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Editorial: Gut microbiota and gastrointestinal disorders, volume II

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Editorial on the Research Topic
Gut microbiota and gastrointestinal disorders, volume II

The human gut microbiota, an intricate ecosystem of bacteria, viruses, fungi, and archaea, plays a pivotal role in maintaining gastrointestinal (GI) homeostasis (1). Recent advances in microbiome research have revealed its profound influence on various GI diseases, such as gastric cancer, inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), acute pancreatitis, and *Clostridioides difficile* infection (CDI) (2). Understanding the interplay between the gut microbiota and these conditions offers promising avenues for novel therapeutic interventions, including next-generation probiotics, fecal microbiota transplantation (FMT), and targeted microbiome-directed modulation (3, 4).

Gastric cancer remains a significant global health burden, ranking as the fourth leading cause of cancer-related mortality. Dysbiosis, characterized by altered microbial diversity and composition, is a hallmark of gastric carcinogenesis (Marashi et al.). *Helicobacter pylori* infection is a well-established risk factor, but eradication alone does not fully restore microbial equilibrium. Studies suggest that certain bacterial species, such as *Lactobacillus*, enhance the response to immunotherapy, whereas antibiotic-induced dysbiosis may reduce the efficacy of chemotherapy (Marashi et al.) (5, 6). Probiotic supplementation after gastrectomy has demonstrated the potential to mitigate inflammation and foster a healthier microbial milieu (Marashi et al.) (7).

IBDs, which include Crohn's disease and ulcerative colitis, are immune-mediated diseases driven by a complex interplay of genetic, environmental, and microbial factors (Ning et al.) (8). Dysbiosis in IBDs is marked by a reduction of beneficial Firmicutes and Bacteroidetes and an overrepresentation of pathogenic Proteobacteria and Actinobacteria (Ning et al.). The intricate crosstalk between gut microbiota and intestinal macrophages plays a crucial role in disease pathogenesis by influencing inflammation and immune responses (Ning et al.). Current therapeutic strategies, including 5-aminosalicylic acid, immunomodulators, and biologics, inadvertently alter gut microbiota composition, highlighting the need for microbiome-targeted interventions such as FMT and prebiotic supplementation (Ning et al.) (9).

IBS, a prevalent functional GI condition, is increasingly linked to microbial imbalances (Cheng et al.). Patients exhibit reduced microbial diversity and a distinct shift in gut microbiota composition, with lower *Bifidobacterium* and *Lactobacillus* levels and increased levels of Enterobacteriaceae (Cheng et al.). Notably, alterations in the gut microbiota vary based on ethnic background, as demonstrated in comparative studies between Han and Tibetan populations (Ma et al.). The distinct gut microbial profiles among ethnic groups indicate that cultural and dietary habits influence the gut microbiota and, consequently, disease susceptibility. Probiotics, prebiotics, and dietary modifications have shown efficacy in restoring microbial equilibrium and alleviating IBS symptoms (Cheng et al.).

Acute pancreatitis (AP) is an inflammatory condition with rising global incidence. The gut microbiota plays a critical role in AP pathogenesis through mechanisms involving increased intestinal permeability, bacterial translocation, and systemic inflammation (Li et al.). Dysbiosis in AP is associated with severe complications, including multiple organ dysfunction syndrome (10). Innovative therapies, such as gut microbiota-derived extracellular vesicles, show promise in mitigating AP severity by modulating immune responses (Li et al.). By targeting the underlying microbial imbalances, these therapeutic approaches may significantly improve patient outcomes in AP management (11).

CDI, a leading cause of healthcare-associated diarrhea, is predominantly driven by antibiotic-induced gut dysbiosis (Duo et al.). The loss of microbial diversity facilitates *C. difficile* colonization, leading to recurrent infections in a significant proportion of patients. FMT has emerged as the most effective therapy for recurrent CDI (rCDI), surpassing antibiotics in efficacy by restoring a balanced gut microbiome (Duo et al.) (12). Despite its success, concerns regarding standardization and safety necessitate further research into microbiota-based therapeutics (Duo et al.).

The intricate relationship between the gut microbiota and metabolic functions extends beyond the GI tract. Emerging research has explored the bidirectional connection between the gut microbiota and insulin-like growth factor 1 (IGF-1), a key regulator of metabolic and growth-related pathways (Zheng et al.). Dysbiosis has been implicated in modulating IGF-1 levels, suggesting potential metabolic consequences of gut microbial imbalances. This finding broadens the scope of microbiome-targeted therapies to include metabolic disorders alongside GI diseases.

The expanding knowledge on the role of gut microbiota in GI disorders underscores the need for precision medicine approaches. Personalized microbiome profiling could guide tailored interventions to optimize therapeutic outcomes. Probiotics, prebiotics, synbiotics, and next-generation microbiome-based therapies, including engineered bacterial consortia and postbiotics, offer exciting prospects. Moreover, advances in metagenomics and metabolomics will further elucidate host-microbe interactions, paving the way for novel therapeutic strategies (13).

In conclusion, the published studies in this Research Topic highlight the intricate role of the gut microbiota as an integral determinant of human GI health and disease. From gastric cancer to IBS and IBD, the influence of the gut microbiome is profound and multifaceted (Stange et al.). Harnessing microbiome-based interventions holds immense potential to revolutionize the management of GI conditions, shifting from symptomatic treatment to root-cause modulation (14). As research continues to unravel the complexities of the gut microbiota, the future of gastroenterology lies in leveraging this microscopic powerhouse for transformative healthcare solutions.

Author contributions

AY: Conceptualization, Funding acquisition, Investigation, Project administration, Resources, Supervision, Validation, Writing – original draft, Writing – review & editing. AS-N: Writing – original draft. Y-DW: Writing – review & editing. JO-R: Writing – review & editing.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

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