Suchańska et al.
Medical Journal of Cell Biology 2025
DOI: 10.2478/acb-2025-0006
Received: 19.09.2025
Accepted: 28.10.2025

Surgical modulation of the gut microbiota: a review of intestinal procedures and microbial outcomes

Klaudia Suchańska[1], Jacek Gonos[2], Julia Śnieg[1]

Abstract

Surgical interventions involving the gastrointestinal tract profoundly influence the composition, diversity, and function of the gut microbiota, which plays a central role in human health and disease. Recent advances in sequencing technologies, particularly 16S rRNA gene profiling and metagenomics, have enabled detailed characterization of microbial alterations following different types of intestinal surgery. Bariatric procedures such as Roux-en-Y gastric bypass and sleeve gastrectomy consistently reduce microbial diversity in the short term but are also associated with functional reprogramming of the microbiota, including enhanced capacity for energy harvest and altered bile acid metabolism. Gastrectomy and bowel resections induce region-specific changes, often leading to dysbiosis, small intestinal bacterial overgrowth, and nutrient malabsorption. The creation of intestinal stomas modifies luminal and mucosal microbial communities, frequently promoting the overrepresentation of opportunistic pathogens. In addition, perioperative interventions, including mechanical bowel preparation, perioperative fasting, and antibiotic prophylaxis, exert acute but sometimes long-lasting effects on microbial ecology. These microbial shifts have been linked to a broad spectrum of clinical outcomes ranging from metabolic improvements and enhanced immune modulation to increased susceptibility to infections, impaired wound healing, and long-term complications such as anastomotic leaks or inflammatory conditions. Understanding the relationship between specific surgical procedures, perioperative management, and microbiota modulation is therefore crucial for optimizing patient outcomes. This review integrates current evidence from clinical and translational studies, highlights the mechanistic links between surgical approaches and microbial dynamics, and outlines future directions for research and therapeutic interventions aimed at preserving or restoring a healthy microbiome after intestinal surgery.

Running title: Surgical modulation of the gut microbiota

Keywords: gut microbiota, intestinal surgery, bariatric surgery, microbiome, dysbiosis, metagenomics

[1]Students Scientific Society Anatomia-Klinika-Nauka, Department of Anatomy, Human Morphology and Embryology, Wroclaw Medical University, Wroclaw, Poland
[2]Foundation of Wroclaw Medical University, Wroclaw Medical University, Wroclaw, Poland
***Correspondence:** klaudia.suchanska@student.umw.edu.pl
Full list of author information is available at the end of article

sciendo

Introduction

The gut microbiota is defined as the community of microorganisms inhabiting the human gastrointestinal tract. Although bacteria constitute the predominant group, the term also includes viruses, fungi, and archaea. The total mass of the gut microbiota in adults is estimated at 1–2 kg, and the number of bacterial cells is comparable to the total number of human cells in the body [1]. *Eubiosis* describes a state of microbial balance, which is essential for maintaining health and proper physiological functions.

The microbiota performs numerous functions, including the synthesis of vitamins (e.g., vitamin K and certain B vitamins), participation in digestion and nutrient metabolism, protection against pathogen colonization, and regulation of immune system activity [2,3]. Disruption of this balance, referred to as *dysbiosis*, has been associated with the development of metabolic disorders, inflammatory bowel diseases, and colorectal cancer [4–6].

Surgical interventions can disturb the gastrointestinal microenvironment by altering pH, oxygen availability, or intestinal transit [7–9]. In addition, perioperative factors such as mechanical bowel preparation (MBP), antibiotic administration, and dietary modifications may significantly influence the gut microbiota [10].

In recent years, increasing attention has been directed toward the role of the microbiota in postoperative complications, including anastomotic leakage, surgical site infections, and prolonged postoperative ileus [11,12]. Moreover, the microbiota is now regarded not only as a biomarker but also as a potential therapeutic target, with interventions such as probiotics and fecal microbiota transplantation (FMT) showing promise in improving surgical outcomes [13,14].

Materials and methods

Eligibility criteria

The following sections provide a detailed analysis of studies investigating the impact of gastrointestinal surgery on the composition and function of the human gut microbiota. Both randomized clinical trials, prospective and cohort studies, as well as systematic reviews and meta-analyses were included.

Studies were considered eligible if they met the following criteria:

- published in peer-reviewed scientific journals,
- conducted in human subjects aged ≥18 years,
- focused on gastrointestinal surgical procedures (intestinal resections, gastrectomy, bariatric surgery, stoma creation or closure),
- assessed the impact of the intervention on microbiome parameters such as composition, diversity, or function,
- employed modern microbiome analysis techniques (e.g., 16S rRNA sequencing, metagenomics, metabolomics).

Studies were excluded if they:

- were limited to animal models,
- focused solely on the effects of drugs or diet,
- did not report microbiological outcomes.

Data sources and search strategy

The literature search was performed using PubMed, Scopus, and Web of Science databases. The search covered studies published between 2010 and 2025, reflecting the rapid development of sequencing technologies and the growing body of research on the gut microbiota during this period.

Study selection and data analysis

The included publications were evaluated with respect to study design, number of participants, sample type and timing of collection, analytical methods applied, and the main findings regarding microbiota alterations following the surgical procedures.

Characteristics of the human gut microbiota in health

The human gut microbiota consists predominantly of bacteria, which account for approximately 99% of all microorganisms. The remaining fraction is composed of viruses, fungi, and archaea [15]. The number of microbial cells inhabiting the adult human intestine is estimated to be comparable to the total number of human cells, corresponding to approximately 3.9×10^{13} bacterial cells [1].

In the healthy adult gut, four major bacterial phyla dominate: **Firmicutes** (e.g., *Faecalibacterium*, *Ruminococcus*), **Bacteroidetes** (e.g., *Bacteroides*, *Prevotella*), **Actinobacteria** (mainly *Bifidobacterium*), and, to a lesser extent, **Proteobacteria** [16]. Particular importance is attributed to species such as *Faecalibacterium prausnitzii*, which supports intestinal barrier integrity and exerts anti-inflammatory effects through the production of short-chain fatty acids (SCFAs) [17].

The gut microbiome is highly variable among individuals and undergoes dynamic changes over time. Its composition is shaped by multiple factors, including diet [18], age [19], antibiotic use [20], as well as genetic and environmental determinants [21].

In this context, eubiosis refers to a state of balanced and diverse microbiota that supports host health, whereas dysbiosis is characterized by reduced diversity, loss of commensal bacteria, and overgrowth of opportunistic pathogens. Dysbiosis has been associated with several diseases, including inflammatory bowel disease [17], type 2 diabetes [5], obesity [4], and colorectal cancer [6].

The impact of surgical procedures on the gut microbiota

Surgical procedures significantly affect the microbial balance of the gastrointestinal tract, with the magnitude of changes depending on the type, extent, and technique of surgery (**Tab. 1**). These consequences may manifest during early recovery and in the long-term clinical course.

Colorectal cancer surgery

Colorectal resections induce lasting alterations in the gut microbiota, with the magnitude and nature of changes varying according to the site of resection. Studies have reported distinct alterations in the abundance of key bacterial genera, including *Bifidobacterium* and *Faecalibacterium*, as well as increases in *Escherichia-Shigella* and *Enterococcus* following right- versus left-sided resections [22]. Particular attention has been directed toward the microbiota at the anastomotic site, which exhibits a distinct microbial profile that may critically influence the healing process. The presence of pathobionts, especially *Enterococcus faecalis*, has been associated with a higher risk of anastomotic leakage [23,24], and analysis of mucosal microbiota sampled intraoperatively may hold predictive value for this complication before clinical symptoms occur [25].

Gastrectomy and reconstruction

Physiological alterations in the gastrointestinal environment following gastrectomy include reduced gastric acid secretion, modified intestinal transit, and altered bile flow. These alterations result in the so-called 'oralization' of the microbiota, characterized by the colonization of distal intestinal segments by oral-associated bacteria, such as *Streptococcus* spp. [8]. Reconstruction using the Roux-en-Y method has been shown to induce more pronounced alterations in the gut microbiota compared with the Billroth I method, accompanied by increased fecal calprotectin levels and activation of intestinal inflammatory responses [26,27].

Bariatric surgery (RYGB, SG, BPD-DS)

Bariatric procedures such as the sleeve gastrectomy (SG), Roux-en-Y gastric bypass (RYGB), and biliopancreatic diversion with duodenal switch (BPD-DS) cause profound and sustained remodeling of the gut microbiota. Multiple studies have documented an increase in aerobic and opportunistic bacteria, particularly members of the *Enterobacteriaceae* family, alongside changes in the relative abundance of the dominant phyla *Firmicutes* and *Bacteroidetes* [28,29]. These structural shifts are accompanied by functional modifications, including elevated shor-

TABLE 1 Summary of studies assessing the impact of gastrointestinal surgery on gut microbiota (n = number of patients included in each study)

SURGERY TYPE	REFERENCE (EXAMPLE)	n	METHOD	MAIN MICROBIOTA CHANGES	CLINICAL CONSEQUENCES
Colorectal resection	[22]	30	16S rRNA	↓ *Bifidobacterium*, ↓ *Faecalibacterium*, ↑ *Escherichia-Shigella*, ↑ *Enterococcus*	Risk of anastomotic leakage, impaired healing
Gastrectomy (Billroth I vs RYGB)	[26]	58	16S rRNA	"Oralization" (↑ *Streptococcus spp.*), more dysbiosis in RYGB	↑ Inflammation, ↑ fecal calprotectin
Bariatric (RYGB, SG, BPD-DS)	[30]	50	Metagenomics + metabolomics	↑ *Enterobacteriaceae*, altered Firmicutes/Bacteroidetes, ↑ SCFA, ↓ LPS	Better glucose/lipid metabolism
Bariatric (malabsorptive)	[31]	40	Shotgun metagenomics	Microbiota modulated by thiamine & magnesium	Nutrient deficiency risk
Ileostomy (stoma)	[9]	20	16S rRNA + metabolomics	↓ Diversity, ↑ aerobes, postprandial shifts	Altered barrier, delayed recolonization
Ileostomy closure	[32]	25	16S rRNA + metabolomics	Gradual recovery, not always baseline	Partial regeneration, mucosal protection

t-chain fatty acid (SCFA) production and reduced serum lipopolysaccharide (LPS) levels [9,30]. Such mechanisms are believed to contribute to improvements in glycemic control and lipid metabolism, independent of weight loss. Interestingly, preliminary evidence suggests that the microbiota composition in patients undergoing malabsorptive procedures may be influenced by dietary intake of nutrients such as thiamine and magnesium [31].

Stoma formation and closure

Temporary ileostomy, which reroutes intestinal contents away from the colon, provides an opportunity to directly study the small intestinal microbiota. It is characterized by reduced microbial diversity and a predominance of aerobic species. Moreover, the stoma microbiota undergoes dynamic postprandial changes, with bacterial biomass increasing within hours after food intake [9]. Following stoma closure, the colonic microbiota gradually reconstitutes, demonstrating partial regenerative capacity. However, the postoperative microbial composition does not always fully reflect the baseline state, which may be clinically relevant for the recolonization processes and the protective functions of the mucosal barrier [32].

Perioperative procedures and the gut microbiota

Pre- and postoperative interventions, including bowel preparation, antibiotic prophylaxis, and microbiota-supporting strategies, exert a substantial impact on the gut ecosystem (**Tab. 2**). Imbalances during this period may increase the risk of postoperative complications such as surgical site infections (SSI) or anastomotic leakage (AL). At the same time, an increasing number of studies highlight controversies and inconsistencies regarding the necessity of some traditional preparation protocols.

Bowel preparation

Mechanical bowel preparation (MBP), which involves the administration of laxatives to clear the colon of fecal content, together with oral antibiotics (OA), has long been an integral component

TABLE 2 Summary of studies evaluating the impact of perioperative procedures on gut microbiota (n = number of patients included in each study)

PERIOPERATIVE PROCEDURE	REFERENCE (EXAMPLE)	N	METHOD	MAIN MICROBIOTA CHANGES	CLINICAL CONSEQUENCES
Mechanical bowel preparation (MBP)	[33]	40	16S rRNA + metabolomics	↓ *Faecalibacterium prausnitzii*, ↓ diversity, ↑ opportunistic pathogens	Increased risk of dysbiosis, impaired mucosal defense
MBP + Oral antibiotics (OA)	[34]	250	Clinical + microbiota analysis	Stronger reduction in microbial load, transient dysbiosis	↓ SSI, ↓ AL risk, but transient dysbiosis
Oral antibiotics + MBP (left-sided resections)	[35]	150	16S rRNA + clinical outcomes	↓ Commensals, altered inflammatory markers	↓ Inflammatory response, better short-term recovery
Selective bowel decontamination (SBP)	[36]	ICU patients (n not specified)	Clinical + microbial culture	Reduced Gram-negative bacteria, risk of resistant strains	Controversial benefit, risk of resistance
Antibiotic prophylaxis (cephalosporins)	[37]	Review of RCTs	Review (various methods)	↓ Diversity, ↑ resistant strains	↑ Risk of C. difficile infection, impaired immunity
Antibiotics (broad spectrum)	[38]	Experimental & clinical	Metagenomics	Expansion of resistance genes, altered phageome	Long-term ecological disruption

of standard preoperative protocols in colorectal surgery. Their primary purpose is to reduce bacterial load and minimize the risk of postoperative infections. However, growing evidence indicates that MBP alone leads to a significant decline in protective commensal species, such as *Faecalibacterium prausnitzii*, while promoting the overgrowth of potentially pathogenic organisms [33]. In contrast, combining MBP with OA, particularly in Enhanced Recovery After Surgery (ERAS) protocols, has proven more effective in reducing the risk of SSI and AL compared with either intervention alone [34,35]. Nonetheless, this strategy induces an acute, though usually transient, dysbiosis, which may be particularly detrimental in older adults and patients with comorbidities. An alternative approach is selective bowel decontamination (SBP), but its use in gastrointestinal surgery remains controversial due to concerns about selecting antibiotic-resistant strains and the lack of conclusive evidence supporting clinical benefit [36].

Antibiotics

Antibiotic prophylaxis is an essential component of surgery, but its effects on the gut microbiota are profound and long-lasting. Even short courses, such as those involving cephalosporins, have been shown to reduce microbial diversity and promote the dominance of resistant strains [37,38]. Such antibiotic-induced dysbiosis increases susceptibility to opportunistic infections, including *Clostridioides difficile*, may disrupt host metabolism, and adversely affect wound healing and immune responses [37]. Against this backdrop, microbiota-targeted interventions are attracting increasing attention. Randomized trials suggest that probiotics may reduce postoperative infection rates and shorten hospital stays, although clear recommendations on the optimal strains, dosages, and timing are still lacking. Moreover, the effectiveness of probiotics and postbiotics appears to depend strongly on the clinical context and the patient's baseline microbiota composition [39].

Clinical consequences of microbiota alterations

Surgery- and perioperatively induced alterations in the gut microbiota carry significant clinical implications. Microbial imbalance can affect not only the risk of early postoperative complications but also the long-term regulation of metabolic and immune homeostasis.

One of the best-documented complications associated with dysbiosis is anastomotic leakage (AL). It shows that the microbiota composition at the anastomotic site at the time of surgery may have predictive value for AL, with particular attention given to *Enterococcus faecalis* strains exhibiting collagenolytic activity [24]. Postoperative microbial disturbances are also linked to an increased risk of surgical site infections (SSI), with reduced microbial diversity correlating with higher susceptibility to infections, particularly those caused by multidrug-resistant organisms [40]. Another concern is impaired gastrointestinal motility – dysbiosis may disrupt communication along the microbiota–enteric neuron axis, contributing to prolonged postoperative ileus and delayed peristalsis [41]. Moreover, emerging evidence suggests that altered microbiota profiles may play a role in the pathogenesis of low anterior resection syndrome (LARS), although available data remain limited [42].

The role of the microbiota extends beyond mechanical and infectious complications. Commensal bacteria such as *Faecalibacterium prausnitzii* are key producers of short-chain fatty acids (SCFAs), which support epithelial integrity and exert anti-inflammatory effects. A reduction in butyrate-producing species is a hallmark of dysbiosis observed in inflammatory bowel disease [17]. Conversely, disrupted microbial composition can promote excessive lipopolysaccharide (LPS) production, bacterial translocation through a compromised intestinal barrier, and exacerbated inflammatory responses, as demonstrated in experimental models [43]. Metabolic consequences are also relevant – after bariatric surgery and gastrectomy, microbiota composition can modulate glucose and lipid metabolism, influencing the metabolic outcomes of surgical treatment (**Fig. 1**) [30].

For these reasons, microbiota-targeted interventions are gaining attention. Probiotics are the most extensively studied approach; their use has been shown to reduce SSI risk, and some studies also report shortened postoperative ileus and improved tolerance of oral feeding [13]. Complementary strategies include prebiotics and postbiotics, which provide substrates for beneficial bacteria or deliver metabolites such as SCFAs that support immune and metabolic homeostasis [44]. In cases of severe or persistent dysbiosis, fecal microbiota transplantation (FMT) is increasingly considered. Although data in gastrointestinal surgery remain limited, preliminary findings suggest its potential efficacy in patients with recurrent infections or malabsorptive conditions [14].

Limitations and future research directions

Current studies investigating the impact of surgery on the gut microbiota have provided important insights; however, their interpretation requires caution due to substantial methodological limitations. The lack of standardization remains the most significant challenge – different techniques are applied, ranging from 16S rRNA sequencing to metagenomics and metabolomics, each offering distinct levels of taxonomic resolution and detection depth [45]. Another difficulty lies in the heterogeneity of sampling timelines: some studies focus on the very

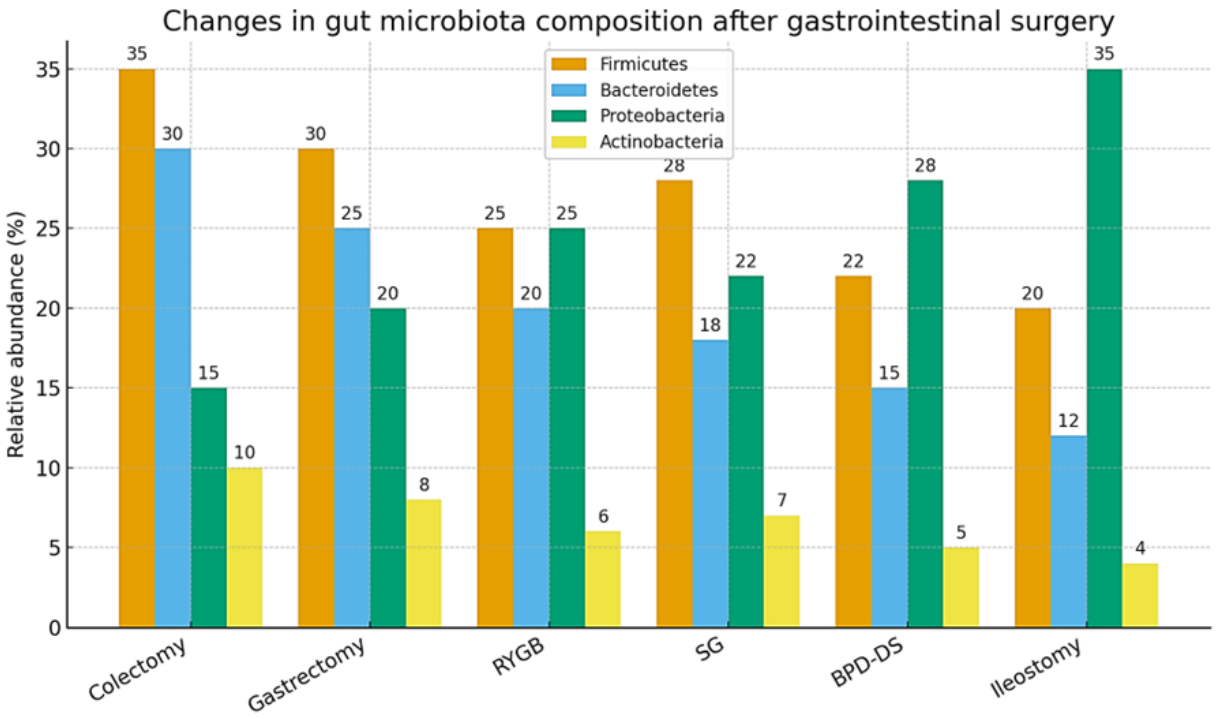

FIGURE 1 Relative abundance of dominant bacterial phyla after selected gastrointestinal surgical procedures. Data are illustrative, based on reviewed studies

early postoperative period (24–48 h), while others assess only long-term outcomes, thereby limiting comparability and generalizability of findings [46].

To improve the quality of evidence, harmonized research standards are needed. These should include clearly defined sampling time points, standardized bioinformatic pipelines, and parallel collection of clinical data such as BMI, glycemia, and antibiotic use. Multicenter prospective studies will also be crucial for validating findings and increasing statistical power [47].

An emerging concept is the personalization of surgical management based on the patient's microbiota profile. Potential applications include identifying individuals at high risk of complications (e.g., anastomotic leakage), implementing targeted probiotic therapy or fecal microbiota transplantation (FMT) in the perioperative setting, and optimizing the choice of reconstructive techniques. Although this field is still in its early stages, preliminary evidence suggests that such approaches may improve surgical outcomes [48,25].

Conclusions

Alterations in the gut microbiota following surgical procedures represent a dynamic and multidimensional process, influenced by the type, extent, and reconstructive technique of the operation, as well as perioperative interventions [49,46,41]. The most profound modifications in microbiota composition and function are observed after procedures that involve radical anatomical and physiological changes in the gastrointestinal tract, such as gastrectomy and bariatric surgery [50,30].

Available evidence indicates that postoperative dysbiosis may not only increase the risk of complications, including anastomotic leakage, surgical site infections, short bowel syndrome, and low anterior resection syndrome (LARS), but also modulate host immune responses and metabolic processes [24,42,51].

Advances in analytical methods, including 16S rRNA sequencing, shotgun metagenomics, and metabolomics, have enabled more detailed characterization of the interplay between surgery and the human microbiome [45]. Nevertheless, standardization of research protocols, improved control of confounding factors, and prospective clinical studies with appropriate control groups are still required [47].

In the future, the gut microbiota may serve not only as a biomarker of postoperative risk but also as a target for preventive and therapeutic interventions such as probiotics, prebiotics, dietary modulation, fecal microbiota transplantation (FMT), or pharmacological approaches [13,14]. Personalization of surgical management based on the patient's microbiota profile emerges as a promising direction within precision medicine [48].

Ethical approval
This was a descriptive review. No human or animal subjects were involved in this research.

Acknowledgments
Not applicable.

Corresponding author
Klaudia Suchańska, Wroclaw Medical University, Students' Scientific Society Anatomia-Klinika-Nauka, Human Morphology and Embryology, Department of Anatomy, Wrocław, Poland; e-mail: klaudia.suchanska@student.umw.edu.pl.

Conflict of interest
The authors declare no conflict of interest.

References
1. Sender R, Fuchs S, Milo R. Revised estimates for the number of human and bacteria cells in the body. PLoS Biol. 2016;14(8):e1002533; DOI:10.1371/journal.pbio.1002533.
2. Sekirov I, Russell SL, Antunes LC, Finlay BB. Gut microbiota in health and disease. Physiol Rev. 2010;90(3):859–904; DOI:10.1152/physrev.00045.2009.
3. Kho ZY, Lal SK. The human gut microbiome: a potential controller of wellness and disease. Front Microbiol. 2018;9:1835; DOI:10.3389/fmicb.2018.01835.
4. Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. Nature. 2006;444(7122):1027–31; DOI:10.1038/nature05414.
5. Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, Liang S, Zhang W, Guan Y, Shen D, Peng Y, Zhang D, Jie Z, Wu W, Qin Y, Xue W, Li J, Han L, Lu D, Wu P, Dai Y, Sun X, Li Z, Tang A, Zhong S, Li X, Chen W, Xu R, Wang M, Feng Q, Gong M, Yu J, Zhang Y, Zhang M, Hansen T, Sanchez G, Raes J, Falony G, Okuda S, Almeida M, LeChatelier E, Renault P, Pons N, Batto JM, Zhang Z, Chen H, Yang R, Zheng W, Li S, Yang H, Wang J, Ehrlich SD, Nielsen R, Pedersen O, Kristiansen K, Wang J. A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature. 2012;490(7418):55–60; DOI:10.1038/nature11450.
6. Arthur JC, Gharaibeh RZ, Mühlbauer M, Perez-Chanona E, Uronis JM, McCafferty J, Fodor AA, Jobin C. Microbial genomic analysis reveals the essential role of inflammation in bacteria-induced colorectal cancer. Nat Commun. 2014;5:4724; DOI:10.1038/ncomms5724.
7. Ohigashi S, Sudo K, Kobayashi D, Takahashi O, Takahashi T, Asahara T, Nomoto K, Onodera H. Changes of the intestinal microbiota, short chain fatty acids, and fecal pH in patients with colorectal cancer. Dig Dis Sci. 2013;58(6):1717–26; DOI:10.1007/s10620-012-2526-4.
8. Horvath A, Bausys A, Sabaliauskaite R, Dauksaite A, Sadauskas M, Stratilatovas E, Strupas K, Dambrauskas Z. Distal gastrectomy with Billroth II reconstruction is associated with oralization of gut microbiome and intestinal inflammation: a proof-of-concept study. Ann Surg Oncol. 2021;28(2):1198–1208; DOI:10.1245/s10434-020-08678-1.
9. Yilmaz B, Fuhrer T, Morgenthaler D, von Eckardstein A, Sander P, Benes V, Peterli R, Lê KA, Sunagawa S. Plasticity of the adult human small intestinal stoma microbiota. Cell Host Microbe. 2022;30(12):1773–86; DOI:10.1016/j.chom.2022.10.002.
10. Jalanka J, Salonen A, Salojärvi J, Ritari J, Immonen O, Marciani L, Gowland P, Hoad C, Garsed K, Lam C, Palva A, Spiller RC, de Vos WM. Effects of bowel cleansing on the intestinal microbiota. Gut. 2015;64(10):1562–8; DOI:10.1136/gutjnl-2014-307240.
11. Boatman S, Kohn J, Jahansouz C. The influence of the microbiome on anastomotic leak. Clin Colon Rectal Surg. 2023;36(2):127–32; DOI:10.1055/s-0043-1760718.
12. Lianos GD, Frountzas M, Kyrochristou ID, Karampa A, Mitrousias A, Misiakos EP, Schizas D, Liakakos T. What is the role of the gut microbiota in anastomotic leakage after colorectal resection? A scoping review of clinical and experimental studies. J Clin Med. 2024;13(22):6634; DOI:10.3390/jcm13226634.
13. Han Y, Wang Y, Guan M, Li X, Sun Y. Preventive effect of probiotics on infections following colorectal cancer surgery: an umbrella meta-analysis. World J Gastrointest Surg. 2024;16(11):3546–58; DOI:10.4240/wjgs.v16.i11.3546.
14. Xu HM, Huang HL, Zhou YL, Liu YD, Chen HT, Li YQ, Zhou YL, Zhang XW, Zhang J, Chen Y. Fecal microbiota transplantation: a new therapeutic attempt from the gut to the brain. Gastroenterol Res Pract. 2021;2021:6699268; DOI:10.1155/2021/6699268.
15. Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR, Li J, Xu J, Li S, Li D, Cao J, Wang B, Liang H, Zheng H, Xie Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Le Paslier D, Linneberg A, Nielsen HB, Pelletier E, Renault P, Sicheritz-Pontén T, Turner K, Zhu H, Yu C, Li S, Jian M, Zhou Y, Li Y, Zhang X, Li S, Qin N, Yang H, Wang J, Brunak S, Dore J, Guarner F, Kristiansen K, Pedersen O, Parkhill J, Weissenbach J, MetaHIT Consortium, Bork P, Ehrlich SD, Wang J. A human gut microbial gene catalogue established by metagenomic sequencing. Nature. 2010;464(7285):59–65; DOI:10.1038/nature08821.
16. Eckburg PB, Bik EM, Bernstein CN, Purdom E, Dethlefsen L, Sargent M, Gill SR, Nelson KE, Relman DA. Diversity of the human intestinal microbial flora. Science. 2005;308(5728):1635–8; DOI:10.1126/science.1110591.
17. Machiels K, Joossens M, Sabino J, De Preter V, Arijs I, Eeckhaut V, Ballet V, Claes K, Van Immerseel F, Verbeke K, Ferrante M, Verhaegen J, Rutgeerts P, Vermeire S. A decrease of the butyrate-producing species Roseburia hominis and Faecalibacterium prausnitzii defines dysbiosis in patients with ulcerative colitis. Gut. 2014;63(8):1275–83; DOI:10.1136/gutjnl-2013-304833.
18. David LA, Maurice CF, Carmody RN, Gootenberg DB, Button JE, Wolfe BE, Ling AV, Devlin AS, Varma Y, Fischbach MA, Biddinger SB, Dutton RJ, Turnbaugh PJ. Diet rapidly and reproducibly alters the human gut microbiome. Nature. 2014;505(7484):559–63; DOI:10.1038/nature12820.
19. Odamaki T, Kato K, Sugahara H, Hashikura N, Takahashi S, Xiao JZ, Abe F, Osawa R. Age-related changes in gut microbiota composition from newborn to centenarian: A cross-sectional study. BMC Microbiol. 2016;16:90; DOI:10.1186/s12866-016-0708-5.
20. Dethlefsen L, Huse S, Sogin ML, Relman DA. The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing. PLoS Biol. 2008;6(11):e280; DOI:10.1371/journal.pbio.0060280.
21. Zhernakova A, Kurilshikov A, Bonder MJ, Tigchelaar EF, Schirmer M, Vatanen T, Mujagic Z, Vila AV, Falony G, Vieira-Silva S, Wang J, Imhann F, Brandsma E, Jankipersadsing SA, Joossens M, Cenit MC, Deelen P, Swertz MA, LifeLines cohort study, Weersma RK, Feskens EJM, Netea MG, Gevers D, Jonkers D, Franke L, Aulchenko YS, Huttenhower C, Raes J, Hofker MH, Xavier RJ, Wijmenga C, Fu J. Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science. 2016;352(6285):565–9; DOI:10.1126/science.aad3369.
22. Cong J, Zhu H, Liu D, Li T, Zhang C, Zhu J, Zhou H, Dong Q, Wang Y. A pilot study: changes of gut microbiota in post-surgery colorectal cancer patients. Front Microbiol. 2018;9:2777; DOI:10.3389/fmicb.2018.02777.
23. Chen Y, Wu N, Yan X, Zhang L, Zhang J, Xie Y, Wang X, Li J, Zhou Y, Li Y. Impact of gut microbiota on colorectal anastomotic healing: a review. Mol Clin Oncol. 2025;22(6):52; DOI:10.3892/mco.2025.2847.
24. Shogan BD, Belogortseva N, Luong PM, Zaborin A, Lax S, Bethel C, Ward M, Muldoon JP, Singer M, An G, Welch RA, Alverdy JC. Collagen degradation and MMP9 activation by Enterococcus faecalis contribute to intestinal anastomotic leak. Sci Transl Med. 2015;7(286):286ra68; DOI:10.1126/scitranslmed.3010658.
25. Lehr K, Lange UG, Hipler NM, Müller A, Stein J, Bruns C, Jäger C, Hecker M, Lehmann C, Reinert S. Prediction of anastomotic insufficiency based on the mucosal microbiome prior to colorectal surgery: a proof-of-principle study. Sci Rep. 2024;14:15335; DOI:10.1038/s41598-024-65320-w.
26. Imai Y, Lee SW, Sakaguchi S, Kunisaki C, Endo I. Comparison of the gastric microbiome in Billroth I and Roux-en-Y reconstructions after distal gastrectomy. Sci Rep. 2022;12(1):10594; DOI:10.1038/s41598-022-14886-4.
27. He Y, Gao S, Jiang L, Yang J. Changes in gut microbiota after gastric cancer surgery: A prospective longitudinal study. Front Oncol. 2025;14:1533816; DOI:10.3389/fonc.2024.1533816.
28. Graessler J, Qin Y, Zhong H, Zhang J, Licinio J, Wong ML, Xu A, Chavakis T, Bornstein SR, Ehrhart-Bornstein M, Saxena R, Spranger J, Li Y, Wang J. Metagenomic sequencing of the human gut microbiome before and after bariatric surgery in obese patients with type 2 diabetes: correlation with inflammatory and metabolic parameters. Pharmacogenomics J. 2013;13(6):514–22; DOI:10.1038/tpj.2012.43.
29. Furet JP, Kong LC, Tap J, Poitou C, Basdevant A, Bouillot JL, Mariat D, Corthier G, Doré J, Henegar C, Rizkalla SW, Clément K. Differential adaptation of human gut microbiota to bariatric surgery-induced weight loss: Links with metabolic and low-grade inflammation markers. Diabetes. 2010;59(12):3049–57; DOI:10.2337/db10-0253.
30. Tremaroli V, Karlsson F, Werling M, Ståhlman M, Kovatcheva-Datchary P, Olbers T, Fändriks L, le Roux CW, Nielsen J, Bäckhed F. Roux-en-Y gastric bypass and vertical banded gastroplasty induce long-term changes on the human gut microbiome contributing to fat mass regulation. Cell Metab. 2015;22(2):228–38; DOI:10.1016/j.cmet.2015.07.009.
31. Suárez-Sánchez F, Pérez-Ruiz E, Ramírez-Silva CI, García-López V, Domínguez-Muñoz F, Cuevas-Ramos D, López-Taylor JR. A species of *Coprococcus* is related to BMI in patients who underwent malabsorptive bariatric surgery and its abundance is modified by magnesium and thiamin intake [Internet]. arXiv [Preprint]. 2025 [cited 2025 Sep 10]: 37 p. Available from: https://doi.org/10.48550/arXiv.2504.16672.
32. Xu L, Li X, Chen L, Zhang Y, Wang J, Huang J, Wang L, Sun X, Wei H. Gut microbiome and plasma metabolome alterations in ileostomy and

after closure of ileostomy. Microbiol Spectr. 2025;13(4):e0119124; DOI:10.1128/spectrum.01191-24.
33. Nagata N, Tohya M, Fukuda S, Suda W, Nishijima S, Takeuchi F, Ohsugi M, Tsujimoto T, Tsuda S, Miyoshi-Akiyama T, Uchida K, Koike K, Hattori M. Effects of bowel preparation on the human gut microbiome and metabolome. Sci Rep. 2019;9(1):4042; DOI:10.1038/s41598-019-40182-9.
34. Scarborough JE, Mantyh CR, Sun Z, Migaly J. Combined mechanical and oral antibiotic bowel preparation reduces incisional surgical site infection and anastomotic leak rates after elective colorectal resection: An analysis of colectomy-targeted ACS NSQIP. Ann Surg. 2015;262(2):331–7; DOI:10.1097/SLA.0000000000001041.
35. Golder AM, Steele CW, Conn D, O'Neill JR, Moss S, Kinsella J, Marney L, Roxburgh CSD, Horgan PG, McMillan DC, McKay CJ, Carter CR, Jamieson NB. Effect of preoperative oral antibiotics in combination with mechanical bowel preparation on inflammatory response and short-term outcomes following left-sided colonic and rectal resections. BJS Open. 2019;3(6):830–9; DOI:10.1002/bjs5.50224.
36. de Jonge E, Schultz MJ, Spanjaard L, Dankert J, Kesecioglu J. Effects of selective decontamination of the digestive tract on mortality and antibiotic resistance in the intensive-care unit. Curr Opin Crit Care. 2005;11(2):144–9; DOI:10.1097/01.ccx.0000155352.01489.11.
37. Becattini S, Taur Y, Pamer EG. Antibiotic-induced changes in the intestinal microbiota and disease. Trends Mol Med. 2016;22(6):458–78; DOI:10.1016/j.molmed.2016.04.003.
38. Modi SR, Lee HH, Spina CS, Collins JJ. Antibiotic treatment expands the resistance reservoir and ecological network of the phage metagenome. Nature. 2013;499(7457):219–22; DOI:10.1038/nature12212.
39. Anderson AD, McNaught CE, Jain PK, MacFie J. Randomised clinical trial of synbiotic therapy in elective surgical patients. Gut. 2004;53(2):241–5; DOI:10.1136/gut.2003.024620.
40. Ohigashi S, Sudo K, Kobayashi D, Takahashi O, Takahashi T, Asahara T, Nomoto K, Onodera H. Significant changes in the intestinal environment after surgery in patients with colorectal cancer. J Gastrointest Surg. 2013;17(9):1657–64; DOI:10.1007/s11605-013-2270-x.
41. Gibiino G, Binda C, Cristofaro L, Ianiro G, Gambassi G, Gasbarrini A, Cammarota G. Dysbiosis and gastrointestinal surgery: Current insights and future research. Biomedicines. 2022;10(10):2532; DOI:10.3390/biomedicines10102532.
42. Kim MJ, Park S, Park JW, Jeong SY, Park KJ, Park HC, Park JH, Park SC. Gut microbiome associated with low anterior resection syndrome after rectal cancer surgery. Sci Rep. 2023;13(1):8578; DOI:10.1038/s41598-023-34557-2.
43. Schuijt TJ, Lankelma JM, Scicluna BP, de Sousa e Melo F, Roelofs JJ, de Boer JD, Hoogendijk AJ, de Beer R, de Vos A, Belzer C, de Vos WM, van der Poll T, Wiersinga WJ. The gut microbiota plays a protective role in the host defence against pneumococcal pneumonia. Gut. 2016;65(4):575–83; DOI:10.1136/gutjnl-2015-309728.
44. Ríos-Covián D, Ruas-Madiedo P, Margolles A, Gueimonde M, de Los Reyes-Gavilán CG, Salazar N. Intestinal short chain fatty acids and their link with diet and human health. Front Microbiol. 2016;7:185; DOI:10.3389/fmicb.2016.00185.
45. Knight R, Vrbanac A, Taylor BC, Aksenov A, Callewaert C, Debelius J, Gonzalez A, Kosciolek T, McCall LI, McDonald D, Melnik AV, Morton JT, Navas J, Quinn RA, Sanders JG, Swafford AD, Thompson LR, Tripathi A, Xu ZZ, Zaneveld JR, Zhu Q, Caporaso JG, Dorrestein PC. Best practices for analysing microbiomes. Nat Rev Microbiol. 2018;16(7):410–22; DOI:10.1038/s41579-018-0029-9.
46. Zaborin A, Smith D, Garfield K, Quensen J, Shakhsheer B, Kade M, Tirrell M, Gilbert J, Zaborina O, Alverdy JC. Membership and behavior of ultra-low-diversity pathogen communities present in the gut of humans during prolonged critical illness. mBio. 2014;5(5):e01361-14; DOI:10.1128/mBio.01361-14.
47. Integrative HMP (iHMP) Research Network Consortium. The integrative human microbiome project. Nature. 2019;569(7758):641–8; DOI:10.1038/s41586-019-1238-8.
48. Tsalikidis C, Mitsala A, Mentonis VI, Filippidis G, Leventakos K, Ioannidis A, Machairas N, Misiakos E, Zografos G, Pikoulis E. Predictive factors for anastomotic leakage following colorectal cancer surgery: where are we and where are we going? Curr Oncol. 2023;30(3):3111–37; DOI:10.3390/curroncol30030236.
49. Agnes A, Puccioni C, D'Ugo D, Gasbarrini A, Biondi A, Persiani R. The gut microbiota and colorectal surgery outcomes: Facts or hype? A narrative review. BMC Surg. 2021;21(1):83; DOI:10.1186/s12893-021-01087-5.
50. He Y, Gao S, Jiang L, Yang J. Changes in gut microbiota after gastric cancer surgery: A prospective longitudinal study. Front Oncol. 2025;14:1533816; DOI:10.3389/fonc.2024.1533816.
51. van Praagh JB, de Goffau MC, Bakker IS, Harmsen HJM, Olinga P, Havenga K. Mucus microbiome of anastomotic tissue during surgery has predictive value for colorectal anastomotic leakage. Ann Surg. 2019;269(5):911–6; DOI:10.1097/SLA.0000000000002651.