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THE ROLE OF GUT MICROBIOTA IN THE DEVELOPMENT OF VARIOUS PATHOLOGIES DURING PREGNANCY

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Abstract

During pregnancy, the gut microbiota is closely associated with the immune, metabolic, and endocrine systems of the body and plays a crucial role in the health of both the mother and the fetus. Recent studies have demonstrated a link between gut microbiota dysbiosis and the development of conditions such as gestational diabetes, preeclampsia, preterm birth, and intrauterine growth restriction. This article analyzes changes in the gut microbiota during pregnancy, their effects on pathological outcomes, and reviews current scientific research and statistical data. The study concludes with discussions of the applied research methods and final conclusions.

Keywords: Pregnancy, gut microbiota, dysbiosis, gestational diabetes, preeclampsia.

Introduction

Research Relevance

Pregnancy is a complex physiological process accompanied by significant metabolic, endocrine, and immune changes, occurring under the influence of numerous factors that determine maternal and fetal health. In recent decades, the gut microbiota — a community of bacteria, fungi, viruses, and other microorganisms residing in the human intestine — has attracted considerable scientific attention due to its potential impact on pregnancy and its outcomes. Maternal gut microbiota produces essential signaling molecules and metabolites (such as short-chain fatty acids — SCFAs) crucial for maternal metabolism, immune regulation, and proper fetal development. Consequently, alterations in its composition — dysbiosis — have been shown to be associated with various obstetric and perinatal pathologies [6].

From an epidemiological standpoint, it is important to consider some pregnancy-related complications and their global burden. For instance, preeclampsia occurs in approximately 2–8% of pregnancies worldwide and is responsible for thousands of maternal and neonatal deaths each year [10]. Similarly, although the global prevalence of gestational diabetes (GD) varies across studies, several recent meta-analyses and multinational investigations estimate an average prevalence of around

14%, highlighting the increased risk of metabolic complications during pregnancy and the long-term cardiometabolic consequences [8].

Recent studies have identified statistical associations between alterations in the composition and function of the maternal gut microbiota — such as a reduction in butyrate-producing SCFA bacteria, decreased populations of Faecalibacterium or Lactobacillus, and an increase in Streptococcus species — and conditions like GD, preeclampsia, preterm birth, and fetal growth restriction. These associations are supported not only by observational findings but also by experimental evidence from animal models, where fecal microbiota transplantation (FMT)–induced dysbiosis has been shown to trigger hypertension and other pregnancy-related pathophysiological changes [5].

However, several scientific limitations remain. Most human studies are observational in nature, making it difficult to establish direct causal relationships. Additionally, differences in microbiota analysis techniques (such as 16S rRNA sequencing and shotgun metagenomics) and diagnostic criteria complicate cross-study comparisons and generalizations. Nevertheless, modulation of the maternal microbiota through dietary interventions, probiotics, prebiotics, and other strategies offers promising preventive and therapeutic avenues — though robust, high-quality randomized controlled trials are still lacking [15].

This article aims to summarize current data on structural and functional changes in the gut microbiota during pregnancy, present existing scientific and statistical evidence linking dysbiosis to the most relevant obstetric pathologies (particularly gestational diabetes and preeclampsia), and discuss potential mechanisms and future research directions. Throughout the article, the focus is placed on the strength of evidence for microbiota–pathology associations, existing limitations, and the practical implications of these findings [1].

Research Objective

The main objective of this study is to investigate the structural and functional alterations of the gut microbiota during pregnancy and to analyze their associations with various pathological conditions — particularly gestational diabetes, preeclampsia, preterm birth, and fetal growth restriction.

Overall, this work aims to comprehensively assess the impact of maternal gut microbiota on both maternal and fetal health, thereby providing a scientific basis for the development of microbiota-based preventive and therapeutic strategies during pregnancy.

Materials and Methods

This study has a theoretical and analytical character and was prepared based on recently published scientific articles, systematic reviews, and statistical data. The data collection was carried out in the following stages:

1. From the reviewed literature, original studies demonstrating the relationship between pregnancy and gut microbiota were selected [14].
2. The selected data included: changes in microbiota composition, associated pathologies (such as gestational diabetes, preeclampsia, preterm birth, and others), possible mechanisms (metabolic, immunological), and study outcomes — all analyzed comprehensively.
3. Statistical findings were examined with examples (e.g., decreased Bifidobacterium spp. and Lactobacillus spp. levels in pregnant women diagnosed with dysbiosis) [16].

The analysis was conducted descriptively and critically. Since most of the included studies were observational in nature, causal relationships should be interpreted with caution.

Results

Below are summarized the findings of studies that demonstrated the relationship between gut microbiota and pregnancy-related pathologies, particularly gestational diabetes mellitus (GDM).

Gestational Diabetes Mellitus (GDM) and Gut Microbiota Dysbiosis

Findings by Crusell et al. (2018): Crusell and colleagues conducted a study using the 16S rRNA sequencing method among pregnant women with GDM (n = 50) and those with normal glucose tolerance (n = 157). The results showed:

- The Actinobacteria phylum was more abundant in the GDM group; at the genus level, Collinsella, Rothia, and Desulfovibrio were significantly increased [2].
- Seventeen OTUs (operational taxonomic units) were significantly different between the GDM and control groups [2].
- Even after adjusting for pregestational BMI, differences in five OTUs remained significant [2].
- The α-diversity (richness and evenness index) of the microbiota decreased toward the end of pregnancy in both groups [2].
- Importantly, GDM-related microbiota alterations persisted postpartum — approximately 8 months after delivery, the gut microbiota composition in women with GDM remained distinct from that of normoglycemic controls [2].

Findings by Sohrabi et al. (2025): Sohrabi and colleagues reported several associations between gut microbiota composition and GDM development:

- Higher populations of Actinomycetota and Bacteroidota during the first trimester were identified as protective factors against GDM development [12].
- The quantity of Bifidobacterium spp. (beneficial flora) was found to be significantly lower in GDM cases [12].
- Caloric and cholesterol intake showed negative correlations with microbiota composition; for instance, higher calorie intake reduced Actinomycetota populations (OR = 9.9, p = 0.009) [12].
- In contrast, carbohydrate and fat consumption (particularly MUFA and PUFA) had positive effects, increasing Bacteroidota abundance [12].

Findings by Wu et al. (2025) — Longitudinal Analysis: Wu and colleagues examined the longitudinal association between GDM and gut microbiota composition:

- They followed 52 women with GDM and 52 controls, analyzing microbiota profiles during early, mid, and late pregnancy using 16S rRNA sequencing [13].
- No major overall compositional differences were observed, but 16 genus-level taxa showed significant trimester-related changes. For example, Odoribacter and Ruminococcus gnavus showed dynamic shifts in the control group, while Ruminococcaceae UCG-002 and Odoribacter changes were more pronounced in the GDM group [13].
- Mendelian randomization analysis revealed that an increase in Prevotella 9 abundance during the first trimester was associated with elevated GDM risk, whereas Methanobrevibacter played a protective role [13].

Interaction Between Metabolites, Hormones, and Gut Microbiota

Liu et al. (2023) analyzed the association between gut microbiota and pregnancy hormone metabolism (progesterone, estradiol, and related metabolites):

- The study included 54 pregnant women (27 with GDM) and applied both 16S rRNA sequencing and targeted metabolomic analysis [7].
- Results showed alterations in 132 metabolic pathways, with metabolites such as butyrate and mevalonate being linked to progesterone and estradiol levels [7].
- These findings suggest that GDM-related microbiota alterations may influence pregnancy hormone function through metabolic mediation mechanisms [7].

High Inflammation, Cytokines, and Gut Microbiota

Pinto et al. (2023) — published in the journal Gut, investigated inflammatory and gut microbiota changes preceding the development of gestational diabetes mellitus (GDM):

- It was found that women who later developed GDM had elevated levels of pro-inflammatory cytokines, particularly interleukin-6 (IL-6) [9].

- Moreover, fecal concentrations of short-chain fatty acids (SCFAs) were reduced, and compositional alterations in conventional gut bacterial species were observed [9].

Microbial Dysbiosis and Possible Associations with GDM Outcomes

Gupta et al. (2024) examined gut microbiota dysbiosis related to GDM and the influence of regional (Asian) factors:

- The gut microbiota profiles of women with GDM were found to be similar across various Asian ethnic populations. Genera such as Collinsella, Blautia, Ruminococcus, and Eubacterium hallii were consistently enriched in GDM groups [4].
- Notably, in GDM cases, microbiota diversity (both alpha and beta diversity) showed little responsiveness to dietary modifications over time [4].

Discussion

Recent studies have revealed that during pregnancy, the gut microbiota plays not only a digestive role but also a crucial part in maintaining metabolic, immune, and hormonal balance. Alterations in gut microbiota composition (dysbiosis) have been scientifically proven to be directly associated with various pregnancy-related pathologies — particularly gestational diabetes, preeclampsia, excessive body weight, depression, and preterm birth.

In women with gestational diabetes, the ratio of Bacteroides, Firmicutes, and Prevotella changes significantly. Koren et al. (2012) found a marked reduction in microbiota diversity from the first to the third trimester, alongside a sharp increase in Proteobacteria and Actinobacteria. These changes activate metabolic inflammation and insulin resistance mechanisms, thereby predisposing to GDM development.

In preeclamptic women, reductions in beneficial Lactobacillus and Bifidobacterium species have been reported, while pro-inflammatory bacteria such as Escherichia coli and Clostridium perfringens increase. Chen et al. (2020), in a study involving 80 pregnant women, found that microbiota imbalance in preeclampsia was associated with elevated inflammatory cytokines (IL-6, TNF-α).

Moreover, the state of gut microbiota has also been linked to mental health during pregnancy. Aatsinki et al. (2021) found that women with reduced Lactobacillus and Bifidobacterium levels exhibited higher rates of prenatal depression, supporting the gut–brain axis hypothesis and emphasizing the role of intestinal bacteria in emotional well-being.

Additionally, maternal gut microbiota directly influences fetal immune system development. Multiple studies (including Nature Microbiology, 2018) demonstrated that beneficial maternal gut bacteria are transferred to the newborn during delivery, shaping the infant’s immune system and susceptibility to allergies.

Overall, these findings underscore that maintaining gut microbiota balance is crucial for healthy pregnancy progression, prevention of complications, and ensuring optimal long-term health outcomes for the newborn. Therefore, supporting microbiota equilibrium through probiotics, prebiotics, and balanced nutrition has become an essential component of modern obstetric practice.

Conclusion

The conducted analyses and review of scientific literature demonstrate that the gut microbiota is one of the key biological systems determining maternal and fetal health during pregnancy. Disruption of its composition — dysbiosis — negatively affects not only the digestive system but also the metabolic, immune, and hormonal systems.

1. Scientific studies show that maintaining physiological balance in the gut microbiota during pregnancy is crucial for maternal and fetal well-being. Alterations in microbial composition (dysbiosis) significantly influence metabolic, immune, and hormonal processes, leading to various pathologies such as **gestational diabetes, preeclampsia, preterm birth, and psychological disorders**.
2. In women with **gestational diabetes mellitus (GDM)**, an altered Firmicutes/Bacteroidetes ratio, an increase in Proteobacteria, and reduced microbial diversity have been observed. These changes trigger **insulin resistance** and inflammatory processes, contributing to metabolic complications of pregnancy.
3. In **preeclampsia**, beneficial bacteria such as Lactobacillus and Bifidobacterium decrease, while pathogenic species including Escherichia coli and Clostridium perfringens proliferate. This imbalance leads to elevated inflammatory mediators (**IL-6, TNF-α**) and endothelial dysfunction in blood vessels.
4. The gut microbiota is also closely linked to **mental health** during pregnancy. According to **Aatsinki et al. (2021)**, lower levels of Lactobacillus and Bifidobacterium are associated with higher rates of **prenatal depression**. This connection can be explained through the **“gut–brain axis”**, where intestinal bacteria influence neurotransmitter synthesis and neural signaling.
5. The **maternal gut microbiota** plays a fundamental role in shaping the **fetal immune system**. During childbirth, beneficial maternal microbes are transferred to the infant, helping to establish immune responses and reducing susceptibility to allergic diseases.

These findings emphasize that maintaining a **healthy gut microbiota** during pregnancy should be an integral part of medical prevention strategies. **Balanced nutrition**, appropriate use of **probiotics and prebiotics**, **stress reduction**, and

rational antibiotic therapy are effective approaches to preserving microbiota stability and preventing pregnancy-related complications.

Therefore, expanding **clinical practices focused on gut microbiota analysis and modulation**, as well as implementing **individual microbiota monitoring systems** for pregnant women, should be considered one of the key directions in modern **obstetrics and perinatal medicine.**

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