THE ROLE OF GUT MICROBIOTA IN CHRONIC GASTRITIS: RECENT ADVANCES AND FUTURE PERSPECTIVES

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Abstract: *Chronic gastritis is a common gastrointestinal disorder characterized by persistent inflammation of the gastric mucosa. Although Helicobacter pylori remains the primary etiological factor, increasing evidence suggests that alterations in the gastric and intestinal microbiota significantly influence disease progression, immune responses, and therapeutic outcomes. Advances in next-generation sequencing technologies have expanded our understanding of microbial diversity and its relationship with gastric inflammation.*

This review summarizes current evidence regarding the role of gut microbiota in chronic gastritis, emphasizing microbial dysbiosis, immune regulation, host–microbiome interactions, and emerging microbiota-based therapeutic approaches. Current findings indicate that modulation of gut microbiota through probiotics, prebiotics, dietary interventions, and microbiome-targeted therapies may represent promising adjunctive strategies in chronic gastritis management.

Keywords: *Chronic gastritis, gut microbiota, dysbiosis, Helicobacter pylori, probiotics, gastrointestinal microbiome.*

Introduction

Chronic gastritis affects millions of individuals worldwide and remains one of the leading causes of upper gastrointestinal morbidity. Traditionally, Helicobacter pylori infection has been considered the principal cause of chronic gastritis. However, recent studies have demonstrated that the gastric environment contains a diverse microbial ecosystem that contributes to mucosal homeostasis and disease development. The gut microbiota consists of trillions of microorganisms that regulate immune function, nutrient metabolism, epithelial barrier integrity, and inflammatory responses. Disturbances in microbial composition, commonly referred to as dysbiosis, have been associated with various gastrointestinal disorders, including chronic gastritis, peptic ulcer disease, inflammatory bowel disease, and gastric cancer.

Modern sequencing technologies have revealed that alterations in microbial diversity may influence the severity of gastric inflammation, bacterial virulence, treatment response, and long-term clinical outcomes.

Aim of the Study

To review current scientific evidence regarding the role of gut microbiota in chronic gastritis and evaluate emerging microbiota-based therapeutic strategies.

Materials and Methods

A narrative review of scientific literature was conducted using PubMed, Scopus, Web of Science, and Google Scholar databases. Publications between 2020 and 2026 related to chronic gastritis, gut microbiota, gastric microbiome, dysbiosis, probiotics, prebiotics, and Helicobacter pylori infection were included.

Original clinical studies, systematic reviews, meta-analyses, and international consensus guidelines published in English were evaluated. Conference abstracts, duplicate studies, editorials, and publications lacking adequate methodological quality were excluded. Information regarding microbiota composition, inflammatory pathways, diagnostic methods, therapeutic interventions, and clinical outcomes was extracted and critically analyzed.

Results

Current evidence demonstrates that patients with chronic gastritis exhibit significant alterations in both gastric and intestinal microbial composition. Besides Helicobacter pylori, several bacterial genera including Streptococcus, Lactobacillus, Prevotella, Veillonella, and Fusobacterium have been associated with different stages of gastric inflammation. Reduced microbial diversity has been linked to increased inflammatory cytokine production, oxidative stress, epithelial barrier dysfunction, and progression toward gastric atrophy and intestinal metaplasia.

Several clinical studies have demonstrated that probiotic supplementation during H. pylori eradication therapy improves treatment tolerance, reduces gastrointestinal adverse effects, and may modestly increase eradication success.

Prebiotic-rich diets and dietary fiber have also been shown to promote beneficial microbial populations, enhance mucosal integrity, and reduce inflammatory activity.

Emerging microbiome-based diagnostic biomarkers have shown potential for identifying patients at increased risk of disease progression and gastric carcinogenesis.

Discussion

The human gastric microbiome has become an important focus of modern gastroenterological research. While Helicobacter pylori remains the dominant pathogen, increasing evidence indicates that disease progression results from complex interactions among microbial communities, host immunity, environmental factors, and genetic susceptibility.

Gut microbiota influences both innate and adaptive immune responses through regulation of cytokine production, dendritic cell activation, T-cell differentiation, and production of short-chain fatty acids. Dysbiosis may therefore contribute to chronic inflammation and impaired mucosal healing.

Probiotics containing Lactobacillus, Bifidobacterium, and Saccharomyces boulardii have demonstrated beneficial effects by restoring microbial balance, reducing inflammation, and improving eradication therapy tolerance. Nevertheless, variations in probiotic strains, treatment duration, and study methodology limit direct comparison among clinical trials.

Future therapeutic strategies may include personalized microbiome modulation, precision nutrition, microbial metabolite analysis, fecal microbiota transplantation in selected conditions, and artificial intelligence-assisted prediction of treatment response. Further multicenter randomized controlled trials are required to establish standardized microbiota-based treatment recommendations for chronic gastritis.

Conclusion

Growing evidence supports the important role of gut microbiota in the pathogenesis and progression of chronic gastritis. Microbial dysbiosis contributes to immune dysregulation, persistent inflammation, and impaired gastric mucosal integrity. Microbiota-targeted interventions, including probiotics, prebiotics, dietary modification, and personalized therapeutic approaches, represent promising complementary strategies for chronic gastritis management. Continued research into host–microbiome interactions will improve diagnostic accuracy and facilitate the development of innovative therapeutic options.

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