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MATERNAL GUT MICROBIOME AND ITS IMPACT ON FETAL OUTCOMES: A FOCUS ON MATERNAL NUTRITION

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Abstract

Background: During pregnancy, maternal microbiota transfer and modifiable factors such as diet may contribute to fetal development. This review aims to clarify how maternal gut microbiota and diet interact to influence fetal nutrition and long-term health outcomes. **Methods**: A literature review was conducted on PubMed, Scopus, and Google Scholar. The search focused on studies investigating the links between maternal gut microbiota composition, dietary patterns, microbial metabolites, and fetal nutrition outcomes. Keywords included “pregnancy”, “gut microbiota”, “nutrition”, “maternal diet”, and “fetal growth”. **Results:** The maternal gut microbiota undergoes notable changes in late pregnancy, and its composition can be further influenced by external factors. Maternal diet and microbial transfer may impact fetal immune, metabolic, and neurodevelopment processes. Short-chain fatty acids and trimethylamine N-oxide are among key microbial metabolites implicated in fetal development. Although probiotic and prebiotic interventions during pregnancy show promise, current evidence remains limited and inconsistent across populations. **Conclusion:** Optimizing maternal gut microbiota through diet may support fetal nutrition and developmental outcomes. However, more longitudinal and ethnically diverse studies are needed.

Keywords: Gut microbiota, pregnancy, fetal nutrition, maternal diet, dysbiosis

Introduction

Pregnancy is a critical period during which maternal physiological and metabolic states directly influence fetal development. The maternal gut microbiome, often referred to as a 'microbial organ', consists of a complex ecosystem of trillions microorganisms residing in the gastrointestinal tract, contributing to many essential functions of the host.[1] During the first thousand days of life, epigenetic programming of the fetal gut microbiome occurs, including in the *in utero* period.[2, 3]

The maternal gut microbiota has been linked to infant immune function[4,5], and neurodevelopmental outcomes later in childhood.[6,7] From the second to third trimester, it undergoes significant shifts, including reduced alpha diversity and increased inflammatory taxa, which are thought to support fetal growth through metabolic adaptation.[8, 9] These shifts are influenced by modifiable factors such as maternal diet, pre-pregnancy obesity, smoking, and stress.[10-12] However, the mechanisms by which the maternal microbiota affects fetal development and long-term health outcomes remain to be fully elucidated.

This review explores how maternal gut microbiota and diet interact to influence fetal nutrition and development. It examines microbial changes across pregnancy, modifiable maternal factors, and the potential for targeted interventions to improve maternal and fetal health.

Method

This narrative literature review synthesized current evidence on maternal gut microbiota composition, dietary patterns, microbial metabolites, and fetal nutrition outcomes. Relevant articles were identified through searches on Google Scholar, PubMed, and Scopus.

The review included studies published in English using keywords “pregnancy”, “gut microbiota”, “nutrition”, “maternal diet”, and “fetal growth”, with with a particular emphasis on human studies.

Results and Discussion

1. Changes in the gut microbiota in healthy pregnancy

The maternal body undergoes metabolic and physiological changes to support fetal growth and accumulate energy stores during a healthy pregnancy.[13] As gestation progresses, increased levels of estrogen, progesterone, prolactin, and thyroid hormones contributes to reduced insulin sensitivity and increased fat deposition.[14] Immunological adaptation during pregnancy occurs in three distinct phases: an initial pro-inflammatory state in early pregnancy to support implantation, followed by an anti-inflammatory phase during the mid-second trimester to facilitate fetal growth, and a return to a pro-inflammatory state near term.[15] A mild systemic inflammatory state in late pregnancy is partly related to adipose tissue accumulation which secretes adipokines and inflammatory mediators.[16]

In general, the healthy gut microbiome consist of six phyla, dominated by *Firmicutes* and *Bacteroidetes,* followed by *Actinobacteria, Proteobacteria, Fusobacteria,* and *Verrucomicrobia.*[17] The gut microbiome profile does not differ significantly from non-pregnant women in early pregnancy, which might be reflected by the relatively unaltered metabolism.[16, 18] In contrast, in the third trimester, individual richness (α-diversity) decreased, β-diversity increased, butyrate-producing bacteria reduced, and the stool collected was associated with greater inflammation and energy content.[18]

The relative abundance of certain bacterial groups, particularly *Proteobacteria* and *Actinobacteria*, increases during late pregnancy.[18] Elevated levels of *Proteobacteria* have been associated with increased gut permeability and a proinflammatory state.[19] However, rising levels of progesterone in late pregnancy may counterbalance this by enhancing gut barrier function through the upregulation of occludin, a key tight junction protein. Notably, progesterone is also linked to a greater abundance of *Bifidobacteria*, a beneficial genus within the *Actinobacteria* phylum.[20] Other study have reported that gestation is linked to increased abundance of the genus *Blautia* and *Streptococcus*, and a lower abundance of *Roseburia*.[21] These microbial changes are believed to contribute to the modulation of the maternal immune system and metabolic adaptations necessary for supporting a healthy pregnancy. Specifically, such changes may enhance glucose diffusion into the intestinal lumen, thereby promoting gestational weight gain and fetal development.[22]

2. Diet and factors influencing maternal gut microbime

Variations in the gut microbiome are modulated by multiple factors, including diet, age, ethnicity, antibiotic medications, metabolic phenotypes, and environmental exposures.[23] The imbalance in the gut microbial community that may contribute to the development of various diseases is termed gut dysbiosis.[24] Environmental exposures such as nicotine and microplastics increase the risk of gut dysbiosis in pregnancy.[25] Nicotine exposure decreased the abundance of *Firmicutes* and suppress the expression of genes in the colonic microbiota that are normally upregulated during pregnancy, including *FFAR2* that is activated by short-chain fatty acids (SCFAs).[26]

Maternal diet determines the gut microbiome profile in pregnancy. There is a shift to a greater abundance of acetate/ butyrate-producing bacteria in second trimester stools of women who consumed a vegetarian compared to an omnivorous diet.[27] The intake of fat and carbohydrate seem to have the greatest impact on the gut microbiome. In a study by Ruebel et al., *Paraprevotella* abundance was shown to be inversely correlated with energy and fat intake in pregnant women with normal weight.[28] *Prevotella,* a closely related genus, is highly abundant in people who consume an agrarian-type diet rich in carbohydrate and fibers,[29] highlighting its role in fermenting dietary fibers. Increased carbohydrates during pregnancy have also been associated with increased *Bacteroidetes* prior to delivery.[30] In general, a typical Western diet high in saturated fat increases *Firmicutes,* decreases *Bacteroides,* and is associated with lower levels of SCFAs.[31, 32] On the other hand, a Mediterranean diet during pregnancy was associated with greater diversity in the maternal gut microbiome and a higher abundance of bacteria responsible for producing SCFAs.[33] In overweight and obese pregnant mothers, overall diet quality was linked to a greater diversity (Shannon index) in the gut microbiome.[34] Similar finding was also observed in a study by Röytiö et al. that found adherence to fat and fiber recommendation to be related to higher microbiota richness in overweight pregnant women.[35] However, the MUMS study that examined the gut microbiome of women at Trimester 1 and 3 found no correlation between diet quality and microbial alpha diversity.[36] These discrepancies may be attributed to differences in the tools and methodologies used to assess dietary quality.

Obesity could further worsen the metabolic syndrome-like condition in pregnancy, increasing circulating levels of proinflammatory cytokines and disrupting maternal SCFAs levels.[37,38] High prematernal body mass index (BMI) is associated with higher odds of developing preeclampsia and gestational diabetes mellitus (GDM).[39-41] In people with obesity, gut membrane permeability increases. Lipopolysaccharide (LPS), a component found in the outer membrane of gram-negative bacteria, is prevalent in the gastrointestinal tract and can translocate to the circulatory system, triggering inflammation.[42] Excessive gestational weight gain (GWG) is also linked to reduced numbers of fecal bacteria abundant in lean individuals (i.e., *Bifidobacterium* and *Bacteroides*) and increased numbers of pathogenic bacteria, such as *Enterobacteriaceae* and *E.coli*.[43, 44] In another study, *Prevotella* (genus) and *Prevotellaceae* (family) were found to be reduced with excessive GWG, independent of prematernal BMI.[28]

Studies have reported alterations in the gut microbiota profiles of pregnant women with gestational disorders. For instance, in pregnant women with GDM, the abundance of *Streptococcus* has been found to significantly increase, while *Faecalibacterium* and *Lachnoclostridium* are reduced compared to healthy pregnant women.[21] *Faecalibacterium prausnitzii,* a key butyrate-producing bacterium, plays a crucial role in maintaining intestinal barrier integrity through its anti-inflammatory properties and ability to support intestinal barrier repair.[45] Similarly, in preeclampsia, the abundance of butyrate-producing bacteria is also diminished. *Prevotella*, for example, is found at lower levels in the gut microbiota of women who develop preeclampsia compared to healthy controls.[46] Butyrate promotes vasodilatation and lower oxidative stress, and It has also been associated with decreased levels of plasminogen activator inhibitor-1, contributing to blood pressure regulation during pregnancy.[47, 48]

3. Maternal gut microbiome, transgenerational transfer, and fetal development

The placenta is suggested to allow microbial transfer between mothers and fetus.

Recent findings indicated that maternal microbiome may be transferred to their offsprings in the intrauterine environment and contribute to shaping the gut microbiome of the fetus.[49-51] Research has shown that antibiotic-induced dysbiosis in the maternal gut during pregnancy is associated with a reduced transmission of microbial species from mother to infant.[52] Additionally, He et al. found that early life gut microbiota in meconium came largely from the amniotic fluid microbiota.[53]

The mechanism of transgenerational microbial transfer remain an emerging area of investigation. Yang et al. proposed that that prenatal establishment of the infant gut microbiota is determined by 1) maternal microbiome profile and 2) intrauterine environment, particularly the placenta and amniotic fluid.[54] It has been hypothesized that small molecular compounds can cross the placental barrier after entering the maternal bloodstream.[50] Trimethylamine N-oxide (TMAO), a bacterial metabolite derived from the metabolism of dietary phosphatidylcholine, choline, and carnitine (abundant in red meat and full-fat dietary product), was reported to be elevated in preeclampsia and hypertensive disorders.[55, 56] These findings suggest that increased maternal TMAO may contribute to transgenerational risk of cardiometabolic diseases. In contrast, the maternal-fetal transfer of SCFAs has been proposed to support immune development in the offspring. Moreover, fetal ingestion of amniotic fluid facilitates microbial transfer to the fetal gut, suggesting its role in establishing the infant microbiota.[53, 57] The overview of gut microbiome changes during pregnancy and their potential impact on *in utero* microbial transfer Is presented in **Figure 1.**

Maternal diet during pregnancy might influence the composition of the infant gut microbiota. Selma-Royo et al. found that higher maternal intake of fats, particularly saturated and monounsaturated fatty acids, was positively associated with the abundance of *Firmicutes* in the neonatal gut, while higher consumption of dietary fiber, plant-based proteins, and vitamins was inversely associated.[30] Among infants delivered via Cesarean section, higher dairy intake was associated with increased odds of the infant's gut microbiota being classified within the cluster of high *Clostridium* and low *Streptococcus* and *Ruminococcus*.[58] Additionally, exposure to a high-fat maternal diet during pregnancy has been linked to a significant reduction in *Bacteroides* abundance in neonates.[59]

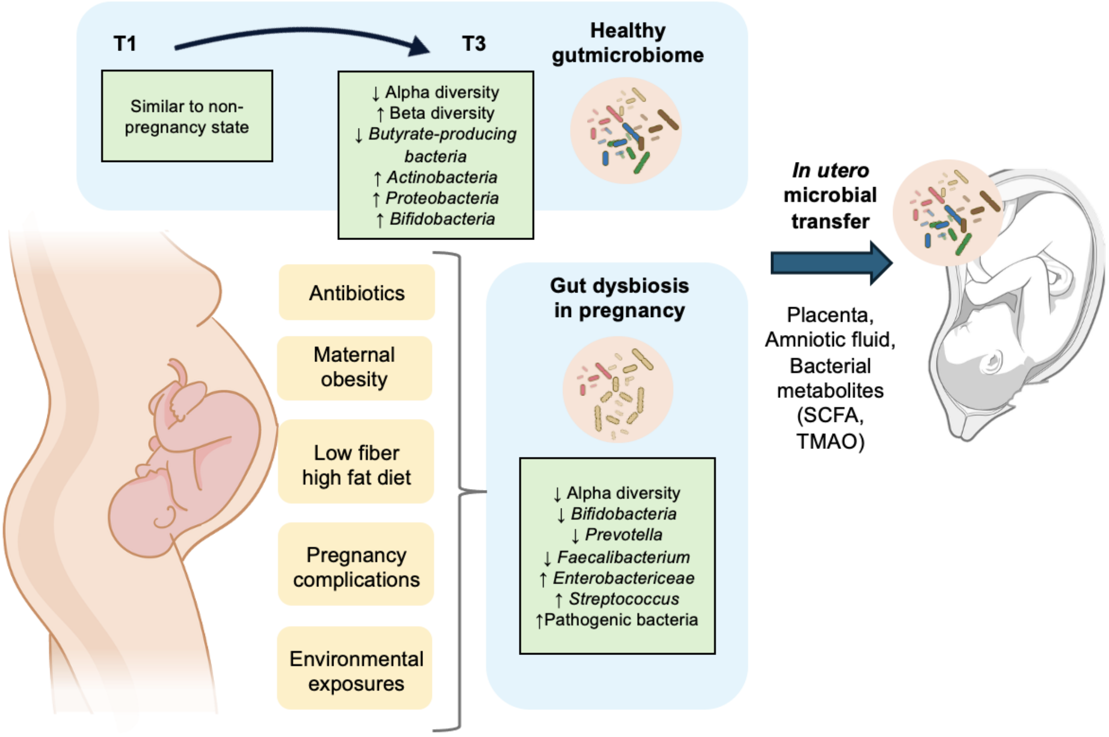

Figure 1. Overview of gut microbiome changes during pregnancy, modifying factors, and *in utero* microbial transfer. T1, first trimester; T3, third trimester; SCFA, short-chain fatty acids; TMAO, trimethylamine N-oxide

The impact of maternal diet and gut microbiome on intrauterine fetal development is subject to further research.[60] According to the Developmental Origins of Health and Disease

(DOHaD) framework, microbial communities and their metabolites may modulate epigenetic processes.[50] Maternal gut microbiota, including their metabolic products, have been linked to the offspring's immune system maturation and allergy susceptibility, although current evidence is predominantly derived from preclinical studies.[5, 61-63] Furthermore, the gut–brain axis has emerged as a promising field of study, highlighting the potential role of maternal gut health in shaping offspring neurodevelopment.[7] For instance, Dawson et al. found that a higher abundance of butyrate-producing families, *Lachnospiraceae* and *Ruminococcaceae*, in mothers was associated with normative child behaviour, and that a healthy prenatal diet was indirectly linked to reduced child internalising behaviours via increased maternal microbial diversity.[6] A detailed discussion of fetal gut–brain axis development is available elsewhere.[64] Overall, recent findings underscore the role of maternal nutrition as a key modifiable factor shaping the early-life gut microbiota and potentially the neonates long term health outcomes **(Table 1).**

Table 1. Summary of human studies investigating the interplay between maternal diet, gut microbiota, and fetal outcomes

Author (Year)	Study Population (Country)	Maternal Dietary Factors	Key Findings in Maternal Gut Microbiota	Fetal/ Infant Outcomes
Selma-Royo et al[30] (2021)	73 mother-infant pairs (Spain)	Daily intake of nutrients during pregnancy	↑ *Firmicutes*, ↓*Bacteroides* abundance with high fat intake, and low carbohydrate intake	↑Neonatal microbial richness (Chao index) with higher plant-based protein and fiber intake ↑Neonatal *Firmicutes* abundance with higher saturated/ mono-unsaturated fat intake, and lower fiber, plant-based protein, and total carbohydrate intake
Dawson et al.[6] (2021)	213 mother-child pairs (Australia)	Healthy dietary pattern during pregnancy (derived using principal	↑Maternal gut microbial diversity with	Better child behavioral outcomes were linked to

Author (Year)	Study Population (Country)	Maternal Dietary Factors	Key Findings in Maternal Gut Microbiota	Fetal/ Infant Outcomes
		component analysis)	higher healthy dietary pattern scores	maternal alpha diversity, but not to maternal dietary patterns
Lundgren et al.[58] (2018)	145 mother-infant pairs (US)	Dietary factors including alternate Mediterranean (aMED) Diet Quality Score, and food group (servings/day)	N/A	Gut microbiota in the neonates at 6 weeks of age: ↑*Streptococcus* with higher maternal fish and seafood intakes ↑*Enterobacteriaceae* and ↓*E. Coli* with higher maternal aMED scores Infant born with C-section: ↑Odds of the high *Clostridium* cluster with higher maternal dairy intake Infant born with vaginal birth: ↑Odds of the high *Streptococcus* and *Clostridium* cluster with higher maternal fruit intake
Chu et al.[59] (2016)	75 mother-infant pairs (US)	High-fat maternal diet (vs controls)	N/A	↓*Bacteroides* in the neonates at birth and at 6 weeks with high-fat maternal diet
Miller et al.[59] (2021)	41 multi-ethnic pregnant women (US)	Adherence to Mediterranean diet, using aMED Score	↑Microbial diversity and ↑ abundance of SCFA-producing bacteria with increased aMED score	N/A
Ruebel et al.[28] (2021)	140 pregnant women: 60 normal weight and 80 overweight/ obese (US)	Daily intake of nutrients during pregnancy	↑Alpha diversity indices with increased saturated fat and animal protein intake in overweight/ obese ↓*Paraprevotella,* ↑*Ruminococcus* with higher energy, total fat, and mono-unsaturated fat intake in normal weight	N/A
Laitinen and	84 pregnant women in T1 (Finland)	Dietary quality, assesses using index of diet quality (IDQ)	Higher microbiota diversity in highest IDQ	N/A

Author (Year)	Study Population (Country)	Maternal Dietary Factors	Key Findings in Maternal Gut Microbiota	Fetal/ Infant Outcomes
Mokkala[34] (2019)			quartile compared to lowest IDQ quartile	
Barrett et al.[27] (2018)	27 pregnant women: 9 vegetarians, 18 omnivores (Australia)	Vegetarian diet	↑Acetate/ butyrate producers in vegetarians compared to omnivores during early pregnancy	N/A
Röytiö et al[35] (2017)	88 pregnant overweight/ obese women in early pregnancy (Finland)	Daily intake of nutrients during pregnancy	↑Gut microbiota richness, ↓*Bacteroidaceae* abundance with adherence to dietary references of fat and fiber	N/A
Mandal et al.[65] (2016)	60 pregnant women (Norway)	Daily intake of nutrients during pregnancy	↑*Proteobacteria* at Day 4 post delivery with increased intakes of vitamin D, cholesterol, and retinol	N/A

T1, first trimester; T3, third trimester, N/A, not available; SCFA, short-chain fatty acids

↑: Increased; ↓: Decreased

4. Targeted interventions to improve maternal gut microbiome and outcomes

Probiotics and prebiotics have emerged as a potential strategy to improve maternal and neonatal health outcomes.[66-70] Probiotics are live microorganisms that confer health benefits to the host when administered in adequate amounts, whereas prebiotics are non-digestible dietary fibers that selectively promote the growth and activity of beneficial gut bacteria, particularly within the genera *Bifidobacterium* and *Lactobacillus*.[71, 72] A recent meta-analysis reported that probiotic supplementation during pregnancy improved glycemic control and was associated with a reduced rate of neonatal intensive care unit admissions among individuals with GDM.[73] Moreover, maternal intake of multi-strain probiotics was linked to a modest (4%) reduction in the risk of food allergies in offspring.[74]

Despite these promising findings, a recent umbrella review emphasized that the clinical evidence for probiotic use in pregnancy remains inconclusive, particularly regarding outcomes beyond GDM.[75] The findings from a trial of multistrain probiotic supplementation in obese pregnant women also found no significant effects on maternal or neonatal inflammatory markers or body composition, despite increased maternal microbial diversity.[76, 77] It is also important to note that the probiotic strain used in these studies varied considerably,[78] limiting the comparability of findings. Furthermore, research on prebiotic supplementation in pregnant populations remains scarce and underexplored in clinical settings.[79] Given these limitations, more robust, large-scale clinical trials are needed to better understand the effectiveness and safety of probiotic and prebiotic supplementation

Additionally, studies have reported differences in gut microbiome composition across racial and ethnic groups, which may influence responses to targeted interventions such as probiotics.[80, 81] Ethnicity-specific microbial baselines can affect the efficacy of these interventions. For example, contrary to previous findings,[18] Dunlop et al. found that gut microbiota remained stable throughout pregnancy in African American women.[82] Traditional diets rich in prebiotics may also yield varying effects. A study among healthy Indonesian adults identified *Prevotella* as a dominant genus, particularly in younger individuals,[83] likely reflecting a plant-rich diet common in non-Western populations.[84] Notably, most microbiome studies have been conducted in predominantly Caucasian populations, limiting the generalizability of findings. There is a critical need for longitudinal, multi-ethnic cohort studies to elucidate microbiome-mediated mechanisms in diverse pregnant populations.

Conclusion

The maternal gut microbiota is increasingly recognised as a key determinant of fetal development. Maternal nutrition directly shapes gut microbial composition and metabolite production, influencing fetal growth, immunity, and even neurodevelopment. Understanding these complex interactions underscores the importance of optimizing maternal gut health during pregnancy as a potential strategy to support fetal nutrition and promote favorable developmental trajectories. Although observational data support associations between microbial composition and maternal–fetal health, causality remains to be confirmed in diverse populations.

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Conflict of Interest

There is no conflict interest of this publication.

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