ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

Clinical Applications, Host-Microbiome Interactions, and Current Developments in Intestinal Microbiology (review)

Salim Shamkhi Jaafar[1]

[1] DNA Research Center/ Universityo Babylon, Alhilla, Babylon ,Iraq.

***Corresponding author**

DOI: https://doi.org/10.51583/IJLTEMAS.2026.151100058

Received: 01 November 2026; Accepted: 06 November 2026; Published: 26 November 2026

ABSTRACT

The highly diverse and dynamic microbial community residing in the human gut is vital to host health through its roles in nutrient metabolism, immune modulation, pathogen resistance, maintenance of epithelial barrier integrity, and systemic physiological activities. Intestinal microorganisms communicate with host tissues through direct interactions and the production of bioactive metabolites, such as short-chain fatty acids, bile acid derivatives, and tryptophan-derived metabolites, which regulate mucosal immunity, epithelial homeostasis, metabolism, and the gut–brain axis. Changes in microbial composition and function, known as dysbiosis, are strongly linked to inflammatory bowel disease. Clinical applications of microbiome research are growing quickly, including metabolic disorders, colorectal cancer, Clostridium difficile infection, and other chronic illnesses. Standardized microbiome-based treatments and fecal microbiota transplantation have demonstrated notable effectiveness, especially for recurrent C. difficile infection. Probiotics, prebiotics, postbiotics, defined microbial consortia, engineered microorganisms, bacteriophage therapy, microbial metabolites, and microbiome-based diagnostics are additional emerging approaches. Despite these developments, significant obstacles still exist, such as inter-individual variability, challenges in establishing causal relationships, methodological heterogeneity, safety concerns, and the requirement for standardized clinical protocols,this review summarizes recent advances in intestinal microbiology, host–microbiome interactions, microbial metabolites, dysbiosis-associated diseases, and current and emerging therapeutic applications, highlighting the potential of microbiome science to support precision medicine and improve disease prevention, diagnosis, and treatment.

Keywords: intestinal microbiology; gut microbiota; gut microbiome; host–microbiome interactions; dysbiosis; microbial metabolites; intestinal barrier; probiotics; fecal microbiota transplantation

METHODOLOGY

This review was conducted as a narrative synthesis of the literature, aiming to summarize recent developments in gut microbiology, host-microbiome interactions, microbial metabolites, diseases associated with microbial dysbiosis, and microbiome-based therapeutic approaches. A comprehensive literature search was performed using electronic databases, including PubMed/MEDLINE, Scopus, Web of Science, and Google Scholar. The search focused primarily on recently published articles, while also incorporating foundational earlier studies where necessary to provide historical context The search strategy combined Medical Subject Headings (MeSH) with free-text keywords,

1. INTRODUCTION

Microbes are far more abundant within the human digestive system than in other parts of the body. It contains bacteria, archaea, fungi, viruses, bacteriophages, and other microorganisms that interact continuously with the host. The collective microbial community is generally referred to as the intestinal microbiota, while its genetic content and functional potential are described as the intestinal microbiome The intestinal microbiome is

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

influenced by numerous factors, including age, genetics, diet, geographical environment, medication exposure, immune status, lifestyle, and disease. Consequently, substantial variation exists between individuals. Nevertheless, important functional pathways are shared among individuals, suggesting that microbial ecosystems may differ taxonomically while maintaining partially overlapping metabolic capabilities (1(

The human microbiome is now recognized as a dynamic biological system rather than a passive collection of microorganisms. It participates in digestion, nutrient metabolism, maintenance of the intestinal barrier, immune development, protection against pathogens, and communication with distant organs (1,2) Advances in sequencing and computational technologies have substantially expanded knowledge of this ecosystem and demonstrated that microbial functions may be more informative than microbial taxonomic composition alone----During recent years, intestinal microbiology has increasingly moved toward clinical translation. Multi-omics approaches and mechanistic studies have identified microbial signatures associated with disease and have provided new strategies for modifying microbial ecosystems. FDA-approved microbiome therapies for recurrent C. difficile infection represent an important milestone in this transition (2,3).

2. THE INTESTINAL MICROBIOTA'S ORGANIZATION AND COMPOSITION

The vast community of bacteria that make up the intestinal microbiota varies in density and composition throughout the gastrointestinal tract. Due to gastric acidity, bile, digestive enzymes, and quick intestinal transit, the stomach and proximal small intestine have comparatively low microbial populations. The distal small intestine is where microbial abundance rises, and the colon is where it peaks ,Accordingly it is appropriate to view the gut microbiota as a dynamic ecosystem influenced by a variety of environmental factors, as well as by responses to dietary changes, inflammation, infection, and antibiotic use; researchers have found that gut health is significantly affected by microbial resilience and ecological stability (1).The phyla Bacillota, Bacteroidota, Actinomycetota, and Pseudomonadota comprise major groupings of bacteria. Individual differences in microbial makeup, however, are substantial.

Microorganisms inhabit specific niches in the intestinal lumen, the mucus layer, and the contact with the epithelial cells, demonstrating the spatial organization of the gut ecosystem, Microorganisms in the intestinal lumen are more heavily impacted by nutrients and luminal contents, while those near epithelial cells can interact directly with host receptors and immune cells. This spatial arrangement is of enormous biological consequence (1, 4).

3. ADVANCES IN INTESTINAL MICROBIOLOGY

3.1: 16S rRNA Sequencing

Given the inability of many gut bacteria to grow on traditional culture media, the emergence of gene sequencing-based technologies particularly metagenomic sequencing targeting the 16S rRNA gene has helped overcome some of these challenges and brought about a paradigm shift in microbiome research. Advanced sequencing techniques based on 16S rRNA have also contributed to establishing the pivotal role of the gut microbiome in human health; the Human Microbiome Project (an initiative of the National Institutes of Health) and the MetaHIT project European initiative) helped create a foundational framework for microbiome analysis, paving the way for numerous studies aimed at defining the role of the gut microbiome in human health and disease(5),The earliest and most widely used approach for microbiome profiling is 16S ribosomal RNA (16S rRNA) gene sequencing.

This method targets conserved and hypervariable regions of the bacterial 16S rRNA gene, allowing taxonomic identification and estimation of microbial diversity within a sample. Due to its relatively low cost, straightforward workflow, and suitability for large-scale studies, 16S rRNA sequencing has become the standard technique for investigating bacterial community composition. However, it is generally limited to bacterial and archaeal identification, provides relatively low taxonomic resolution at the species level, and does not directly reveal the functional capabilities or metabolic activities of the microbiome (6,7).

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

3.2. Shotgun Metagenomic Sequencing

Advances in sequencing technology led to the development of shotgun metagenomic sequencing, which analyzes all genomic DNA present in a biological sample rather than targeting a single marker gene. This approach enables comprehensive characterization of bacteria, archaea, fungi, viruses, and other microorganisms while simultaneously identifying genes involved in metabolic pathways, antimicrobial resistance, and virulence. Compared with 16S rRNA sequencing, shotgun metagenomics offers higher taxonomic resolution, often reaching species- or strain-level identification, and provides valuable insights into the functional potential of microbial communities. Nevertheless, this method is more expensive and requires substantial computational resources and sophisticated bioinformatics analyses (6,8,9).

3.3. Metatranscriptomics

More recently, metatranscriptomics has emerged as an advanced multi-omics approach for investigating the functional activity of microbial communities. Unlike DNA-based methods, metatranscriptomics sequences messenger RNA (mRNA) extracted from a sample, thereby identifying genes that are actively expressed at the time of sampling. Consequently, this technique provides direct information about microbial metabolism, physiological activity, and host–microbe interactions under specific environmental or disease conditions. Despite these advantages, metatranscriptomics is technically challenging because RNA molecules are highly unstable and require careful sample collection, preservation, and specialized computational analyses (10,11,12). The evolution from 16S rRNA gene sequencing to shotgun metagenomics and subsequently metatranscriptomics reflects the transition from determining "who is present", to "what genetic functions are encoded", and ultimately "which genes are actively functioning" within the gut microbiome (6,11). These sequencing technologies have been instrumental in establishing the pivotal role of the gut microbiome in human health and disease. Large international initiatives, including the Human Microbiome Project (HMP) and the Metagenomics of the Human Intestinal Tract (MetaHIT) project, established standardized methodologies and comprehensive reference datasets that have significantly accelerated microbiome research and facilitated the identification of microbial biomarkers associated with numerous diseases (13).

3.4: Shotgun Metagenomics

Shotgun metagenomic sequencing is a current and practical technique to environmental DNA sequencing, enabling better insight into the richness and activities of microbial communities. However, because of the complexity of the data, evaluating metagenomic sequences is difficult. Thankfully, these difficulties have been addressed by the development of new instruments and data sources, which allow researchers to identify the microorganisms that are present in a community and ascertain their possible role(14)**.**

3.5: Metatranscriptomics

Metatranscriptomics analyzes microbial RNA and therefore provides information regarding genes that are actively expressed. This is important because the presence of a microbial gene does not necessarily indicate that its associated pathway is biologically active, The term "metatranscriptomics" refers to the set of techniques used to study microbial gene expression in natural environments—specifically, the study of the complete set of active gene transcripts(15)**.**

3.6: Metabolomics

Metabolomics examines small molecules produced by microorganisms, the host, or their interaction. This approach is particularly valuable because microbial metabolites provide a functional link between microbial activity and host physiology (16).

3.7: Culturomics

To obtain a comprehensive picture of the diversity of the gut microbial ecosystem and to study this complex system, it is necessary to combine both culture-based and molecular (culture-independent) techniques(17).

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

4. MICROBIAL METABOLITES

Microbial metabolites are among the most important mediators of host–microbiome communication. Important groups include short-chain fatty acids, bile acid derivatives, tryptophan metabolites, polyamines, and other bioactive molecules (18).

4.1: Short-Chain Fatty Acids

Short-chain fatty acids (SCFAs) serve as important mediators between the gut microbiota and epigenetic states. Mutations in acetyltransferase enzymes can lead to the silencing of normal genes (such as tumor suppressor genes). Numerous studies have demonstrated that SCFAs can inhibit histone deacetylase enzymes albeit to varying degrees, with butyrate being the most potent thereby playing a significant role in suppressing cancer cell proliferation, influencing cell differentiation, regulating insulin secretion, and maintaining immune homeostasis in addition to enhancing the production of interleukin-22(19).

4.2: Bile Acid Metabolism

The intestinal microbiota transforms primary bile acids into secondary and other modified bile acids. These molecules can interact with host receptors such as FXR and TGR5 and thereby influence metabolism, immunity, and epithelial function ,Recent research has revealed considerable diversity in microbial bile acid metabolism, increasing interest in specific bacterial enzymes as potential therapeutic targets (20).

4.3: Tryptophan Metabolism

Numerous metabolites that are involved in many facets of human nutrition and metabolism are derived from tryptophan. Tryptophan metabolites, particularly serotonin (5-hydroxytryptamin), may play a part in intestinal (patho) physiology, according to mounting data, albeit the exact mechanisms of action are still unclear. Gastrointestinal disorders may result from changes in serotonin metabolism.Other tryptophan metabolites, namely those from the kynurenine pathway, have been shown to be involved in controlling gut function(21)According to a research by Liu et al., fecal microbiota transplantation (FMT) shields the colonic epithelial barrier and stops inflammatory cell death caused by lipopolysaccharide (LPS). Mechanistically, FMT modifies the gut microbiota by raising the levels of tryptophan metabolites (ILA, IAld, and IAA) and *Lactobacillus reuteri* in the colon. This prevents inflammatory cell death and protects the intestinal epithelial barrier. Notably, the benefits of *Lactobacillus reuteri* and its tryptophan metabolites in reducing inflammatory cell death depend on the AhR/NLRP3 axis (22).

5. THE INTESTINAL BARRIER

The intestinal barrier consists of mucus, epithelial cells, tight junctions, antimicrobial molecules, and immune components. Its major function is to allow controlled absorption of nutrients while preventing inappropriate penetration of microorganisms and harmful molecules.

Microbial metabolites can strengthen epithelial barrier function, whereas dysbiosis may contribute to altered permeability, epithelial injury, and inflammation (23)The relationship between barrier integrity and disease is particularly important in inflammatory bowel disease. However, increased intestinal permeability should be considered one component of a complex disease process rather than a universal cause of all gastrointestinal disorders.

6. MICROBIOME AND MUCOSAL IMMUNITY

The first line of defense in the organism's physiological barrier is the mucus layer that covers the surface of epithelial cells. In reaction to bacteria or pathogens in the gut lumen, Paneth cells at the base of crypts in the small intestine epithelia can secrete antimicrobial peptides (AMPs), which aid in intestinal innate host defense,The AMPs include lysozymes, RegIII, and α-defensins (HD5 and HD6 in humans and cryptdins in mice) The mucosal barrier that keeps symbiotic bacteria out is made up of the mucus layer and AMPs.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

Innovative research has shown that AMPs play a significant role in the host mucosal defense, suggesting that they have a direct impact on the intestinal lumen's microbiome, Epithelial cells signal the mucosal immune system by producing cytokines and chemokines; these cytokines play either a defensive or a pathogenic role during inflammation. Epithelial cells produce interleukin-22, which contributes to maintaining homeostasis and promoting healing processes during intestinal infections. (24).

7. DYSBIOSIS AND DISEASE

Maintaining intestinal homeostasis requires continual interaction between mucosal immunity and gut bacteria. However, intestinal immune dysfunction can result in a number of illnesses, including inflammatory bowel disease (IBD), once this equilibrium is upset. Intestinal inflammation caused by an aberrant immune response is the hallmark of IBD, a group of disorders affected by genetic, environmental, and microbiological factors. IBD is commonly associated with Crohn's disease (CD) and ulcerative colitis (UC)(25) According to studies, dysbiosis, or an imbalance in the gut microbiota, causes an aberrant adaptive immune response that worsens inflammation and damages the digestive tract. As a result, altering the gut microbiota has become a successful method of preventing and treating inflammation. Fecal microbiota transplantation (FMT) is one of these approaches that is thought to be a successful IBD therapy [26] Recent studies have demonstrated that a key gene regulating the development of IBDspecifically the gene encoding the CARD9 protein (Caspase Recruitment Domain-containing protein 9) is responsible for intracellular signaling that triggers inflammation. Alterations in gut microbiota composition and increased susceptibility to intestinal fungal infections have been observed in mice lacking the *CARD9* gene, suggesting that the deletion of this gene leads to microbiota imbalance associated with inflammatory bowel disease (27).

8. INFLAMMATORY BOWEL DISEASE

Inflammatory Bowel Disease (IBD) comprising Crohn's Disease (CD) and Ulcerative Colitis (UC) is a group of disorders characterized primarily by chronic intestinal inflammation that affects individuals across various age groups. Its prevalence continues to rise globally, particularly in industrialized regions; this not only negatively impacts patients' quality of life but also emerges as a major public health issue and a significant burden on healthcare systems, necessitating the development of new, safer, and more effective therapies. Worldwide, the number of IBD cases has reached 6.8 million. Persistent inflammation of the intestinal mucosa and tissue damage are the primary pathological features of the disease. At the microbiological level, structural changes and functional disturbances in the gut microbiota have been identified as key drivers of the onset and persistence of inflammation, operating through metabolic interactions and immune regulatory pathways. Furthermore, the overproduction of reactive oxygen species (ROS) and an imbalance in the antioxidant system not only cause direct damage to intestinal mucosal cells but also influence immune cell differentiation and intestinal barrier repair by modulating signaling pathways, thereby creating a vicious cycle that exacerbates inflammation. The figure below illustrates some characteristics of these molecular regulatory pathways and their interrelationships(28).

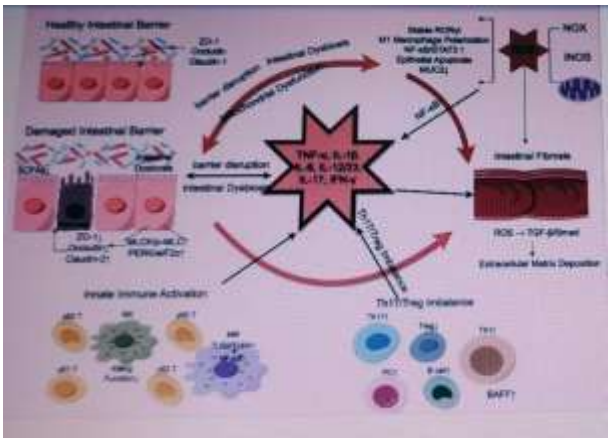

Figure (1) Core pathogenic circuitry in inflammatory bowel disease. In the healthy state, the epithelial

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

barrier is sealed by high ZO-1, Occludin and Claudin-1, crowned by a dense mucus layer rich in short-chain fatty acid–producing commensals. Disease begins with barrier disintegration: tight-junction proteins are down-regulated, Claudin-2 is aberrantly up-regulated, MLCK and PERK/eIF2α stress pathways are activated, and epithelial apoptosis increases while butyrate-generating microbiota decline and pathobionts expand. Subjacent lamina-propria macrophages sense translocating microbes via TLR2/4, triggering NF-κB–dependent release of TNF-α, IL-1β, IL-6 and IL-23. NK and γδ-T cells lose cytotoxic competence yet secrete IL-17. Th1 and Th17 lineages expand, Treg cells are functionally silenced, and BAFF-stimulated plasma cells accumulate, generating a cytokine storm. NADPH oxidase, inducible nitric-oxide synthase and dysfunctional mitochondria jointly produce reactive oxygen species that stabilize RORγt, sustain M1 macrophage polarization, activate STAT3, deplete MUC2, and, via TGF-β/Smad signalling, drive extracellular-matrix deposition and intestinal fibrosis (28).

9. CLOSTRIDIOIDES DIFFICILE INFECTION

Due to overlapping symptoms, difficult diagnosis, and unique treatment concerns, Clostridium difficile infection (CDI) presents a significant clinical issue in patients with inflammatory bowel disease (IBD). Disrupted gut microbiota, immunological dysregulation, and disease-specific risk factors are all involved in the relationship between CDI and IBD. CDI in IBD results from a complicated combination of microbiological, immunological, and therapeutic variables. Improving care and prevention in this high-risk group requires an understanding of these processes(29)**.**

10. COLORECTAL CANCER AND GUT MICROBIOTA

The second most common cause of cancer-related deaths worldwide and the third most common kind of cancer, colorectal cancer is more common in developed countries than in developing ones. Obesity, a high-fat diet, smoking, and excessive alcohol intake are among the variables that are thought to be associated with colon carcinogenesis. Elevated levels of β-catenin, c-Myc, and proliferating cell nuclear antigen (PCNA), transcription factors or proteins linked to the development of cancer, have been seen in colon cells cultured with the bacteria Streptococcus gallolyticus (30, 31).

11. METABOLIC DISEASES

The generation of SCFA, bile acid conversion, host energy metabolism, and inflammatory control are all influenced by the gut flora. As a result, changes in intestinal microbial populations have been linked to type 2 diabetes, obesity, and insulin resistance ,One of the most powerful environmental factors influencing microbial metabolism is diet. Although dietary patterns dominated by highly processed foods may change microbial composition and metabolic output, dietary fiber can encourage fermentation and the production of microbial metabolites (32). However, the relationships between microbiome and metabolic diseases are extremely complex, and microbiome-based treatments necessitate customized approaches.

12. GUT–BRAIN AXIS

The gut microbiome communicates with the nervous system through immune, endocrine, neural, and metabolic pathways. Microbial metabolites can influence neuroactive signaling and systemic inflammation (33) Disruption of the gut-brain axis has been linked to autism spectrum disease, according to some research. The profiles of amino acids, carbohydrates, and fats linked to autism spectrum disorder, which are primarily encoded by microbial species from the genera Prevotella, Bifidobacterium, Desulfobacterium, and Bacteroides, are linked to changes in brain gene expression and restricted dietary patterns. Morton, J. T and his colleagues discovered a functional structure along the GBA axis that is associated with the diversity of autism spectrum disorder patterns. and profiles of proinflammatory cytokines (34)Research on the gut–brain axis has expanded rapidly, but many reported associations remain observational. Future studies must establish whether specific microbial alterations directly contribute to neurological or psychiatric conditions or instead reflect dietary, behavioral, or medication-related changes.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

13. PROBIOTICS, PREBIOTICS, SYNBIOTICS, AND POSTBIOTICS

Probiotics are live microorganisms administered with the intention of providing health benefits. Their effects are strain-specific, and evidence supporting one strain should not automatically be generalized to an entire species,Prebiotics are substrates selectively utilized by microorganisms and can promote beneficial microbial functions. Synbiotics combine live microorganisms with substrates designed to support their activity.

Postbiotics represent another emerging approach in which non-living microbial preparations or components are used to produce biological effects,These approaches may influence pathogen resistance, epithelial integrity, immune signaling, and microbial metabolism (35).The gut microbiota—the community of microorganisms residing in the digestive tract—constitutes a complex and dynamic ecosystem that is fundamental to an organism's metabolic, immunological, and physiological processes. In recent years, there has been growing interest in probiotics, prebiotics, synbiotics, and postbiotics as means to modulate the gut microbiota and improve the health and productivity of farm animals. Studies indicate that these additives contribute to maintaining intestinal homeostasis, enhancing immune responses, and boosting animal productivity(36).

14. HOST–MICROBIOME INTERACTIONS

Stool samples are frequently used in research as a measure of the human gut flora. Stool samples have the benefit of being simple to collect, allowing for comprehensive, long-term sampling from the same subjects The diversity and role of microbial communities in the human colon are probably well represented by these samples , Nevertheless, microbial communities in the proximal gut or those connected to the mucus layer are unlikely to be reliably captured by such techniques. Moreover, these results might alter quickly in response to dietary modifications or antibiotic use(4, 37).

15. MICROBIOME ENGINEERING AND PHAGE THERAPY

The hunt for novel antimicrobial remedies has increased due to the worldwide challenge of antibiotic resistance. Because of their capacity to self-replicate, their selectivity in targeting specific hosts, and their shown effectiveness against biofilm-associated illnesses and multidrug-resistant diseases, bacteriophages are attracting fresh interest (38) Targeting Aβ deposits in vivo confirmed that the engineered phages successfully reached the central nervous system—thanks to the properties of the phage-based delivery vehicle—and bound to Aβ peptides with high specificity, all without exhibiting any detectable toxicity. Given the characteristics of this phage-based delivery system, the targeting of Aβ deposits in vivo demonstrated that the modified phages were capable of reaching the central nervous system and binding to Aβ peptides with great selectivity, without showing any notable adverse effects(39)

16. DEVELOPMENTS IN MICROBIOME RESEARCH

In the future, microbiome research will concentrate on understanding the complex interactions between microbial and host biological components The dynamic dynamics of microbial ecosystems and their adaptive responses to changing host and environmental circumstances will need a comprehensive systems biology approach (Fig. 2).Researchers can clarify how several biological layers interact to affect health and illness by examining multi-omics interactions, opening the door to extremely targeted therapeutic approaches. Achieving these goals will require significant improvements in data integration, with improved computational tools and machine learning algorithms being essential in connecting host physiology and disease outcomes with microbial gene expression, protein synthesis, and metabolic activity. In addition to advancing our knowledge of the microbiome, these integrated approaches will propel the creation of cutting-edge treatments and diagnostics, which will be a critical step toward genuinely customized medicine(40).

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

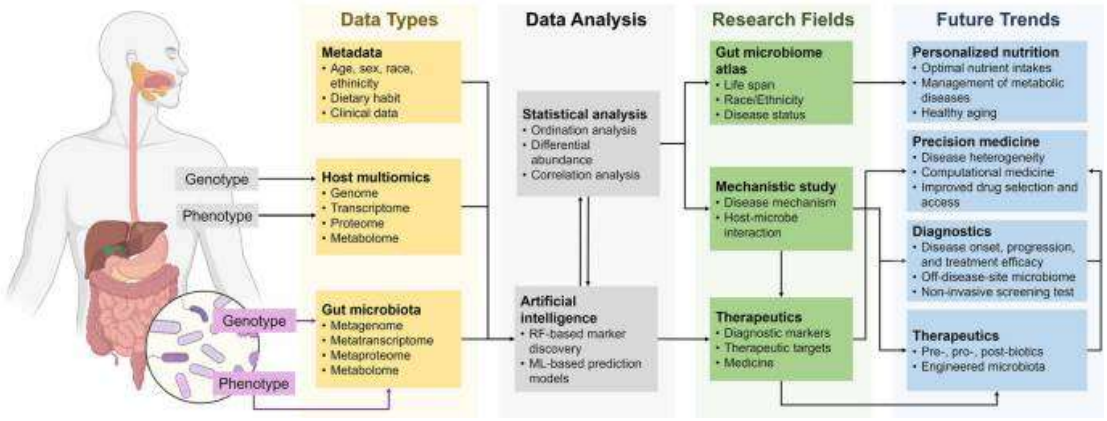

Figure:2A future framework for advancing the study of microbes(40).

The balance and harmony among the various types of microbes—such as bacteria, fungi, viruses, and archaea—residing in the digestive tract maintain the integrity of the intestinal barrier and promote immune tolerance. This is achieved through the production of short-chain fatty acids, which nourish the colon and facilitate the differentiation of regulatory T cells via genetic and receptor-mediated pathways. These processes lead to an increase in anti-inflammatory cytokines, such as interleukin-10 and transforming growth factor-beta (TGF-β). Furthermore, epithelial antimicrobial peptides (AMPs) enhance resistance to colonization by reducing excessive microbial adhesion and maintaining spatial organization within the mucus layer. Meanwhile, commensal fungi, such as *Saccharomyces cerevisiae* (baker's yeast), participate in inter-kingdom metabolic interactions that support the stability of microbial networks; simultaneously, methane-producing archaea, such as *Methanobrevibacter smithii*, consume hydrogen generated during fermentation, thereby supporting metabolic cross-feeding and the efficiency of the intestinal tract. By regulating microbial populations and mucosal colonization, bacteriophages (phages) support ecological balance without triggering inflammation. Overall, these coordinated interactions between microbes and the host preserve mucosal homeostasis by maintaining the integrity and selective permeability of the epithelial barrier (see Figure 3)(41).

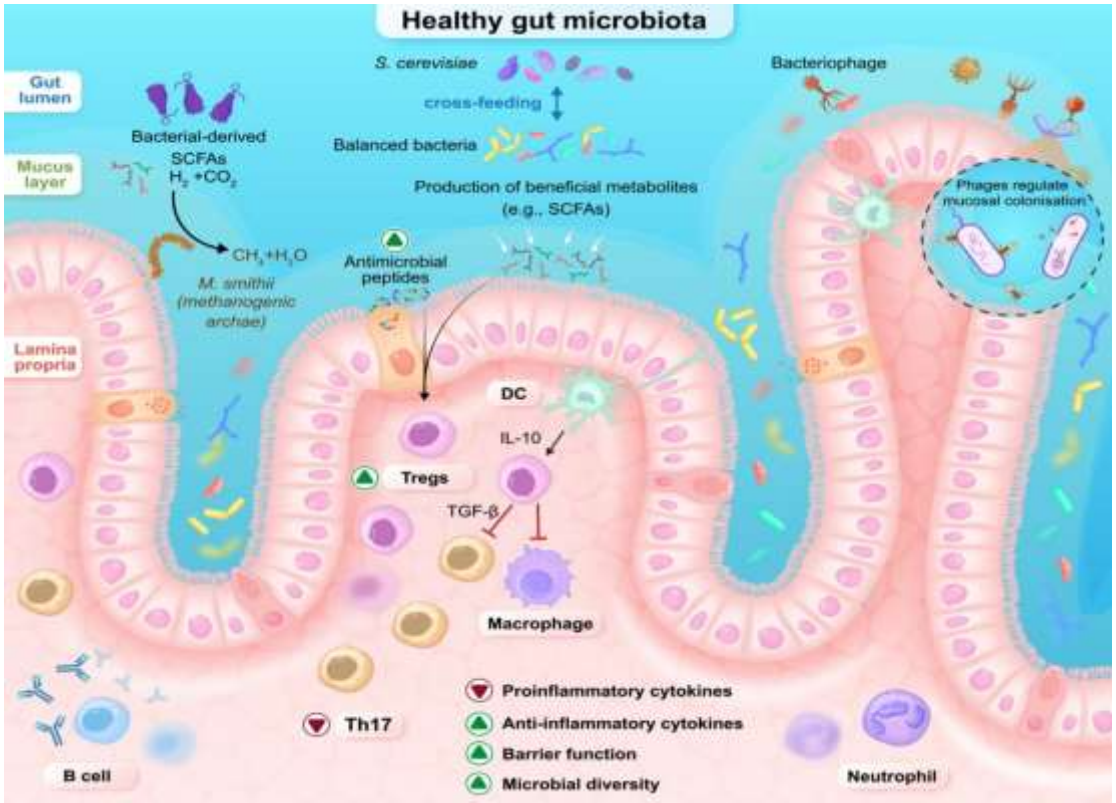

Figure 3. Homeostatic multikingdom interactions in the healthy gut mucosa. The healthy gastrointestinal tract harbors a diverse multikingdom microbiota composed of bacteria, archaea, fungi,

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

and viruses that collectively maintain epithelial barrier integrity and immune tolerance. Balanced bacterial communities ferment dietary substrates to produce short-chain fatty acids (SCFAs), which fuel colonocytes, strengthen tight junctions, and promote regulatory T cell (Treg) differentiation via epigenetic and receptor-mediated pathways, increasing anti-inflammatory cytokines such as interleukin-10 (IL-10) and transforming growth factor-beta (TGF-β). (41).

CONCLUSION

From the study of intestine infections, intestinal microbiology has developed into a multidisciplinary discipline that examines a complex microbial environment that significantly affects human health.According to available data, microorganisms affect pathogen resistance, metabolism, mucosal immunity, epithelial integrity, and communication with distant organs through direct interactions and microbial metabolites, Inflammatory bowel illness, recurrent C. difficile infections, colorectal cancer, and metabolic problems have all been linked to dysbiosis. Clinical translation is moving quickly, especially in recurrent C. difficile infection, where microbiome-based treatments have shown definite therapeutic efficacy. However, causal linkages are still complicated and require mechanistic confirmation, Integrating multi-omics, spatial biology, microbial ecology, host genetics, immunology, and clinical data will be critical to the future of intestinal microbiology. The creation of safer and more accurate microbiome-based diagnostics and treatments may be made possible by such integration To address concerns regarding the potential development of bacterial resistance to bacteriophages, strategies must be implemented to disable the ability of these phages to replicate outside the laboratory.

REFERENCES

1. 1-Ma Z, Zuo T, Frey N, et al. A systematic framework for understanding the microbiome in human health and disease: from basic principles to clinical translation. Signal Transduction and Targeted Therapy. 2024;9:237.
2. Gilbert JA, Azad MB, Bäckhed F, et al. Clinical translation of microbiome research. Nature Medicine. 2025;31:1099–1113.
3. Yadegar A, et al. Fecal microbiota transplantation: current challenges and future landscapes. Clinical Microbiology Reviews. 2024;37(2).
4. Wang S, Gong X, Xiao F, Yang Y. Recent advances in host-focused molecular tools for investigating host-gut microbiome interactions. Frontiers in Microbiology. 2024;15:1335036.
5. Shahi, S. K., Zarei, K., Guseva, N. V., & Mangalam, A. K. (2019). Microbiota analysis using two-step PCR and next-generation 16S rRNA gene sequencing. JoVE (Journal of Visualized Experiments), (152), e59980.
6. Knight R, Vrbanac A, Taylor BC, et al. Best practices for analysing microbiomes. Brief Bioinform. 2020.
7. Remondini D, et al. Comparison between 16S rRNA and shotgun sequencing data for the taxonomic characterization of the gut microbiota. Sci Rep. 2021;11:3030.
8. Quince C, Walker AW, Simpson JT, Loman NJ, Segata N. Shotgun metagenomics, from sampling to analysis. Nat Biotechnol. 2017;35:833–844.
9. Yatsunenko T, et al. Next-generation sequencing: insights to advance clinical investigations of the microbiome. J Clin Invest. 2022.
10. Zhang Y, Thompson KN, Branck T, Yan Y, Nguyen LH, Franzosa EA, et al. Metatranscriptomics for the Human Microbiome and Microbial Community Functional Profiling. Annu Rev Biomed Data Sci. 2021;4:279–311.
11. Tyagi S, Katara P. Metatranscriptomics: A Tool for Clinical Metagenomics. OMICS. 2024;28(8):394–407.
12. Marchesi JR, Ravel J. Concepts and applications of metatranscriptomics in microbiome research. (Discussed in comprehensive reviews of metagenomics and metatranscriptomics.)
13. Human Microbiome Project Consortium. Structure, function and diversity of the healthy human microbiome. Nature. 2012;486:207–214; and the MetaHIT consortium publications establishing reference human gut microbiome datasets.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

14. Sharpton, T. J. (2014). An introduction to the analysis of shotgun metagenomic data. Frontiers in plant science, 5, 209.
15. Filiatrault MJ (October 2011). "Progress in prokaryotic transcriptomics". Current Opinion in Microbiology. 14 (5): 579–86. doi:10.1016/j.mib.2011.07.023. PMID 21839669
16. Gut microbiota-derived metabolites tune host homeostasis fate. Seminars in Immunopathology. 2024;46:2.
17. O'Sullivan, D. J. (2000). Methods for analysis of the intestinal microflora. Current issues in intestinal microbiology, 1(2), 39-50.
18. Kanai T. Tryptophan metabolic pathway of the microbiome and host cells in health and disease. International Immunology. 2024;36(12):601–616.
19. Liu, M., Lu, Y., Xue, G., Han, L., Jia, H., Wang, Z., ... & Zhou, Y. (2024). Role of short-chain fatty acids in host physiology. Animal models and experimental medicine, 7(5), 641-652.
20. Lee MH, Nuccio SP, Mohanty I, et al. How bile acids and the microbiota interact to shape host immunity. Nature Reviews Immunology. 2024;24:798–809.
21. Keszthelyi, D., Troost, F. J., & Masclee, A. A. M. (2009). Understanding the role of tryptophan and serotonin metabolism in gastrointestinal function. Neurogastroenterology & Motility, 21(12), 1239-1249.
22. Liu, M., Li, S., Cui, Y., Zhu, X., Wang, Z., Sun, H., ... & Shi, Y. (2026). Tryptophan metabolism mediated by the gut microbiota inhibits pyroptosis via the AhR signaling pathway to maintain intestinal epithelial homeostasis. Microbiome, 14(1), 136.
23. Gastrointestinal microbiota-directed nutritional and therapeutic interventions for inflammatory bowel disease: opportunities and challenges. Gastroenterology Report. 2024.
24. Shi, N., Li, N., Duan, X., & Niu, H. (2017). Interaction between the gut microbiome and mucosal immune system. Military Medical Research, 4(1), 14.
25. Berg D, Clemente JC, Colombel JF. Can inflammatory bowel disease be permanently treated with short-term interventions on the microbiome? Expert Rev Gastroenterol Hepatol. 2015;9:781–95.
26. Wang ZK, Yang YS, Chen Y, Yuan J, Sun G, Peng LH. Intestinal microbiota pathogenesis and fecal microbiota transplantation for inflammatory bowel disease. World J Gastroenterol. 2014;20:14805–20.
27. Lamas B, Richard ML, Leducq V, Pham HP, Michel ML, Da CG, et al. CARD9 impacts colitis by altering gut microbiota metabolism of tryptophan into aryl hydrocarbon receptor ligands. Nat Med. 2016;22:598–605.
28. Yang, X., Guo, H., & Zou, M. (2026). Inflammatory bowel diseases: Pathological mechanisms and therapeutic perspectives. Molecular Biomedicine, 7(1), 2.
29. Ali, A., & AlHussaini, K. I. (2026). Diagnostic challenges and treatment approaches for Clostridioides difficile infection in IBD patients. Frontiers in Microbiology, 17, 1740387.
30. Olovo CV, Huang X, Zheng X, Xu M. Faecal microbial biomarkers in early diagnosis of colorectal cancer. J Cell Mol Med. 2021;25:10783–10797. doi: 10.1111/jcmm.17010.
31. Quaglio, A. E. V., Grillo, T. G., De Oliveira, E. C. S., Di Stasi, L. C., & Sassaki, L. Y. (2022). Gut microbiota, inflammatory bowel disease and colorectal cancer. World journal of gastroenterology, 28(30), 4053.
32. Ross FC, Patangia D, Grimaud G, et al. The interplay between diet and the gut microbiome: implications for health and disease. Nature Reviews Microbiology. 2024;22:671–686.
33. Host–microbe interactions: communication in the microbiota–gut–brain axis. Current Opinion in Microbiology. 2024;80:102494.
34. Morton, J. T., Jin, D. M., Mills, R. H., Shao, Y., Rahman, G., McDonald, D., ... & Taroncher-Oldenburg, G. (2023). Multi-level analysis of the gut–brain axis shows autism spectrum disorder-associated molecular and microbial profiles. Nature neuroscience, 26(7), 1208-1217.
35. Pitashny M, Kesten I, Shlon D, et al. The Future of Microbiome Therapeutics. Drugs. 2025;85:117–125.
36. Kumar, S., Bhatia, Z., & Seshadri, S. (2023). Probiotics, prebiotics, synbiotics, and postbiotics: human microbiome and human health.
37. Weingarden, A. R. (2026). Strengths and limitations of in vitro and animal models to advance understanding of human diet–microbiome interactions. Gut Microbes Reports, 3(1), 2636336.

ISSN 2278-2540 | DOI: 10.51583/IJLTEMAS | Volume XV, Issue XI, November 2026

38. Samanta, S., Mitra, I., Bhattacharya, A., & Saha, R. P. (2026). Engineering the Phage Revolution: Advances in Bacteriophage Therapy for the Antimicrobial Resistance Era. Molecular Biology, 1-22.
39. Pires, D. P., Cleto, S., Sillankorva, S., Azeredo, J., & Lu, T. K. (2016). Genetically engineered phages: a review of advances over the last decade. Microbiology and Molecular Biology Reviews, 80(3), 523-543.
40. Yang, S. Y., Han, S. M., Lee, J. Y., Kim, K. S., Lee, J. E., & Lee, D. W. (2025). Advancing gut microbiome research: the shift from metagenomics to multi-omics and future perspectives. Journal of microbiology and biotechnology, 35, e2412001.
41. -Houshyar, Y., Zhang, F., Tavakoli, P., Grimm, M. C., & Hold, G. L. (2026). Neglected kingdoms: the gut virome, mycobiome and their role in inflammatory bowel disease. Gut Microbes, 18(1), 2653288.