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FROM GUT TO MIND: THE INFLUENCE OF MICROBIOTA COMPOSITION ON POSTPARTUM DEPRESSION

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ABSTRACT

Background: Postpartum depression is a significant mood disorder affecting women during the first year after childbirth. Emerging evidence indicates that gut microbiota may play a meaningful role in its development through inflammatory, metabolic, and neuroendocrine pathways. The purpose of this review is to synthesize current knowledge on gut microbiota alterations during pregnancy and postpartum and to evaluate their potential contribution to postpartum depression, with emphasis on mechanistic links and opportunities for therapeutic modulation.

Methodology: This review was conducted by analyzing clinical, mechanistic, and translational studies, using PubMed, the Cochrane Library, and Google Scholar databases, that focused on maternal microbiota composition, postpartum mood disturbances, and microbiota-modulating strategies.

Results: The reviewed evidence demonstrates that women with depressive symptoms commonly exhibit reduced levels of anti-inflammatory and short-chain-fatty-acid-producing bacteria and an increased presence of pro-inflammatory taxa. Pregnancy and postpartum are characterized by substantial microbial shifts, including changes in Firmicutes and Bacteroidetes, with postpartum reductions in beneficial genera such as Faecalibacterium and Bacteroides. These alterations may influence inflammation, neurotransmitter metabolism, intestinal barrier function, and stress-axis activity, collectively contributing to depressive risk. Interventions aimed at modulating the maternal microbiota, including dietary strategies and probiotic supplementation, show preliminary potential for reducing depressive symptoms or lowering postpartum depression risk.

Conclusions: Overall, current findings suggest that gut microbiota may represent both a biomarker and a modifiable factor in postpartum depression. Microbiota-targeted approaches warrant further investigation to determine their preventive and therapeutic utility in maternal mental health.

1. Introduction

Postpartum depression (PPD) is a mood disorder that typically occurs within the first six weeks after childbirth, although it may develop at any point within the first year postpartum. PPD is often confused with the "baby blues," a transient mood disturbance that appears shortly after delivery. Approximately 80% of women experience early signs of emotional disturbance within the first few days after childbirth (Buttner et al., 2012). However, differentiating between postpartum depression and baby blues can be challenging, as both conditions share overlapping symptoms such as mood instability, irritability, and fatigue. Furthermore, a substantial proportion of postpartum women exhibit depressive-like symptoms such as changes in appetite, sleep disturbances and reduced energy levels following pregnancy (O'Hara et al., 1991). However, the symptoms of PPD are considerably more severe, persist longer, and frequently require professional intervention. Clinical manifestations of postpartum depression include depressed mood, loss of interest or pleasure, changes in appetite or body weight, sleep disturbances, irritability or psychomotor retardation, feelings of worthlessness or excessive guilt, and suicidal thoughts or behaviors (Javdan et al., 2025). Postpartum depression affects not only the mother but can also have a broad range of consequences for the infant, including impaired mother–infant bonding, which may adversely influence the child's development and increase the risk of future mental health problems (Oliveira et al., 2022). According to a meta-analysis by Wang et al., which included 565 studies from 80 regions worldwide, the global prevalence of postpartum depression is estimated at 17.22% among women after childbirth (Z. Wang et al., 2021).

2. Materials and Methods

A literature search was conducted to identify studies on changes in gut microbiota associated with postpartum depression and the potential consequences of these shifts. The electronic databases PubMed, Google Scholar, and the Cochrane Library were systematically searched using combinations of the following keywords: postpartum depression, postpartum microbiome, gut microbiota, postpartum depression factors, gut microbiota in depression, gut microbiota during pregnancy, postpartum period, microbiota modulation, and microbiota in depression.

3. Postpartum Depression Factors

The etiological landscape of postpartum depression is highly complex and shaped by a wide spectrum of biopsychosocial determinants. Factors highlighted in previous research can be divided into following categories:

Psychological and Emotional Factors:

depression and anxiety during pregnancy, postpartum blues, neuroticism, excessive stress or stressful life events, poor marital relations, low self-esteem, negative maternal attitude (Haga et al., 2012; Zhao & Zhang, 2020)

Social and Environmental Factors:

domestic violence, immigration status, low socioeconomic status, single marital status, lack of social support, acculturation processes, unwanted pregnancy, inadequate access to postpartum care (Goyal et al., 2010; Zhao & Zhang, 2020)

Biological and Medical Factors:

gestational diabetes, hormonal contraception, postpartum anemia, sleep disturbances, nutritional imbalances including selenium deficiency, obesity, and malnutrition, preeclampsia (Zhao & Zhang, 2020)

Obstetric and Infant-Related Factors:

cesarean section (including emergency cesarean section), lack of immediate skin-to-skin contact after birth, obstetrical stressors, preterm delivery, prenatal hospitalization, childbirth-related complications, difficult or grieving infant temperament, poor or deceased infant health (Goyal et al., 2010; Ihongbe & Masho, 2017; Vigod et al., 2010).

The management of PPD primarily involves psychological interventions and pharmacotherapy. Nevertheless, evidence supporting the efficacy of psychological interventions in preventing PPD remains limited. Interpersonal psychotherapy has demonstrated potential in alleviating depressive symptoms among patients with PPD, particularly when administered between 4 and 8 weeks postpartum. It has also been associated with improved family satisfaction, with longer interventions correlating with greater family engagement (X. Wang et al., 2023). Despite its potential benefits, this approach demands substantial resources, including therapist availability, considerable time, financial investment and active family involvement.

Pharmacological treatments may also affect the child's future development and behavior, as most antidepressants are excreted into breast milk, rendering their use inadvisable for breastfeeding mothers (Hawkins, 2023). Adherence to treatment in patients with postpartum depression remains a substantial clinical challenge. Evidence suggests that 50% of individuals diagnosed with affective disorders, prematurely discontinue antidepressants within 6 months (Meng et al., 2024). In this group, the presence of co-occurring substance use disorders and the overall severity of the depressive episode are strongly associated with nonadherence, while the occurrence of adverse effects from antidepressant medications further undermines compliance (Pompili et al., 2009). These challenges highlight the need for alternative, non-pharmacological approaches that can circumvent barriers related to medication adherence and provide effective strategies for managing postpartum depression. In this context, the present review examines the role of gut microbiota in the risk and manifestation of PPD, as well as the potential of its modulation to offer novel preventive and therapeutic strategies.

4. Changes in Gut Microbiota in Depression

Accumulating clinical evidence indicates that deviations in the composition of gut microbiota, relative to healthy individuals, are associated with the development of depression, highlighting the pivotal role of the brain–gut-microbiota axis in its pathophysiology (Liu et al., 2022; Nikolova et al., 2021; Simpson et al., 2021; Yang et al., 2020). Moreover, evidence that microbial or metabolite administration can both induce and mitigate depression-like phenotypes underscores the bidirectional regulatory role of the brain–gut–microbiota axis in depressive disorders (Chang et al., 2022).

Recent studies suggest that patients with major depressive disorder (MDD) tend to exhibit distinct microbial profiles when compared to healthy controls. Specifically, higher levels of *Prevotella*, *Klebsiella*, *Streptococcus*, and *Clostridium XI* have been observed, accompanied by lower levels of *Bacteroidetes* (Lin et al., 2017). Although results across studies remain somewhat inconsistent, a recurring pattern can be observed — an enrichment of pro-inflammatory bacterial taxa together with a depletion of anti-inflammatory species (Liu et al., 2023). This imbalance supports the hypothesis that alterations in the gut microbiome may contribute to systemic inflammation, which is often linked to depressive pathophysiology.

The phyla most commonly altered in depression include ***Firmicutes, Actinobacteria,* and *Bacteroidetes***, with a notably increased ***Bacteroidetes/Firmicutes*** ratio in patients with MDD. This microbial shift is typically characterized by an enrichment of *Bacteroides* and a reduction in beneficial genera such as *Blautia*, *Faecalibacterium*, and *Coprococcus*. Moreover, consistent findings across several studies indicate elevated levels of *Eggerthella* and decreased abundance of *Sutterella* in individuals with MDD (Liu et al., 2022; Nikolova et al., 2021; Simpson et al., 2021). Notably, the abundance of *Faecalibacterium* has been shown to correlate negatively with depression severity, as measured by clinician-rated depression scales, suggesting that this genus may play a protective role against the progression of depressive symptoms (Jiang et al., 2015). A meta-analysis reported reduced abundances of the genera *Coprococcus* and *Faecalibacterium* in individuals with depression compared to non-depressed controls, and noted that depressive symptoms tended to improve in probiotic intervention studies (Sanada et al., 2020). Despite variations in specific microbial patterns reported across studies, converging evidence indicates that gut microbiota composition is markedly altered in depression and may serve as a potential target for its prevention and treatment (Xiong et al., 2023).

5. Gut microbiota Changes During Late Pregnancy and Postpartum Period
5.1 Early postpartum period (<6 weeks)

During the early postpartum period*, Firmicutes* was consistently identified as the predominant phylum(Dahl et al., 2017; Jost et al., 2014; Weerasuriya et al., 2023). Other commonly detected genera included *Bifidobacterium, Streptococcus, Lactobacillus, Faecalibacterium, Roseburia, Staphylococcus, Prevotella, Alloprevotella*, and *Escherichia*, reflecting a diverse microbial ecosystem that begins to reorganize shortly after delivery. These taxa are thought to play important roles in shaping maternal immune function and metabolic recovery during the first weeks after birth(Dahl et al., 2017; Jost et al., 2014).

Longitudinal data indicated that *Bacteroides* remained dominant up to 4–6 weeks postpartum(Jost et al., 2014), suggesting a relatively stable core microbiota despite hormonal fluctuations and physiological stress associated with childbirth. The persistence of *Bacteroides* during this period may be linked to dietary patterns, mode of delivery, and inflammatory responses, all of which are known to influence early postpartum microbiome dynamics. Moreover, the gradual shifts observed across studies highlight the importance of this transitional window for both maternal health and potential microbial transmission to the infant(Dahl et al., 2017; Weerasuriya et al., 2023).

5.2 Late postpartum period (>6 weeks)

Firmicutes persisted as the most abundant phylum in the gut microbial community, including *Lachnospiraceae*, *Clostridiaceae,Streptococcaceae,* and *Ruminococcaceae.*

Ruminococcacee was found as predominant(Butts et al., 2020; Crusell et al., 2018; Paganini et al., 2019; Turroni et al., 2012). *Bacteroidetes* consistently represented the second most prevalent phylum(Butts et al., 2020; Crusell et al., 2018; Paganini et al., 2019). Crusell MKW et al. have focused on changes in gut microbiota in patients with and without GDM (**gestational diabetes mellitus**) during a period of 3–16 months postpartum. They have reported that 42 women with previous GDM had a relative lower abundance of *Firmicutes*. In the postpartum period, women with previous GDM exhibited distinct microbial alterations characterized by an **enrichment of *Collinsella*** and a **depletion of *Bacteroides*, *Faecalibacterium* and *Isobaculum***, mirroring patterns linked to later metabolic dysfunction. *Collinsella* is frequently referred to as a strictly anaerobic pathobiont that produces lactate instead of butyrate or other SCFA (short-chain fatty acids). Increases in lactate amounts induce insulin resistance in skeletal muscle by suppressing glycolysis and impairing insulin signaling(Kunasegaran et al., 2023). Notably, **Ruminococcus2 abundance decreased postpartum in the GDM group compared with normoglycaemic women**, contrasting with its previously reported enrichment in individuals with metabolic disorders. These findings suggest that the postpartum microbiota of women with prior GDM may undergo unique shifts with potential relevance for long-term metabolic risk(Crusell et al., 2018).

5.3 Comparison of gut microbiota during late pregnancy and postpartum

Comparisons between pregnancy and postpartum periods generally showed continuity in gut microbial structure(Weerasuriya et al., 2023). *Firmicutes* remained predominant across both states, although some studies observed competitive fluctuations between *Firmicutes* and *Bacteroidetes*(Crusell et al., 2018; Turroni et al., 2012). Although in a study conducted by Pan R et al. it was shown that after delivery, the relative abundance of several opportunistic pathogens—including *Escherichia/Shigella*, *Enterococcus*, and UBA1819—increased compared with pregnancy. *Escherichia/Shigella* and UBA1819 are pro-inflammatory taxa previously linked to inflammatory conditions(Pan et al., 2024).

6. Possible Mechanisms Linking Gut Microbiota and PPD

Based on the microbial changes mentioned above, several mechanisms may plausibly link postpartum microbiota alterations to PPD. The postpartum depletion of anti-inflammatory taxa such as **Faecalibacterium** and **Bacteroides**, alongside an enrichment of metabolically adverse genera such as **Collinsella**, may promote systemic inflammation, impair immune recovery, and disrupt SCFA-mediated gut–brain communication.

SCFAs, key microbiota-derived metabolites, influence the gut–brain axis by reducing inflammation and modulating neurotransmitter pathways relevant to PPD. Evidence from both animal models and human studies suggests that altered SCFA production and microbial composition can affect serotonin metabolism, HPA-axis (hypothalamic-pituitary-adrenal axis) regulation, and depression-like behaviors. Together, these findings indicate that SCFAs serve as important intermediaries in PPD pathophysiology and represent a potential target for microbiota-based interventions(Zhang et al., 2023). Experimental studies show that gut microbiota strongly influence HPA axis activity, as germ-free animals display exaggerated hormonal stress responses that can be normalized through microbial restoration. Similar findings in PPD models indicate that microbiota disturbances parallel cortisol changes, supporting a regulatory role for gut bacteria in stress-axis activation. Overall, current evidence suggests that gut microbiota can modulate PPD-related behaviors through their impact on the HPA axis(Sudo et al., 2004).

7. Microbiota Modulation as a Preventive or Therapeutic Strategy

To establish microbiota modulation as a preventive or therapeutic strategy, it is essential to identify the key factors that shape the postpartum gut microbiota. Across the analyzed studies, the dominant determinants included timing and mode of delivery, probiotic supplementation, dietary patterns, breastfeeding, and environmental exposures.

With respect to probiotics, *Bifidobacterium* and *Lactobacillus* remain the most widely used strains in clinical practice. Their administration supports gut homeostasis by promoting beneficial microbial communities, limiting pathogen adhesion, enhancing epithelial barrier integrity, and modulating immune responses. Combinations of *Bifidobacterium*, *Lactobacillus*, and *Streptococcus* have been shown to upregulate tight junction proteins such as claudin-1 and occludin while reducing pro-inflammatory cytokines including IL-6 and IL-17. Probiotic supplementation also promotes Treg expansion and increases IL-10 production(Lu et al., 2024). Notably, a study by Slykerman RF et al. demonstrated that pregnant women receiving *Lactobacillus rhamnosus* HN001 exhibited significantly lower postpartum depression and anxiety scores(Slykerman et al., 2017). Given their anti-inflammatory properties, probiotic interventions may therefore hold promise as a preventive strategy for reducing PPD incidence.

A meta-analysis further showed that higher levels of *α-Proteobacteria* appear to increase PPD risk, likely through inflammatory pathways, whereas greater abundances of *Bifidobacterium*, *Ruminococcaceae, Prevotellaceae, Veillonellaceae*, and *Clostridia* are associated with reduced risk. These protective taxa may influence maternal mood by regulating neurotransmitter synthesis, SCFA metabolism, and gut–brain axis function, thereby limiting inflammation and supporting intestinal barrier stability(Guo & Chen, 2025).

Regarding mode of delivery, current evidence indicates minimal impact on the maternal gut microbiome during the postpartum period. Comparative analyses of vaginal and cesarean deliveries reported no significant differences in microbial composition or alpha and beta diversity measures(Butts et al., 2020; Carrothers et al., 2015). In the context of preterm birth, *Firmicutes* was identified as the predominant phylum in both term and preterm deliveries; however, women with preterm birth exhibited higher relative abundances of *Firmicutes* and lower levels of *Actinobacteria*. At more specific taxonomic levels, decreased abundances of *Bifidobacterium*, *Streptococcus*, and *Clostridiales* were noted among women with spontaneous preterm delivery. In contrast, another cohort reported that *Bifidobacterium* remained the dominant genus in mothers of preterm and extremely preterm neonates(Dahl et al., 2017; Morais et al., 2020).

Collectively, the evidence linking gut microbiota composition with PPD-related inflammatory, neuroendocrine, and metabolic pathways suggests that microbiota-targeted interventions represent a promising avenue for prevention and treatment. Approaches such as probiotics, diet-based modulation, and microbiota-directed therapies may provide clinical benefit by enhancing SCFA production, reinforcing gut barrier integrity, and influencing HPA axis activity. Although further research is required, the mechanisms reviewed here indicate that targeted modulation of the microbiota could become a valuable component of PPD.

8. Unresolved questions

Despite growing evidence linking gut microbiota to postpartum depression, several key questions remain unanswered. It is unclear which microbial patterns most reliably predict postpartum depressive symptoms and whether these signatures differ across populations, delivery modes, or metabolic status. The optimal timing, duration, and specificity of microbiota-targeted interventions also remain to be determined. Furthermore, the causal pathways connecting microbial metabolites, neuroendocrine regulation, and maternal mood are not yet fully defined. Addressing these gaps will be essential for translating microbiota-based strategies into effective clinical tools for postpartum mental health.

9. Conclusions

Postpartum depression is a multifactorial disorder shaped by an interplay of psychological, social, hormonal, and biological influences. Growing evidence indicates that the gut microbiota represents an additional, previously underappreciated contributor to PPD susceptibility and symptom expression. Both pregnancy and the postpartum period are characterized by microbial shifts, and alterations such as reductions in anti-inflammatory taxa and enrichments of pro-inflammatory or metabolically adverse genera may disrupt key neuroimmune and neuroendocrine pathways implicated in PPD.

Mechanistic studies support the role of the gut microbiota in modulating short-chain fatty acid production, intestinal barrier function, neurotransmitter synthesis, and HPA axis activity, all of which are central to mood regulation and stress responsiveness(Sudo et al., 2004; Zhang et al., 2023). These findings suggest that microbiota-dependent pathways may serve as critical biological links between postpartum physiological changes and the emergence of depressive symptoms(Guo & Chen, 2025).

Given the observed associations, microbiota-targeted strategies as including probiotic supplementation, dietary interventions and lifestyle modifications all represent promising avenues for preventive and therapeutic innovation. While current evidence is encouraging, clinical validation remains limited, and future research should focus on identifying strain-specific effects, optimal timing and duration of interventions, and the long-term safety and efficacy of microbiota-based therapies in postpartum populations.

Overall, the accumulated data indicate that the gut microbiome holds significant potential as both a biomarker and a modifiable target in postpartum depression. Integrating microbiota-focused approaches into maternal mental health care may ultimately enhance early detection, reduce disease burden, and contribute to more personalized and effective management strategies for women during the postpartum period.

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