



Global Conference on Medical and Health Sciences

Hosted Online from Madrid, Spain

Date: 14th September, 2026

Website: <https://econferencia.com>

GUT MICROBIOME IN NAUSEA, VOMITING, AND HYPEREMESIS GRAVIDARUM DURING PREGNANCY: CURRENT EVIDENCE

Kayumova D. T.

Fayzullakhodjaeva A. O.

Tashkent State Medical University;

City Maternity Complex No. 3, Tashkent, Uzbekistan

Rakhimova Sh.M.

Kimyo International University in Tashkent, Tashkent, Uzbekistan

Abstract

Nausea and vomiting are among the most common symptoms of early pregnancy, while hyperemesis gravidarum (HG), the most severe clinical manifestation, may result in dehydration, weight loss, and metabolic disturbances. In addition to hormonal mechanisms, increasing evidence suggests that the gut microbiome may contribute to the pathophysiology of nausea and vomiting during pregnancy and HG. This review aimed to summarize current evidence regarding the association between gut microbiome composition and functional characteristics and the severity of nausea and vomiting during pregnancy, as well as the development of HG. The available evidence indicates that alterations in gut microbiome composition may be associated with nausea, vomiting, and HG. However, the causal role of these microbial alterations remains uncertain.

Keywords: Gut microbiome; nausea and vomiting during pregnancy; hyperemesis gravidarum; 16S rRNA sequencing; shotgun metagenomics; Mendelian randomization; PUQE.



Global Conference on Medical and Health Sciences

Hosted Online from Madrid, Spain

Date: 14th September, 2026

Website: <https://econferencia.com>

Introduction

Nausea and vomiting are among the most prevalent symptoms of early pregnancy. Hyperemesis gravidarum, the most severe form of nausea and vomiting during pregnancy, is characterized by an inability to maintain adequate oral intake, dehydration, weight loss, and metabolic disturbances. Hormonal factors, particularly growth differentiation factor 15 (GDF15), play an important role in its pathophysiology. However, substantial interindividual variation in symptom severity suggests that additional mechanisms, including alterations in the gut microbiome, may also be involved.

Materials and Methods

A narrative review of original studies investigating the gut microbiome in nausea and vomiting during pregnancy and HG was performed. Studies employing 16S rRNA gene sequencing, whole-genome shotgun metagenomic sequencing, and two-sample Mendelian randomization were reviewed. Study design, sample characteristics, alpha- and beta-diversity, associated microbial taxa, functional metabolic pathways, and limitations affecting causal interpretation were compared.

Results

The reviewed studies demonstrated differences in gut microbiome composition among women with HG and among pregnant women with varying severity of nausea and vomiting. However, findings regarding alpha-diversity were inconsistent across studies. In a small 16S rRNA sequencing study, women with HG demonstrated higher Shannon, ACE, and Chao1 indices. In contrast, the larger SweMaMi study reported a decrease in microbial species richness and



Global Conference on Medical and Health Sciences

Hosted Online from Madrid, Spain

Date: 14th September, 2026

Website: <https://econferencia.com>

Shannon diversity with increasing Pregnancy-Unique Quantification of Emesis and Nausea (PUQE) scores.

Shotgun metagenomic analyses indicated that symptom severity was associated with specific microorganisms, including *Bifidobacterium dentium*, *Prevotella copri*, and *Blautia* spp., as well as microbial metabolic pathways related to glutamine degradation, inositol biosynthesis, and lactate production. Two-sample Mendelian randomization analyses suggested potential inverse associations between certain microbial taxa and the risk of HG, while *Coprococcus2* showed a potential protective association.

Interpretation of these findings requires consideration of potential confounding factors, including dietary patterns, psychological status, and medication use, particularly proton pump inhibitors. Because these factors cannot be completely separated from microbiome alterations in observational studies, it remains unclear whether the observed microbial changes contribute to the development of symptoms or occur as a consequence of them.

Conclusion

Current evidence supports an association between the gut microbiome and nausea, vomiting, and hyperemesis gravidarum during pregnancy. The gut microbiome may represent one component of the multifactorial pathophysiology of HG. Nevertheless, the available evidence is insufficient to establish specific microbial alterations as diagnostic or therapeutic biomarkers. Large-scale prospective and interventional studies are needed to clarify the temporal and causal relationships between gut microbiome alterations and HG and to determine their potential clinical relevance.



Global Conference on Medical and Health Sciences

Hosted Online from Madrid, Spain

Date: 14th September, 2026

Website: <https://econferencia.com>

References

1. Fejzo M., Rocha N., Cimino I., et al. GDF15 linked to maternal risk of nausea and vomiting during pregnancy. *Nature*. 2024;625:760–767.
2. González-Valdivia C., Tong B., Hjalmarsson S., et al. The gut microbiome in early pregnancy is associated with the severity of nausea and vomiting: a nested case-control study. *Gut Microbes Rep*. 2025;3(1):2603861.
3. Koçak Ö., Sharafi P., Gökdemir Ş., et al. Changes in gut microbiome profile in pregnant women with hyperemesis gravidarum: a comparative study based on 16S rRNA sequencing. *Mikrobiyol Bul*. 2026;60(1):53–71.
4. Xu D., Zhang L., Zhang J. Causal association between gut microbiota and hyperemesis gravidarum: a two-sample Mendelian randomization study. *Front Microbiol*. 2024;15:1307729.
5. Koren O., Goodrich J.K., Cullender T.C., et al. Host remodeling of the gut microbiome and metabolic changes during pregnancy. *Cell*. 2012;150(3):470–480.