

4. Dunlop, A. L., Satten, G. A., Hu, Y. J., Knight, A. K., … Corwin, E. J. (2021). Vaginal Microbiome Composition in Early Pregnancy and Risk of

Spontaneous Preterm and Early Term Birth Among African American Women. Frontiers in cellular and infection microbiology, 11, 641005. https://doi.org/10.3389/fcimb.2021.641005

5. Fettweis, J. M., Serrano, M. G., Brooks, J. P., Edwards, D. J., Girerd, P. H., Parikh, H. I., Huang, B., Arodz, T. J., … Buck, G. A. (2019). The vaginal microbiome and preterm birth. *Nature medicine*, *25*(6), 1012–1021. https://doi.org/10.1038/s41591-019-0450-2

6. Ravel, J., Gajer, P., Abdo, Z., Schneider, G. M., Koenig, S. S., McCulle, S. L., Karlebach, S., … Forney, L. J. (2011). Vaginal microbiome of reproductive-age women. *Proceedings of the National Academy of Sciences of the United States of America*, *108 Suppl 1*(Suppl 1), 4680–4687. https://doi.org/10.1073/pnas.1002611107

7. Bayar, E., Bennett, P. R., Chan, D., Sykes, L., & MacIntyre, D. A. (2020). The pregnancy microbiome and preterm birth. *Seminars in immunopathology*, *42*(4), 487–499. https://doi.org/10.1007/s00281-020-00817-w

8. Witkin, S. S., & Linhares, I. M. (2017). Why do lactobacilli dominate the human vaginal microbiota? *BJOG: an international journal of obstetrics and gynaecology*, *124*(4), 606–611. https://doi.org/10.1111/1471-0528.14390

9. Pillay, N., Short, C. S., Mzobe, G. F., Mtshali, A., & Ngcapu, S. (2026). The vaginal microbiome in pregnancy and preterm birth: mechanisms, disparities, and therapeutic opportunities. *NPJ biofilms and microbiomes*, *12*(1), 89. https://doi.org/10.1038/s41522-026-00945-5

10. Leitich, H., Bodner-Adler, B., Brunbauer, M., Kaider, A., Egarter, C., & Husslein, P. (2003). Bacterial vaginosis as a risk factor for preterm delivery: a meta-analysis. *American journal of obstetrics and gynecology*, *189*(1), 139–147. https://doi.org/10.1067/mob.2003.339

11. Brown, R. G., Marchesi, J. R., Lee, Y. S., Smith, A., Lehne, … MacIntyre, D. A. (2018). Vaginal dysbiosis increases risk of preterm fetal membrane

rupture, neonatal sepsis and is exacerbated by erythromycin. *BMC medicine*, *16*(1), 9. https://doi.org/10.1186/s12916-017-0999-x

12. Kindinger, L. M., Bennett, P. R., Lee, Y. S., Marchesi, J. R., Smith, A., Cacciatore, S., Holmes, E., Nicholson, J. K., Teoh, T. G., & MacIntyre, D. A. (2017). The interaction between vaginal microbiota, cervical length, and vaginal progesterone treatment for preterm birth risk. *Microbiome*, *5*(1), 6. https://doi.org/10.1186/s40168-016-0223-9

13. Romero, R., Dey, S. K., & Fisher, S. J. (2014). Preterm labor: one syndrome, many causes. *Science (New York, N.Y.)*, *345*(6198), 760–765. https://doi.org/10.1126/science.1251816

14. Menon, R., Richardson, L. S., & Lappas, M. (2019). Fetal membrane architecture, aging and inflammation in pregnancy and parturition. *Placenta*, *79*, 40–45. https://doi.org/10.1016/j.placenta.2018.11.003

15. Gilman-Sachs, A., Dambaeva, S., Salazar Garcia, M. D., Hussein, Y., Kwak-Kim, J., & Beaman, K. (2018). Inflammation induced preterm labor and birth. *Journal of reproductive immunology*, *129*, 53–58. https://doi.org/10.1016/j.jri.2018.06.029

16. Powell, A. M., Khan, F. Z. A., Ravel, J., & Elovitz, M. A. (2024). Untangling Associations of Microbiomes of Pregnancy and Preterm Birth. *Clinics in perinatology*, *51*(2), 425–439. https://doi.org/10.1016/j.clp.2024.02.009

17. Kimura, I., Miyamoto, J., Ohue-Kitano, R., Watanabe, K., Yamada, T., Onuki, M., Aoki, R., Isobe, … Hase, K. (2020). Maternal gut microbiota in pregnancy influences offspring metabolic phenotype in mice. *Science (New York, N.Y.)*, *367*(6481), eaaw8429. https://doi.org/10.1126/science.aaw8429

18. Vinturache, A. E., Gyamfi-Bannerman, C., Hwang, J., Mysorekar, I. U., Jacobsson, B., & Preterm Birth International Collaborative (PREBIC) (2016). Maternal microbiome - A pathway to preterm birth. *Seminars in fetal & neonatal medicine*, *21*(2), 94–99. https://doi.org/10.1016/j.siny.2016.02.004

19. García-Rios, P., Rodríguez-Lozano, F. J., González-Murcia, R., Murcia, L., Victoria-Montesinos, D., & García-Muñoz, A. M. (2026). The role of oral dysbiosis in pregnancy complications: a systematic review and meta-analysis of preterm birth. *Journal of oral microbiology*, *18*(1), 2617757. https://doi.org/10.1080/20002297.2026.2617757

20. Xie, Z., Chen, Z., & Ma, G. (2025). Dynamic changes in the pregnancy microbiome and their role in preterm birth. *Frontiers in cellular and infection microbiology*, *15*, 1683610. https://doi.org/10.3389/fcimb.2025.1683610

21. Thomas, C., Ahmed, S., Berghella, V., Brignardello-Petersen, R., El-Rabbany, M., Devion, C., & Ronzoni, S. (2026). Effect of dental treatments on reduction of preterm birth: a systematic review and meta-analysis. *American journal of obstetrics & gynecology MFM*, *8*(3), 101884. https://doi.org/10.1016/j.ajogmf.2025.101884

22. Goodrich, J. K., Waters, J. L., Poole, A. C., Sutter, J. L., Koren, O., Blekhman, R., Beaumont, M., … Ley, R. E. (2014). Human genetics shape the gut microbiome. *Cell*, *159*(4), 789–799. https://doi.org/10.1016/j.cell.2014.09.053

23. Stafford, G. P., Parker, J. L., Amabebe, E., Kistler, J., Reynolds, S., Stern, V., Paley, M., & Anumba, D. O. C. (2017). Spontaneous Preterm Birth Is Associated with Differential Expression of Vaginal Metabolites by Lactobacilli-Dominated Microflora. *Frontiers in physiology*, *8*, 615. https://doi.org/10.3389/fphys.2017.00615

24. Donders, G., Bellen, G., Janssens, D., Van Bulck, B., Hinoul, P., & Verguts, J. (2017). Influence of contraceptive choice on vaginal bacterial and fungal microflora. *European journal of clinical microbiology & infectious diseases: official publication of the European Society of Clinical Microbiology*, *36*(1), 43–48. https://doi.org/10.1007/s10096-016-2768-8

25. Jarde, A., Lewis-Mikhael, A. M., Moayyedi, P., Stearns, J. C., Collins, S. M., Beyene, J., & McDonald, S. D. (2018). Pregnancy outcomes in women

taking probiotics or prebiotics: a systematic review and meta-analysis. *BMC pregnancy and childbirth*, *18*(1), 14. https://doi.org/10.1186/s12884-017-1629-5

26. Lev-Sagie, A., Goldman-Wohl, D., Cohen, Y., Dori-Bachash, M., Leshem, A., Mor, U., Strahilevitz, J., Moses, A. E., Shapiro, H., Yagel, S., & Elinav, E. (2019). Vaginal microbiome transplantation in women with intractable bacterial vaginosis. *Nature medicine*, *25*(10), 1500–1504. https://doi.org/10.1038/s41591-019-0600-6

27. Dominguez-Bello, M. G., De Jesus-Laboy, K. M., Shen, N., Cox, L. M., Amir, A., Gonzalez, A., … Clemente, J. C. (2016). Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. *Nature medicine*, *22*(3), 250–253. https://doi.org/10.1038/nm.4039

28. Muzny, C. A., & Sobel, J. D. (2022). The Role of Antimicrobial Resistance in Refractory and Recurrent Bacterial Vaginosis and Current Recommendations for Treatment. *Antibiotics (Basel, Switzerland)*, *11*(4), 500. https://doi.org/10.3390/antibiotics11040500

29. Tareke, A. A., Melak, E. G., Mengistu, B. K., Hussen, J., & Molla, A. (2024). Association between maternal dietary diversity during pregnancy and birth outcomes: evidence from a systematic review and meta-analysis. *BMC nutrition*, *10*(1), 151. https://doi.org/10.1186/s40795-024-00960-9