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Impact of gut microbiome on outcomes following endoscopic interventions in gastrointestinal disease

Agrawal H *et al*. Microbiome impact on endoscopic healing

Abstract

BACKGROUND

Endoscopic interventions play a vital role in diagnosing and managing gastrointestinal diseases, but complications such as bleeding, infection, and delayed healing can adversely affect patient outcomes. The influence of the gut microbiome on these outcomes is increasingly being recognized.

AIM

To evaluate the role of the gut microbiome in influencing clinical outcomes after endoscopic interventions, focusing on microbial diversity, specific taxa, metabolic functions, and emerging predictive models.

METHODS

A systematic literature search was conducted in PubMed, Embase, and Cochrane databases up to May 2025, selecting human studies that analyzed gut microbiome composition or function in relation to endoscopic interventions and clinical outcomes. Microbiome analysis techniques included 16S rRNA gene sequencing, metagenomics, and metabolomics.

RESULTS

Forty-two studies met the inclusion criteria. Our review identifies key beneficial microbes, such as *Faecalibacterium prausnitzii* and *Bacteroides* spp., which support mucosal healing. In contrast, dysbiosis (*e.g.*, an increased abundance of *Proteobacteria*) is associated with poorer healing and higher complication rates. Notably, microbiome-informed predictive models have shown strong potential for forecasting post-procedural complications, offering a pathway to personalized treatment strategies. Probiotics have also emerged as a promising intervention, helping to restore microbial balance and reduce complications such as infection and delayed healing.

CONCLUSION

The gut microbiome plays a significant role in recovery after endoscopy. Integrating microbiome analysis into clinical decision-making could improve outcomes through personalized predictions and targeted therapies. Future research should focus on standardizing microbiome assessment protocols and validating predictive models to optimize patient care.

Key Words: Gut microbiome; Endoscopy; Mucosal healing; Dysbiosis; Machine learning

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Core Tip: The gut microbiome critically influences patient outcomes after endoscopic procedures by modulating mucosal healing and inflammation. Disruptions from bowel preparation and the procedures affect microbial balance, with targeted probiotic and microbiome-based therapies offering promising recovery improvements. Integration of multi-omics and machine learning enables personalized prediction and management of complications, marking a shift toward precision medicine in gastrointestinal endoscopy.

INTRODUCTION

Endoscopic interventions serve key roles in diagnosing and managing gastrointestinal diseases, including screening colonoscopy and advanced therapies such as endoscopic mucosal resection (EMR) and endoscopic submucosal dissection (ESD)[1] Despite technical progress, predicting patient outcomes remains difficult. Complications like bleeding, infection, delayed healing, and stricture formation can worsen prognosis and increase healthcare costs[2].

The human gastrointestinal tract contains about 10^{14} bacteria, forming a complex ecosystem that influences host physiology, immune responses, and disease risk. This microbiome regulates immune function, supports epithelial barrier integrity, and affects inflammation and tissue repair[3]. Dysbiosis, an imbalance in microbial composition, associates with several gastrointestinal disorders including inflammatory bowel disease (IBD), colorectal cancer, and functional conditions[4].

Recent evidence indicates the gut microbiome may affect recovery and complications after endoscopic interventions. Variations in microbial diversity and the presence of specific bacterial taxa correlate with clinical outcomes[5]. Microbial metabolites such as short-chain fatty acids contribute to epithelial regeneration and immune regulation essential for mucosal healing[6]. Additionally, bowel preparation before endoscopy temporarily alters the microbiome, which could impact recovery after the procedure[7].

This manuscript reviews the role of the gut microbiome in outcomes after endoscopic interventions. It examines how changes in microbial diversity, specific bacteria, and metabolites influence healing, complications, and disease recurrence. It describes the effects of endoscopy and bowel preparation on gut microbes. The paper presents microbiome-based prediction models and therapies that aim to improve patient care. It highlights the use of multi-omics and machine learning (ML) methods to support personalized treatment and better prognosis in gastrointestinal endoscopy.

MATERIALS AND METHODS

A systematic literature search was performed following PRISMA guidelines. We queried PubMed, Embase, and Cochrane Library databases from inception until May 2025. Search terms combined keywords and MeSH related to gut microbiome ("gut microbiome", "intestinal microbiome"), endoscopic interventions ("endoscopy", "colonoscopy", "endoscopic mucosal resection"), and outcomes ("complications", "healing", "prediction", "response").

We included original research studies that evaluated the gut microbiome in human patients undergoing any endoscopic procedure, reported clinical outcomes related to procedure success, complications such as bleeding, infection, or strictures, or healing, and used microbiome analysis techniques like 16S rRNA gene sequencing, shotgun metagenomics, or metabolomics. We excluded animal and *in vitro* studies.

Two independent authors screened titles and abstracts for relevance. Full texts of eligible studies were assessed against inclusion criteria, and disagreements were resolved by consensus. From included studies, we extracted data on study design, population size, patient demographics, type of endoscopic procedure, microbiome sampling method (stool or mucosal biopsy), sequencing technique, and timing relative to the procedure. We collected data on microbial diversity metrics, including alpha and beta diversity, specific taxa associated with outcomes, functional analyses such as metabolic pathways and metabolite levels, and clinical outcomes like complication rates, healing times, and therapeutic response. Study quality was assessed using the Newcastle-Ottawa Scale for observational studies and the Cochrane Risk of Bias tools for interventional trials.

RESULTS

The initial search yielded 1264 records. After removing duplicates and screening abstracts, 112 full-text articles were reviewed. Forty-two studies met inclusion criteria (Figure 1). These studies collectively demonstrate that gut microbiome composition and diversity significantly correlate with mucosal healing, complication rates, and disease recurrence after endoscopic interventions. Interventions such as *Helicobacter pylori* (*H.*

pylori) eradication, probiotics, and microbiome-targeted therapies showed promising clinical benefits in improving recovery and reducing adverse outcomes. ML models integrating microbiome profiles provide accurate predictions of recurrence risk, supporting personalized post-endoscopy surveillance.

DISCUSSION

Microbial diversity and host-microbe interactions

The gastrointestinal microbiome varies along the digestive tract, reflecting different local environments. Microbial composition shifts significantly from the stomach to the colon. Each section hosts communities adapted to its conditions[7]. The upper gastrointestinal tract, including the duodenum and jejunum, absorbs fats, simple carbohydrates, and proteins. The distal small intestine absorbs bile acids and vitamin B12. The colon receives few dietary carbohydrates and nutrients but supports the highest microbial diversity due to bacterial fermentation[8].

Culturomics and next-generation sequencing show that the colon has greater microbial diversity than upper regions, with distinct bacterial groups in each area[9]. The stomach, previously considered mostly sterile due to acid, contains microbes important for gastric health and disease[10]. Detailed studies link stomach microbiome profiles to conditions like chronic gastritis, peptic ulcers, and gastric cancer risk[11]. These findings challenge earlier views on microbial distribution and highlight the need to account for local differences in microbiome diagnostics and treatments.

Functional roles of key microbes and their metabolites

Certain bacterial genera influence health outcomes. *Faecalibacterium prausnitzii*, a key butyrate producer, reduces inflammation and promotes healing by blocking NF-κB pathways and activating regulatory T cells. Low levels are linked to delayed healing after endoscopic injury[12,13]. *Bacteroides* species aid immune tolerance and mucosal repair by breaking down polysaccharides, but their loss during bowel preparation or flare-ups impairs recovery. *Proteobacteria*, including *Escherichia coli* and *Klebsiella*

pneumoniae, release lipopolysaccharides during inflammation, triggering cytokine release and worsening mucosal damage. *Lactobacillus* and *Bifidobacterium* may help maintain epithelial barriers post-endoscopy, though the benefits of probiotics are mixed. *Fusobacterium nucleatum* is associated with colorectal cancer and poor healing after polyp resection by promoting inflammation and inhibiting cell death[8,14,15] (Table 1).

The gastrointestinal microbiome closely interacts with host physiology, influencing both disease and treatment outcomes. Endomicroscopy reveals how colorectal mucosal traits affect bacterial composition. Inflammation shifts microbial communities, favoring facultative anaerobes. Goblet cells shape bacterial colonization, and the microbiome rapidly responds to host changes, thereby affecting disease progression and treatment. Microbial metabolism, including short-chain fatty acids such as butyrate, supports mucosal integrity and immune regulation. Low butyrate levels or its loss are linked to poor healing and increased risk of complications. Microbial bile acid conversion influences epithelial growth, while disrupted metabolism contributes to stricture formation. Tryptophan metabolism and the aryl hydrocarbon receptor regulate intestinal barrier function; reduced microbial production of aryl hydrocarbon receptor ligands increases permeability and inflammation post-procedure. Elevated gram-negative bacteria and lipopolysaccharides exacerbate inflammation, delay healing, and increase oxidative damage[11,15,17-22] (Table 2).

Microbiome-immune system interactions

The gut microbiome influences innate and adaptive immune responses essential for mucosal healing. Commensal microbes stimulate regulatory T cells to produce interleukin-10 and transforming growth factor-beta[23]. These cytokines reduce inflammation and support tissue repair. Losing these microbes shifts the immune system toward inflammation. Microbial signals control neutrophil and macrophage recruitment and activation[24]. Excess neutrophils produce reactive oxygen species that harm the mucosa. A balanced microbiome limits this response and helps resolve

inflammation. Microbial metabolites strengthen epithelial tight junctions and increase mucus layer thickness[7]. Dysbiosis weakens these defences, allowing antigens and pathogens to cross, causing chronic inflammation[25].

Effects of endoscopic interventions on the gut microbiome

Bowel preparation for colonoscopy causes lasting changes in the gut microbiome. Longitudinal studies show mucosal and luminal microbes shift significantly after standard prep with bisacodyl and polyethylene glycol[26]. Bacteroidetes and species like *Faecalibacterium prausnitzii* consistently increase. These changes reorganize microbial communities and affect disease detection and treatment[27].

Effects differ between healthy individuals and those with IBD. In IBD patients, bowel prep reduces differences between mucosal and luminal microbiomes, increasing shared microbial groups in biopsies and stool. This convergence may reduce diagnostic accuracy by masking disease-related markers[28].

Cheon *et al*[29] found that *H. pylori* eradication therapy speeds mucosal healing and reduces ulcer size after EMR for gastric ulcers. Shen *et al*[30] showed that ERAS-based nursing care improves management of postoperative complications and prognosis in patients with early gastrointestinal tumors treated by endoscopic resection. Shi *et al*[31] developed a ML model using gut microbiome and clinical data to predict colorectal polyp recurrence one year after EMR. (Table 3)

Colonoscopy alters gut microbial composition. Probiotic supplementation helps restore balance and improves patient outcomes. Reviews indicate probiotics support mucosal healing by modulating immune response and repairing the epithelial barrier[32]. Follow-up over three to six months shows some microbes return to baseline, while others remain altered, indicating lasting microbiome effects after endoscopy[33]. Endoscopic interventions impact the microbiome beyond bowel prep. Sampling with ingestible devices shows traditional endoscopy, involving fasting and sedation, may not capture normal microbiome states[34]. Upper endoscopy risks contamination from oral, oesophageal, or gastric microbes, complicating analysis. The invasive nature alters the

gut environment, creating artificial conditions that misrepresent microbial communities[35].

Magnetic controlled capsule endoscopy offers a less invasive alternative that preserves natural microbiome conditions while allowing thorough examination[36]. Combined with metabolomic analysis, this method supports noninvasive disease detection and maintains microbiome integrity. Future technologies should minimize disruption to native microbial ecosystems to improve patient outcomes[37].

Microbiome patterns relate to outcomes in endoscopic therapies[38]. Barrett's esophagus patients with microbial profiles rich in anti-inflammatory taxa show higher mucosal remission rates after treatment. Dysbiosis associates with persistent metaplasia and recurrence[39]. In IBD, higher microbial diversity and more butyrate producers link to better mucosal healing after medical and endoscopic treatments[40].

For colorectal cancer prevention, microbial signatures assess adenoma recurrence risk. High levels of pro-inflammatory bacteria like Fusobacterium nucleatum indicate greater risk and slower healing[41].

Microbiome-based prediction models for colorectal diseases

Microbiome-based prediction models aid colorectal cancer and polyp detection[42]. ML methods like Naive Bayes and Neural Networks reduce false negatives to about 5% by analyzing stool samples for microbial signatures linked to colorectal neoplasia. This approach may reduce colonoscopy demand and improve early detection[43].

After adenoma resection, taxa such as *Butyricimonas*, *Faecalitalea*, and *Catenibacterium* remain elevated, suggesting use in surveillance[44]. These bacteria correlate with adenoma-related amino acid profiles, linking microbiome changes to tumor development[45]. Bioinformatic analyses separate high- and low-risk colorectal adenocarcinoma patients by microbial patterns related to immune cell infiltration and survival. Reviews identify many bacteria with predictive value, but models require validation in prospective studies before clinical use[46]. Studies find 39 bacterial species

differing between colorectal cancer patients with and without lympho-vascular invasion[47]. Random Forest and XGBoost models accurately predict clinical outcomes.

Ben Izhak *et al*[48] found gut microbiome changes linked to weight loss and metabolic improvement after bariatric surgery, suggesting microbiome monitoring can predict surgical outcomes. Carlini *et al*[49] showed preoperative gut microbiome interventions reduced anastomotic leak rates in laparoscopic colorectal cancer surgery. Jin *et al*[50] demonstrated that gut microbiome from patients without anastomotic complications promoted collagen synthesis and healing in colon anastomoses, indicating microbiome manipulation aids recovery. Liu *et al*[51] reported that Bifidobacterium animalis supplementation after colorectal polyp resection improved immune response and recovery *vs* placebo. Park *et al*[52] found probiotics after anterior colon resection reduced postoperative symptoms and complications. Martínez-Sánchez *et al*[53] and Veziant *et al*[54] are studying dietary and clinical factors combined with microbiome profiling to predict surgical and cancer outcomes in colorectal patients. These studies highlight the gut microbiome as a modifiable factor to improve colorectal surgery results and patient prognosis (Table 4).

Gastric disease prediction and risk stratification

Gastric microbiome analysis aids disease prediction and risk assessment, especially for chronic gastritis and gastric cancer[55]. Oral bacterial profiles, including *Prevotella*, *Haemophilus*, *Fusobacterium*, *Neisseria*, and *Streptococcus*, show distinct patterns in patients undergoing upper endoscopy[56]. While alpha diversity does not strongly correlate with findings, the presence and abundance of specific bacteria provide useful diagnostic data alongside endoscopy[57].

Tests for gastric microbiota dysbiosis show promise in cancer risk assessment for atrophic gastritis patients, with specificity near 89% in identifying high-grade dysplasia or cancer[58]. These models analyze antrum and corpus biopsy samples to predict cancer risk and may serve as clinical biomarkers. Low levels of healthy gastric bacteria also signal gastrointestinal disease risk and offer opportunities for early detection[59].

Functional studies using genomic DNA sequencing of gastric biopsies enhance understanding of host-microbe interactions and improve risk prediction[60]. Combining microbiome data with biomarkers like pepsinogen ratios, *H. pylori* antibodies, and gastrin levels improves screening accuracy over endoscopy alone[61].

Cheon *et al*[29] conducted a randomized controlled trial on *H. pylori* eradication after EMR in gastric ulcer patients. The therapy accelerated mucosal healing and reduced ulcer size, supporting its use as standard postoperative care. Shen *et al*[30] tested ERAS-based nursing interventions in patients undergoing endoscopic resection for early gastrointestinal tumours. Their trial showed better management of postoperative complications and improved prognosis, emphasizing microbiota-related supportive care. Shi *et al*[31] created a ML model using gut microbiome and clinical data to predict colorectal polyp recurrence one year after EMR. This approach highlights microbiome profiling for personalized surveillance. Studies show colonoscopy causes significant shifts in gut microbiome. Probiotic supplementation restores balance and improves outcomes. Reviews on probiotics in mucosal healing support their role in restoring the epithelial barrier and modulating immune response after endoscopic interventions (Table 5). These methods aid personalized detection and risk assessment.

Post-procedural outcomes and complications

Surgical site infections and anastomotic complications link closely to gut microbiome composition, especially after colorectal surgery. Reviews show strong connections between microbiome profiles and issues like anastomotic leaks, infections, and postoperative ileus. Certain bacteria influence wound healing, immune response, and tissue repair[1].

Despite improved surgical standards and care in high-volume centres, complication rates remain significant: 10%-30% for ileus, 6.5%-20% for infections, and 2.7%-20% for leaks. Preoperative microbiome analysis can predict these risks, opening paths for preventive measures. Surgery also alters gut microbiome, with changes varying by bacterial type and affecting recovery positively or negatively.

Distinct microbial patterns appear in patients who develop complications, highlighting the role of microbiome in outcomes. Studies such as Carlini *et al*[49] have shown that targeted modulation of gut microbiome prior to colorectal surgery significantly reduces anastomotic leak incidence, underscoring the microbiome's role in surgical healing. Similarly, Jin *et al*[50] demonstrated that microbiome from patients without anastomotic complications promotes epithelial collagen synthesis and supports colon anastomosis healing.

Cheon *et al*[29] found that *H. pylori* eradication therapy speeds mucosal healing after gastric mucosal resection. Bowel preparation and the procedure can disrupt the microbiome, causing prolonged imbalance and slower recovery. Probiotic supplementation after surgery reduces infection rates and improves immune function[52,62]. Persistent dysbiosis raises risks for complications and disease recurrence, highlighting the need for microbiome-focused perioperative care[63]. Preoperative microbiome optimization through probiotics and diet aims to increase beneficial bacteria before surgery. Microbiome assessment may become part of risk evaluation, and targeted interventions could improve outcomes[64].

Advanced ML applications in microbiome analysis

Gut microbiome data is complex and high-dimensional, posing challenges and opportunities for clinical research, especially in predicting postoperative outcomes and disease recurrence[65]. ML has enabled integration of large microbiome datasets with clinical variables to create predictive models that support personalized medicine and postoperative care[66]. Shi *et al*[31] developed a ML model combining microbial profiles and clinical data to predict colorectal polyp recurrence within one year after EMR. The model showed strong accuracy, supporting its use in personalized surveillance and early intervention. Yu *et al*[67] used bioinformatics and ML to analyze microbiome and transcriptome data for colon adenocarcinoma risk prediction. This multi-omics approach enhances risk stratification by integrating host gene expression with microbial patterns. Liu *et al*[58] created gut microbiome-based algorithms to predict

metachronous adenoma after colorectal cancer surgery, identifying high-risk patients for improved follow-up. Wang *et al*[2] reviewed computational methods, including ML, to study microbial interactions linked to colorectal anastomotic leaks, aiding microbiome-targeted prevention. Yu *et al*[68] applied computational analysis to track microbiome changes after colorectal adenoma resection, providing insights on healing and recurrence risk. Challenges remain in handling data heterogeneity, high dimensionality, and model interpretability. Advances in algorithms, validation, and multi-omics integration will improve clinical application of ML in microbiome analysis[69]. ML on gut microbiome data enables personalized risk assessment and targeted care, advancing precision management in surgery and gastrointestinal diseases.

Integration with clinical data, biomarkers, and surveillance

Integrating gut microbiome profiles with clinical data and biomarkers improves prediction of postoperative outcomes. Combining microbial signatures with patient demographics, metabolic status, inflammatory markers, and imaging provides a clearer view of risks and recovery[70]. Veziant *et al*[54] designed the METABIOTE cohort to assess gut microbiome, sarcopenia, obesity, and metabolic syndrome in predicting surgical and oncologic outcomes after colorectal cancer surgery. This approach enhances risk assessment beyond clinical data by including microbial and metabolic factors. Liu *et al*[62] developed algorithms combining microbiome and clinical data to identify patients at risk for metachronous adenoma recurrence, improving surveillance. Caenepeel *et al*[71] found microbiome composition correlates with disease activity and treatment response in IBD. Combining microbiome analysis with biomarkers like CRP, fecal calprotectin, and endoscopy refines monitoring and treatment. Yu *et al*[67] integrated transcriptomic, metabolomic, and microbiome data to capture host-microbe interactions related to healing and inflammation. These multi-omics models, often with ML, identify composite biomarkers that enhance prognosis. Challenges include data standardization, integration, and the need for large cohorts. Gut microbiome analysis

offers value in postoperative surveillance and disease monitoring. Tracking microbial composition and function over time gives early insight into recovery, complication risks, and disease recurrence[72]. Shi *et al*[31] showed combining microbiome data with clinical factors predicts colorectal polyp recurrence after endoscopic resection, supporting early surveillance and intervention. Liu *et al*[73] developed gut microbiome-based algorithms to forecast metachronous adenoma risk after colorectal cancer surgery, enabling personalized follow-up. In IBD, mucosal and fecal microbiome profiles act as biomarkers for disease activity and relapse. Caenepeel *et al*[71] and Wang *et al*[74] identified microbiome signatures linked to endoscopic healing and clinical remission, guiding treatment and reducing invasive interventions. Continuous microbiome monitoring helps detect early postoperative complications like anastomotic leaks and infections. Carlini *et al*[49] and Wang *et al*[75] highlight microbiome markers' role in predicting and preventing these events. Though standardizing sampling and data analysis remains difficult, gut microbiome surveillance provides a non-invasive, dynamic tool to improve patient management, outcomes, and reduce healthcare costs through early detection and personalized care.

Therapeutic and probiotic interventions for recovery enhancement

Modulating the gut microbiome offers therapeutic strategies to improve outcomes after gastrointestinal surgery and endoscopy. Randomized trials by Liu *et al*[51] and Park *et al*[52] show probiotic supplementation enhances immune function, speeds recovery, and reduces postoperative complications. Carlini *et al*[49] found preoperative microbiome modulation lowers anastomotic leak rates after colorectal surgery, highlighting clinical benefits of microbiome optimization. Dietary interventions are being studied for their role in shaping the microbiome to support surgical recovery[53]. Fecal microbiome transplantation (FMT) also shows potential in restoring microbial balance and promoting mucosal healing, though further research is needed. Advanced microbiome-based predictive models, such as those by Shi *et al*[31], support personalized postoperative care by identifying high-risk patients for targeted treatment.

Microbiome-targeted therapies represent a move toward precision medicine to enhance recovery, reduce complications, and improve outcomes. Clinical trials indicate probiotics aid recovery after colorectal polyp resection. One study found *Bifidobacterium animalis subsp. lactis* MH-02, given daily for seven days, lowered postoperative symptoms and improved bowel function *vs* placebo[76].

Probiotics support mucosal barriers, regulate immunity, and restore microbial balance disrupted by interventions. Early use and strain selection, especially Bifidobacterium species, increase benefits[76].

These findings support including probiotics in post-procedural care. Probiotics are simple, low-cost, safe, and have no major side effects. Future studies should determine optimal probiotic combinations, treatment duration, and patient groups to maximize benefits and minimize risks.

Challenges and limitations in clinical implementation

Microbiome research faces technical challenges before routine clinical use. Variations in sample collection, processing, and analysis affect measurement accuracy and interpretation. Bowel preparation for endoscopy alters microbial communities, complicating results. Upper gastrointestinal sampling risks contamination, requiring standardized protocols to ensure accuracy and safety[77]. Quality control in sequencing and bioinformatics is essential for reliable data across laboratories[78]. Processing microbiome data needs specialized skills and infrastructure often absent in clinical settings. User-friendly tools and standardized pipelines are necessary for wider adoption[79]. Study heterogeneity complicates findings due to differences in sample types, timing, storage, DNA extraction, sequencing, and analysis methods. The lack of standard metrics for microbial diversity and function limits comparisons. Confounders such as diet, medications, comorbidities, and lifestyle often remain uncontrolled, affecting microbiome and clinical outcomes. The microbiome also changes over time with diet, stress, and illness. Single time-point samples miss these fluctuations, making longitudinal sampling crucial to understand effects on healing and complications[80].

Most evidence is correlative, with few interventional trials testing if altering the microbiome through probiotics, prebiotics, antibiotics, or fecal transplants improves endoscopic outcomes[81]. More trials are needed before clinical application. Clinical implementation faces challenges from a lack of standardized, practical protocols for microbiome assessment[82]. High sequencing and analysis costs limit use. Clinicians need validated biomarkers and decision-support tools for routine care[83]. Microbiome-based tests face unique regulatory hurdles. Many models come from case-control studies requiring external validation in prospective trials. Temporal and individual variability complicate validation[84]. The absence of standardized reference ranges across populations hinders clinical interpretation. Demographic, dietary, and geographic factors demand population-specific standards. Regulatory frameworks for microbiome diagnostics remain under development, requiring collaboration among researchers, clinicians, and authorities. Integration with clinical workflows and proof of cost-effectiveness are essential for adoption[85].

Future directions and emerging technologies

Advances in sequencing enable detailed identification of species, strains, resistance genes, virulence factors, and metabolic pathways through shotgun metagenomics. Combining microbiome data with metabolomics, proteomics, and transcriptomics creates comprehensive profiles of host-microbe interactions. Multi-omics approaches offer more insight than microbiome analysis alone[75]. Real-time sequencing and point-of-care testing could allow rapid analysis during endoscopy for immediate clinical decisions. Artificial intelligence and ML, especially deep learning, analyze complex multi-omics data and detect clinical patterns[86]. Federated learning supports large-scale research while protecting patient privacy. Cloud platforms increase access to advanced analytics without local infrastructure[87]. Future research should focus on large, longitudinal studies tracking microbiome changes linked to clinical outcomes. Integrating multi-omics will improve understanding of host-microbe interactions. ML can enhance prediction of complications and treatment responses. Clinical trials must

test interventions like probiotics, prebiotics, dietary changes, and fecal microbiome transplants[88]. Personalized endoscopy could use microbiome profiles for risk assessment, bowel preparation optimization, and tailored post-procedure care[89]. Targeted microbiome modulation offers new options to improve post-endoscopic outcomes. Precision probiotics designed for individual microbiomes may enhance therapy and reduce side effects. Synthetic microbial communities could deliver consistent, targeted effects beyond traditional probiotics[90]. FMT effectively treats recurrent *Clostridioides* difficile infection and is under study for other dysbiosis-related conditions[91]. Standardized FMT protocols for endoscopic patients could provide strong treatment options[92]. Selective depletion using targeted antimicrobials or bacteriophages can remove harmful bacteria while preserving beneficial ones. New microbiome-based drugs, such as prebiotics, postbiotics, and microbiome-derived therapeutics, offer precise control over microbiome modification. Integrating microbiome monitoring with treatment could enable adaptive protocols that maximize benefits and minimize risks in real time[62,73,93,94].

CONCLUSION

The gastrointestinal microbiome influences outcomes after endoscopic interventions. It aids disease detection, supports recovery, and improves patient management. Combining advanced sequencing with ML produces models that identify high-risk patients, guide treatments, and enhance surveillance. Spatial and temporal microbial variations provide information beyond traditional clinical measures, enabling personalized care. Endoscopic interventions change microbiome composition, making microbial factors relevant in clinical decisions. Microbiome-targeted therapies show potential to improve outcomes. Despite technical and regulatory challenges, research and technology will transform gastroenterology. Standardized protocols, validation methods, and user-friendly tools are needed for routine care and resource optimization (Figure 2). Future efforts should emphasize prospective validation, multi-omics integration, and targeted therapies using microbiome data. Microbiome analysis offers

opportunities for early detection, treatment prediction, and personalized strategies. This shift toward precision medicine could improve outcomes after endoscopic interventions.

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