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Intestinal and vaginal microbiota in pregnancy

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Abstract

Background: Pregnancy induces profound hormonal, metabolic, and immunological changes that affect both maternal and fetal health. Increasing evidence highlights the role of intestinal and vaginal microbiota in shaping these processes, with dysbiosis linked to complications such as gestational diabetes, preeclampsia, preterm birth, and fetal growth restriction

Objective: To investigate the composition and clinical significance of intestinal and vaginal microbiota during pregnancy,

Methods: A mixed retrospective and prospective study was conducted at Odesa National Medical University (2021–2024). The retrospective analysis included over 600 medical records of pregnant women. The prospective cohort enrolled 412 women: 168 with MS and 244 controls. All underwent standardized clinical, biochemical, hormonal, and microbiological assessment. Placental samples were examined in 94 cases. Microbiota was evaluated using culture-based and molecular methods, with quantitative and qualitative assessment of bifidobacteria, lactobacilli, Enterobacteriaceae, Gardnerella, Candida, and Klebsiella. A subgroup of MS women received symbiotic therapy. Statistical analysis included multivariate regression and predictive modeling

Results: Women with MS showed reduced bifidobacteria and lactobacilli, increased Enterobacteriaceae, and decreased microbial diversity. Vaginal dysbiosis was characterized by

reduced Lactobacillus dominance and higher prevalence of Gardnerella and Candida. Combined dysbiosis strongly correlated with adverse outcomes and placental pathology. Symbiotic therapy improved microbial balance and significantly reduced rates of gestational diabetes, preeclampsia, preterm birth, cesarean delivery, and perinatal losses

Conclusion: Intestinal and vaginal dysbiosis is common in MS pregnancies and predicts adverse outcomes. Symbiotic therapy offers a safe and effective strategy for restoring microbial balance and improving maternal and perinatal health.

Key words: pregnancy; intestinal microbiota; vaginal microbiota; symbiotics; prevention

Pregnancy represents a unique physiological state characterized by profound hormonal, metabolic, and immunological changes that influence both maternal and fetal health [1]. Among the most important but still incompletely understood factors shaping these processes are the intestinal and vaginal microbiota [2, 3]. The maternal gut harbors a complex microbial community that regulates nutrient absorption, energy balance, and immune homeostasis, while the vaginal microbiota serves as a critical barrier against urogenital infections and plays a protective role in maintaining reproductive health.

Accumulating evidence suggests that pregnancy induces significant shifts in microbial composition [4, 5]. In the gut, changes include increased abundance of proinflammatory taxa in later trimesters, which may contribute to metabolic adaptations supporting fetal growth. In the vagina, dominance of Lactobacillus species is typically preserved, but deviations from this protective state have been linked to bacterial vaginosis, preterm birth, and other adverse outcomes [4, 6]. Interactions between intestinal and vaginal microbial ecosystems are increasingly recognized, as translocation of metabolites, immune mediators, and even microbial components can influence systemic physiology and local mucosal environments [2, 7].

Understanding these dynamics is of growing clinical interest. Altered maternal microbiota has been associated with gestational diabetes, preeclampsia, excessive weight gain, and neonatal outcomes such as immune development and susceptibility to allergic disease [4, 5, 8]. Moreover, advances in sequencing technologies have facilitated high-resolution profiling, allowing identification of microbial signatures predictive of complications [9]. This evolving knowledge opens new opportunities for preventive and therapeutic strategies, including probiotic or dietary interventions aimed at optimizing microbial balance during pregnancy.

The aim of this article is to investigate the composition and clinical significance of intestinal and vaginal microbiota during pregnancy

Material and methods. This study was conducted in 2021-2024 in Odesa National Medical Univeristy and it employed a comprehensive design combining retrospective and prospective components. In the retrospective stage, more than 600 case histories and medical records of pregnant women were analyzed to establish the prevalence of metabolic syndrome across different age groups and to evaluate its association with major obstetric and perinatal complications.

The prospective stage included 412 pregnant women, among whom 168 (40.8%) had a confirmed diagnosis of metabolic syndrome and 244 (59.2%) served as controls without clinical or laboratory signs of metabolic disturbances. All participants underwent standardized clinical and laboratory evaluation, including anthropometric measurements, biochemical blood tests, hormonal assays (insulin, leptin, progesterone, estradiol, gonadotropins), and microbiological analysis of the intestinal, vaginal, and urinary microbiota [10]. Placental tissue samples were obtained in 94 cases for morphological examination to assess lipid deposition, vascular changes, and inflammatory infiltration [11].

Microbiota composition was assessed using classical culture-based techniques complemented by molecular methods where appropriate. Quantitative and qualitative characteristics of bifidobacteria, lactobacilli, Enterobacteriaceae, Gardnerella, Candida, and Klebsiella were evaluated. Microbial diversity was determined using the Shannon index [12]. A subgroup of patients received symbiotic therapy as part of preconception care and during pregnancy, enabling the assessment of its effectiveness in restoring microbial balance and preventing complications.

Statistical analysis included variation statistics, correlation analysis, and multivariate regression modeling [13]. A predictive model of adverse perinatal outcomes was developed, integrating 12 clinical, hormonal, and microbiological parameters. The accuracy, sensitivity, and specificity of the model were calculated. Ethical approval was obtained in accordance with national bioethical standards, and all participants provided written informed consen

Results. The present study provided an extensive analysis of intestinal and vaginal microbiota in pregnant women, with a particular focus on those diagnosed with metabolic syndrome (MS). The prospective cohort included 412 women, 168 of whom had clinically verified MS and 244 served as controls. Baseline demographic characteristics revealed that women with MS were of significantly older reproductive age, with more than 60% being above 30 years compared to 37% in the control group. Body mass index values were also markedly higher:

71% of MS women had BMI ≥30 kg/m², whereas only 14% of controls fell into this category. These differences established a clear background of metabolic and hormonal imbalance upon which microbiota alterations were investigated.

Intestinal microbiota analysis revealed profound dysbiotic changes in the MS group. Quantitative studies showed a 37% reduction in bifidobacteria and a 32% reduction in lactobacilli compared to controls. In contrast, Enterobacteriaceae counts increased more than twofold (2.1 times higher than controls). The Shannon diversity index was reduced by 34%, indicating a global decline in microbial richness and evenness (Fig. 1). These shifts suggest that intestinal dysbiosis in MS pregnancies is characterized not only by a deficiency of protective taxa but also by an overgrowth of opportunistic organisms.

Importantly, statistical correlations demonstrated that a pronounced deficiency in bifidobacteria and lactobacilli was associated with an increased incidence of gestational diabetes and preeclampsia. Specifically, women with the lowest quartile of protective taxa had a 2.4-fold higher risk of preeclampsia and a 2.1-fold higher risk of fetal growth restriction.

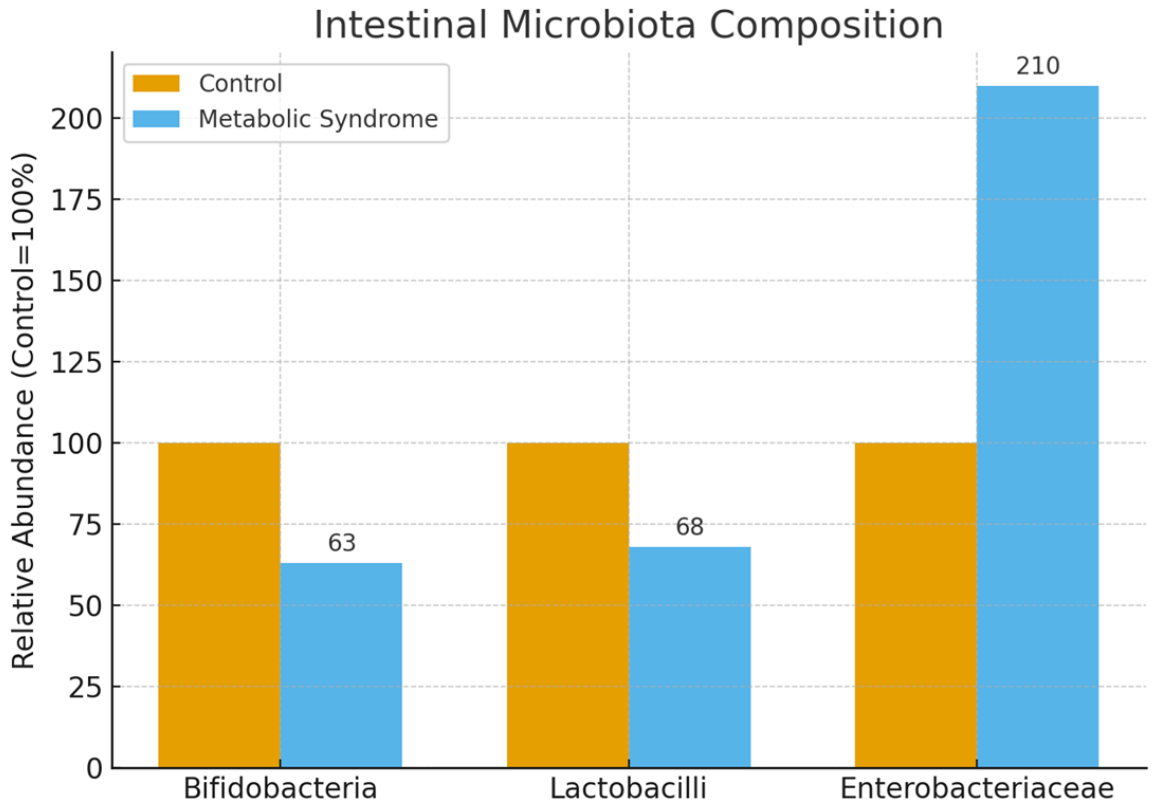

Figure 1 Intestinal microbiota composition in pregnancy

Vaginal microbiota findings reinforced these patterns. Lactobacillus dominance, a hallmark of a healthy vaginal ecosystem, was compromised in MS pregnancies (Fig. 2). A 42% decrease

in lactobacilli concentration was recorded, while Gardnerella species were detected in 38% and Candida in 24% of cases. These alterations were significantly less frequent in the control group. Multivariate analysis showed that low vaginal lactobacilli levels were independently associated with adverse outcomes such as preterm birth, which occurred in 17.9% of MS women compared with 9.4% of controls. The risk of fetal growth restriction was similarly increased in cases with vaginal dysbiosis, supporting the hypothesis that disruption of local protective flora contributes to impaired reproductive outcomes.

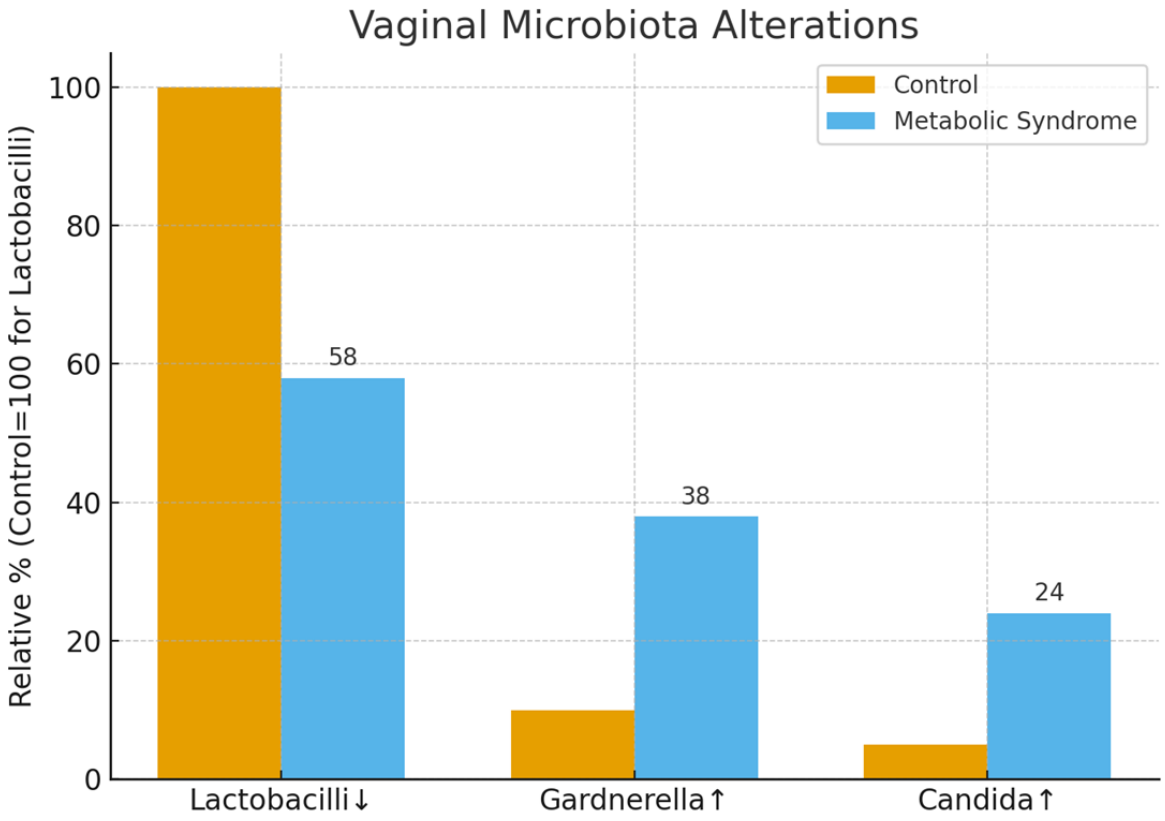

Figure 2 Vaginal microbiota alteration in pregnancy

The combined assessment of intestinal and vaginal microbiota highlighted an important interrelationship. Women with simultaneous depletion of bifidobacteria in the gut and lactobacilli in the vagina experienced the highest incidence of complications, including a twofold rise in composite adverse perinatal outcomes. This dual dysbiosis profile was particularly predictive of placental pathology. Morphological examinations of 94 placentas confirmed excessive lipid accumulation, macrophage infiltration, and vascular sclerosis in MS pregnancies, changes that were more pronounced in women with severe microbial imbalance.

Symbiotic therapy emerged as a potentially effective intervention. In a subgroup of 84 MS women who received combined probiotics and prebiotics before and during pregnancy,

notable improvements in microbial composition were recorded. Bifidobacteria counts increased by 62%, while lactobacilli rose by 47%, restoring microbial balance closer to that observed in healthy controls. In parallel, opportunistic Enterobacteriaceae prevalence decreased by half (Fig. 3). Vaginal microbiota also shifted favorably, with increased lactobacilli dominance and reduced detection rates of Gardnerella and Candida. These microbiological improvements were mirrored by better clinical outcomes: the incidence of gestational diabetes declined from 28.6% in untreated MS women to 14.3% in those receiving symbiotics, preeclampsia decreased from 21.4% to 10.7%, and preterm birth rates fell from 17.9% to 8.3%.

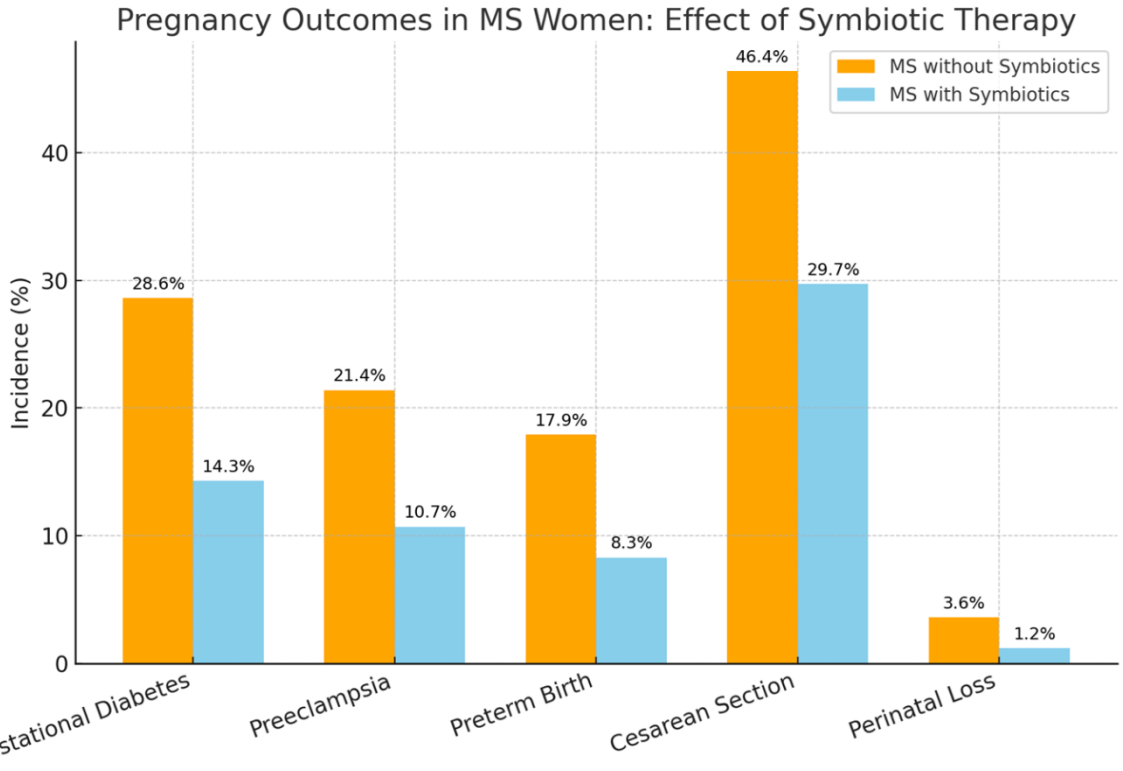

Figure 3. Pregnancy Outcomes in MS Women: Effect of Symbiotic Therapy

Cesarean delivery rates were reduced from 46.4% to 29.7%, and perinatal losses decreased from 3.6% to 1.2%. These data support the concept that targeted correction of dysbiosis can mitigate the risks traditionally associated with MS pregnancies.

Another key result of the study was the predictive modeling of adverse perinatal outcomes. By integrating 12 clinical, hormonal, and microbiological parameters, a risk model was developed that achieved an overall accuracy of 84%, with sensitivity of 81% and specificity of 86%. Among the strongest predictors were maternal BMI, serum insulin and leptin levels, and quantitative measures of intestinal and vaginal microbiota, particularly the ratios of

bifidobacteria and lactobacilli to opportunistic flora. This model enabled early identification of women at highest risk, offering opportunities for individualized preventive strategies.

Thus, the results demonstrate that intestinal and vaginal dysbiosis is common in pregnant women with metabolic syndrome and is closely associated with adverse maternal and perinatal outcomes. Protective species such as bifidobacteria and lactobacilli were consistently reduced, while opportunistic organisms expanded, creating a microbial environment conducive to inflammation, placental dysfunction, and obstetric complications. The dual assessment of gut and vaginal ecosystems provided a more complete risk profile, as combined dysbiosis correlated with the most severe outcomes. Symbiotic therapy proved effective in partially restoring microbial balance and reducing complication rates, supporting its role as an adjunct in pregnancy management.

Conclusion:

Intestinal and vaginal dysbiosis is common in pregnant women with metabolic syndrome and is strongly associated with gestational diabetes, preeclampsia, preterm birth, and adverse perinatal outcomes. Reduced bifidobacteria and lactobacilli alongside the overgrowth of opportunistic flora create conditions for inflammation and placental dysfunction. Dual assessment of gut and vaginal microbiota provides a reliable risk profile, while symbiotic therapy effectively restores microbial balance and reduces complication rates. These findings highlight microbiota as both a predictive marker and a therapeutic target in pregnancy managemen

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