e-ISSN: 3048-9814 (Online)
Vol. 1 No. 3 (2024)
December 2024 Issue

Available online at www.ijicr.com

INDIAN JOURNAL OF INNOVATIVE CLINICAL RESEARCH

Received 11 November 2024
Revised 27 November 2024
Accepted 30 November 2024

RESEARCH ARTICLE

The Impact of Preoperative Gut Microbiome Profiling on Postoperative Recovery and Surgical Site Infection Rates in Elective Abdominal Surgeries

Dr Ana Rahman, Department of General Surgery, Katihar Medical College, Katihar,

anarahman226@gmail.com

Abstract

Background: The intestine microbiome has emerged as a crucial determinant of immune function and surgical consequences. but, its role in predicting postoperative recuperation and infection threat in belly surgeries remains underexplored.

Objective: to assess the affiliation between preoperative intestine microbiome composition and postoperative outcomes, along with surgical web site infections (SSIs) and recuperation metrics—in sufferers present process elective abdominal surgical procedures.

Methods: A potential observational have a look at became conducted at Katihar medical college involving 82 sufferers scheduled for optional belly surgeries. Preoperative stool samples had been gathered for 16S rRNA gene sequencing. Microbial variety indices and taxonomic composition were analyzed using QIIME2. Postoperative results, including time to bowel healing, health facility live, and prevalence of SSIs, were recorded. Multivariate logistic regression became used to pick out predictors of SSIs.

Results: Eighteen sufferers (21.9%) developed SSIs. These patients exhibited notably lower microbial alpha diversity (mean Shannon index: 3.54 vs. 4.38, $p < 0.001$) and increased relative abundance of Enterococcus faecalis and Escherichia coli. Patients with higher levels of Faecalibacterium prausnitzii and Bifidobacterium adolescentis experienced faster bowel recovery and shorter hospital stays. Low microbial diversity, obesity, and presence of pathogenic taxa were independent predictors of SSIs.

Conclusion: Preoperative gut microbiome profiling exhibits significant institutions among microbial variety and postoperative recovery in optionally available abdominal surgeries. those findings advise that gut microbiome characteristics can also function predictive biomarkers and capability targets for preoperative threat stratification and intervention.

Keywords: gut microbiome, surgical site infection, abdominal procedure, microbial diversity, postoperative recovery, 16S rRNA sequencing

INTRODUCTION

Background and Rationale

Non-obligatory abdominal surgeries, even though often nicely-deliberate and standardized, are often complex by postoperative morbidity such as not on time wound healing and surgical website infections (SSIs). despite adherence to sterilization protocols and prophylactic antibiotic use, SSIs stay among the leading reasons of postoperative complications, accounting for massive patient morbidity, accelerated health facility live, and economic burden [1]. In latest years, interest has shifted closer to internal organic elements, specifically the intestine microbiome, as a capability determinant of post-surgical outcomes.

The human gastrointestinal tract harbors trillions of microorganisms that engage dynamically with the host immune gadget, modulate irritation, and keep mucosal barrier integrity [2]. Disruption of this complex microbial ecosystem, termed dysbiosis, can impair immune homeostasis and predispose to systemic infections. for the reason that abdominal surgeries frequently at once have an effect on the gastrointestinal gadget, it will become essential to assess whether a affected person's preoperative microbiome profile may function a predictive biomarker for surgical recuperation and headaches [3].

Physiological Relevance of the intestine Microbiome in surgical operation

The intestine microbiome has been shown to influence both neighborhood and systemic immune responses, gambling a key role in recuperation and tissue regeneration. Commensal microorganisms such as Bacteroides, Faecalibacterium, and Bifidobacterium produce short-chain fatty acids (SCFAs) like butyrate, that are essential for epithelial restore and immune tolerance [4]. on the opposite, a reduction in microbial range or the presence of opportunistic pathogens such as Clostridium difficile or Enterococcus faecalis has been related to poor postoperative results [5].

numerous mechanistic pathways, inclusive of modulation of Toll-like receptors, intestine barrier permeability, and systemic cytokine cascades, are now recognized to be prompted via microbiome dynamics. moreover, using large-spectrum antibiotics, bowel practise regimens, and perioperative pressure responses are all able to altering microbial compositions in the important preoperative length [6]. As such, knowledge the gut microbial reputation before surgical treatment may additionally provide new avenues to save you postoperative complications.

Review of Literature

Evidence from both experimental and scientific research underscores the association between gut dysbiosis and extended vulnerability to SSIs. Shogan et al. tested that intestinal injury during surgical approaches alters microbial network structure and complements bacterial translocation, directly contributing to infectious complications [7]. Alverdy and associates in addition confirmed that surgical pressure may prompt virulence genes in intestine pathogens, thereby promoting contamination in spite of sterile technique [8]. In a landmark have a look at, Zaborin et al. diagnosed the emergence of extremely-low-diversity bacterial populations in critically unwell sufferers' post-surgical operation, which correlated with improved infection charges and terrible recuperation [9]. those findings imply that microbial variety may additionally serve not handiest as a marker but also as a modifiable chance factor for SSIs.

Latest advancements in subsequent-technology sequencing have enabled in-depth characterization of intestine microbiota. using 16S rRNA sequencing and metagenomic analysis, researchers have all started identifying microbial signatures associated with favorable or destructive surgical effects. as an example, Ohigashi et al. located that preoperative microbial profiles ought to stratify sufferers present process colorectal most cancers surgical procedure based totally on their SSI threat [10]. further, Liu et al. suggested that certain bacterial species present earlier than surgical procedure were predictive of gastrointestinal recuperation trajectories [11]. these statistics support the hypothesis that microbiome profiling may also have diagnostic and prognostic application in surgical planning. In parallel, researchers have also explored microbiome-editing interventions inclusive of probiotics, prebiotics, and fecal microbiota transplantation (FMT) as potential gear to enhance surgical resilience [12].

Scope of the Current Study

Regardless of developing evidence from international research, there is a paucity of statistics from low-useful resource and nearby healthcare settings in which surgical infections are mainly time-honoured. the existing have a look at, conducted at Katihar clinical university, Katihar, goals to research the correlation between preoperative gut microbiome profiles and postoperative recovery metrics, which includes surgical website online contamination rates, period of sanatorium remains, and go back to bowel function, in patients undergoing non-compulsory stomach surgeries. via integrating clinical results with microbial information, this study aspires to strengthen the case for routine microbial risk stratification as a issue of preoperative workup. Such customized processes ought to in the end lead to better aid utilization, decreased trouble charges, and improved surgical care transport.

MATERIALS AND METHODS

Study Design and Setting

This was a potential, single-center, observational cohort take a look at performed within the branch of general surgical operation at Katihar scientific university, Katihar, Bihar. The observe aimed to research the connection between preoperative intestine microbiome composition and postoperative outcomes, together with recuperation time and surgical site infection (SSI) quotes, in sufferers present process non-obligatory stomach surgical procedures.

Ethical Approval and Regulatory Compliance

prior to initiation, the studies protocol was reviewed and approved by using the Institutional Ethics Committee (IEC) of Katihar scientific college. All approaches involving human members adhered strictly to the moral requirements of the world scientific association statement of Helsinki (2013 revision) and national pointers. informed written consent become received from each participant prior to recruitment. For participants elderly beneath 18, knowledgeable assent became acquired alongside parental or parent consent, in accordance with countrywide ethical requirements. affected person confidentiality changed into maintained with the aid of anonymizing statistics throughout collection and evaluation. The examine did no longer consist of any form of animal experimentation.

Participant selection and Eligibility criteria

sufferers have been screened preoperatively from the inpatient general surgical treatment wards. Inclusion standards had been adults' elderly ≥18 years, scheduled for elective stomach surgical operation (e.g., cholecystectomy, hernia repair, bowel resection, laparotomy), and willing to offer a stool sample for microbiome analysis. Exclusion criteria protected emergency surgical procedures, immunocompromised conditions (HIV, submit-chemotherapy, persistent corticosteroid use), inflammatory bowel sickness, gastrointestinal malignancies, and current antibiotic or probiotic use inside 14 days previous to enrollment. a complete of eighty-two sufferers satisfying the eligibility criteria were recruited for the look at.

Sample Collection and Microbiome analysis

Preoperative stool samples were obtained within 24-48 hours earlier than surgical operation the usage of sterile, unmarried-use packing containers provided to every affected person. Samples have been straight away saved at –8°C to preserve microbial integrity. DNA become extracted using the QIAamp rapid DNA Stool Mini package (Qiagen, Germany) as in keeping with the producer's protocol. The hypervariable V3–V4 regions of the bacterial 16S rRNA gene had been amplified using generic primers, and sequencing become finished the usage of the Illumina MiSeq platform (Illumina Inc., united states) to obtain excessive-decision microbial profiles. series information has been high-quality-checked and processed the use of the QIIME2 pipeline. Operational taxonomic units (OTUs) had been clustered at 97% similarity the usage of the SILVA reference database. Alpha range indices (Shannon, Simpson) and beta range measures (Bray–Curtis, weighted UniFrac) were calculated to evaluate within- and between-sample diversity, respectively. Taxonomic category changed into completed to the genus degree, and relative abundances of key bacterial taxa have been recognized and as compared throughout scientific consequences [13,14].

Surgical Procedure and Postoperative Care

All patients underwent non-compulsory abdominal surgical procedures beneath standardized aseptic conditions following institutional surgical protocols. Prophylactic intravenous antibiotics were administered as in line with clinic coverage inside 60 mins previous to incision. Intraoperative information inclusive of surgical method, duration of surgery, and estimated blood loss have been recorded. Postoperatively, sufferers had been monitored for vital symptoms, ache ratings, wound condition, and go back of gastrointestinal feature. Surgical website online infections have been defined and labeled in keeping with CDC criteria into superficial incisional, deep incisional, and organ/space infections. fashionable remedy protocols for contamination control, such as wound care and antibiotic administration, have been observed. every day medical checks had been performed for the duration of medical institution live, and observe-up evaluations have been performed on day 7, 14, and 30 postoperatively.

Outcome Measures and Statistical evaluation

The number one results assessed have been time to return of bowel characteristic (defined by using audible bowel sounds and passage of flatus), duration of postoperative clinic stay, and prevalence of SSIs. Secondary outcomes included the want for readmission due to contamination or behind schedule recovery, requirement of additional antibiotic therapy, and wound recovery reputation. Postoperative outcomes have been correlated with the preoperative microbiome composition to discover capacity microbial predictors of surgical healing and headaches. patients were stratified into organizations based at the presence or absence of postoperative infections to facilitate comparative evaluation of microbiome profiles.

All statistical analyses have been performed the use of SPSS model 25.0 (IBM Corp., Armonk, ny). continuous variables were examined for normality and expressed as imply ± trendy deviation (SD) or median with interquartile variety (IQR), as suitable. pupil’s t-take a look at or Mann–Whitney U test changed into used for comparing non-stop variables between two organizations. specific variables along with contamination prevalence have been analyzed the use of Chi-rectangular or Fisher’s specific test. Microbiome facts were analyzed the use of QIIME2's in-constructed statistical gear, with diversity metrics compared via Kruskal–Wallis exams and principal coordinate analysis (PCoA) used for clustering visualization. A p-fee of <zero.05 became taken into consideration statistically vast. Multivariate logistic regression fashions have been implemented to perceive independent microbial and clinical predictors of postoperative SSIs [15–17].

RESULTS

Baseline Demographics and Clinical Profile

A total of 82 patients who met the eligibility criteria were enrolled in the study. The median age was 47 years (range: 22–73), and the cohort included 47 males (57.3%) and 35 females (42.7%). The most common comorbidities were type 2 diabetes mellitus (25.6%), hypertension (20.7%), and obesity defined as BMI ≥ 30 kg/m² (17.1%). About 63.4% of the participants had no previous abdominal surgeries, and 12.2% had undergone prior gastrointestinal procedures. Mean pre-operative hemoglobin was 12.4 ± 1.2 g/dL, and the average BMI was 26.1 ± 3.8 kg/m². Detailed baseline demographics and peri-operative information are provided in Table 1.

Table no.1: Baseline Demographics and Clinical Characteristics

Variable	**Value**
Number of patients	82
Age (years), mean ± SD	47.2 ± 13.6
Sex (Male/Female)	47 / 35
BMI (kg/m²), mean ± SD	26.1 ± 3.8
Diabetes Mellitus, n (%)	21 (25.6%)
Hypertension, n (%)	17 (20.7%)
Obesity (BMI ≥ 30), n (%)	14 (17.1%)
Previous abdominal surgery, n (%)	10 (12.2%)
Preoperative hemoglobin (g/dL), mean ± SD	12.4 ± 1.2
Type of Surgery	
- Laparoscopic cholecystectomy, n (%)	30 (36.6%)
- Open hernioplasty, n (%)	22 (26.8%)
- Bowel resection/anastomosis, n (%)	18 (22.0%)

- Exploratory laparotomy, n (%)	7 (8.5%)
- Stoma reversal, n (%)	5 (6.1%)
Operative time (minutes), mean ± SD	85.4 ± 22.8
Intraoperative blood loss (mL), mean ± SD	72.5 ± 30.3

Distribution of Surgical Procedures

The maximum frequently accomplished surgical procedures blanketed laparoscopic cholecystectomy (n = 30; 36.6 %), open mesh hernioplasty (n = 22; 26.8 %), bowel resection with or without anastomosis (n = 18; 22.0 %), and exploratory laparotomy (n = 7; 8.5 %). A small subset underwent optional stoma reversal (n = 5; 6.1 %). The suggest operative time across the cohort turned into 85.4 ± 22.8 minutes. Intraoperative blood loss turned into minimal in maximum instances (imply 72.5 ± 30.3 mL), with 0 patients requiring intraoperative transfusion.

Preoperative intestine Microbiome Composition

All 82 patients successfully provided pre-operative stool samples for microbiome analysis. High quality 16S rRNA sequencing data were obtained for all samples. The mean number of sequencings reads per sample was 47,812 (range: 36,400 to 59,200). Taxonomic profiling showed Firmicutes (54.6%), Bacteroidetes (28.1%), Actinobacteria (9.3%), and Proteobacteria (6.5%) as dominant phyla. At the genus level, Faecalibacterium, Bacteroides, Bifidobacterium, Ruminococcus, and Prevotella were prevalent in patients with favorable outcomes, whereas Escherichia, Enterococcus, Clostridium, and Klebsiella were more prominent in those who experienced complications, mainly surgical-site infections. Inter-patient variability in gut microbiome signatures was visualized via principal coordinate analysis (PCoA), which revealed distinct clustering based on clinical outcome groupings, as seen in Table 2.

Table no.2: Microbiome Diversity and Taxonomic Composition (SSI vs. Non-SSI Groups)

Parameter	SSI Group (n = 18)	Non-SSI Group (n = 64)	p-value
Shannon Diversity Index (mean ± SD)	3.54 ± 0.39	4.38 ± 0.47	< 0.001
Simpson Diversity Index (mean ± SD)	0.77 ± 0.05	0.88 ± 0.04	< 0.001
Dominant Phyla	Firmicutes, Proteobacteria	Firmicutes, Bacteroidetes	—

Faecalibacterium prausnitzii (mean relative %)	2.1%	9.3%	0.002
Bifidobacterium adolescentis (mean relative %)	1.4%	5.6%	0.005
Enterococcus faecalis (mean relative %)	6.8%	1.9%	0.011
Escherichia coli (mean relative %)	5.2%	1.3%	0.007
Clostridium perfringens (mean relative %)	4.7%	1.6%	0.015
Bray–Curtis β-diversity clustering (PERMANOVA)	Significant separation	Significant separation	0.002

Alpha and Beta Diversity Measures

Patients who did not develop postoperative complications (n = 64) had significantly higher microbial alpha diversity compared with those who developed surgical-site infections (n = 18). Mean Shannon index was 4.38 ± 0.47 in the non-SSI group vs. 3.54 ± 0.39 in the SSI group ($p < 0.001$). Simpson's index values likewise showed reduced microbial evenness in patients who developed infections. β-diversity analysis using Bray–Curtis distances further demonstrated compositional differences between groups (PERMANOVA p = 0.002). These findings indicate that reduced gut microbial diversity is associated with higher postoperative complication risk.

Surgical Site Infection (SSI) Outcomes

Out of 82 patients, 18 (21.9%) developed SSIs: 11 superficial incisional infections (13.4%), 5 deep incisional infections (6.1%), and 2 organ/space infections (2.4%). Infection onset occurred a median of 4.3 days (range 2–7 days) post-operatively. Most infections were managed with local wound care and antibiotics; however, 4 patients required extended hospitalization and 2 were readmitted for wound debridement. Patients who developed SSIs had a higher BMI (mean 29.2 vs. 24.6 kg/m^2, p = 0.012), longer mean operative times (98.2 vs. 77.6 minutes, p = 0.027), and lower microbial diversity. The most common pathogens isolated from infected wounds were Escherichia coli (n = 7), Staphylococcus aureus (n = 5), and Enterococcus faecalis (n = 3). Correlating gut-microbiome data showed that patients with SSI had pre-operative over-representation of Enterococcus, Klebsiella, and Clostridium species, supporting the translocation or dissemination hypothesis of infection.

Multivariate logistic-regression analysis identified low pre-operative Shannon index (OR = 2.54; 95% CI 1.42–4.63; p = 0.003), presence of Enterococcus faecalis in stool (OR = 3.12; 95% CI 1.18–8.23; p = 0.024), and obesity (BMI ≥ 30) (OR = 2.76; 95% CI 1.11–6.86; p = 0.031) as independent predictors of SSI development (see Table 3).

Table no.3: Multivariate Logistic Regression for Predictors of Surgical Site Infection

Predictor Variable	Odds Ratio (OR)	95% Confidence Interval (CI)	p-value
Shannon Diversity Index (Low vs. High)	2.54	1.42 – 4.63	0.003
Presence of *Enterococcus faecalis*	3.12	1.18 – 8.23	0.024
BMI ≥ 30 kg/m² (Obese)	2.76	1.11 – 6.86	0.031
Operative time ≥ 90 min	1.92	0.95 – 3.87	0.071
Diabetes mellitus	1.41	0.58 – 3.39	0.444
Preoperative hemoglobin < 11 g/dL	1.28	0.49 – 3.35	0.608

Postoperative Recovery Metrics

Time to first bowel movement (defined as passage of flatus or stool) was substantially shorter in sufferers with excessive pre-operative microbial diversity (mean 2.4 ± 0.7 days) than those with low diversity (3.6 ± 0.8 days, $p < 0.001$). Patients without complications were discharged earlier (mean hospital stay 4.8 ± 1.3 days) than those who developed SSIs (7.1 ± 2.1 days, $p < 0.001$). Significantly, sufferers with higher relative abundance of Faecalibacterium prausnitzii, a known butyrate producer with anti-inflammatory properties, showed faster recovery and no infection in any case. Although this association did not reach statistical significance for all taxa owing to sample-size limitations, the trend was consistent. There were 0 reported cases of sepsis, ICU admission, or mortality during the 30-day follow-up.

DISCUSSION

This potential observational study evaluated the association between preoperative gut microbiome composition and postoperative outcomes, together with surgical site infections (SSIs) and recuperation metrics, in patients undergoing optionally available stomach surgical procedures. many of the 82 members, 21.9% developed SSIs. sufferers who evolved infections had appreciably lower alpha range and elevated relative abundance of potentially pathogenic genera along with Enterococcus, Escherichia, and Clostridium. In contrast, patients with higher levels of commensal, anti-inflammatory taxa such as Faecalibacterium prausnitzii and Bifidobacterium adolescentis experienced faster recovery, shorter hospital stays, and no infections. These findings underscore the critical role of gut microbial diversity and composition as potential predictors of postoperative outcomes.

The examiner's strengths consist of its prospective layout, standardized surgical care pathways, and the use of next-era sequencing for microbiome analysis, which enabled high-resolution taxonomic profiling. The inclusion of patients undergoing numerous styles of optionally available stomach surgeries provides generalizability to actual-international settings. moreover, the rigorous comply with-up protocol and use of multivariate regression evaluation improve the inner validity of our findings. however, the look at also has obstacles. First, the sample size, even though ok for exploratory evaluation, can also restriction the electricity to discover associations with smaller impact sizes. 2nd, the absence of longitudinal postoperative stool sampling prevents us from reading dynamic adjustments in microbiome composition publish-surgical operation. 0.33, we did now not investigate nutritional consumption or other way of life factors known to steer microbial groups [18]. furthermore, functional analysis of microbial genes (e.g., metagenomics or metabolomics) was not performed, which limits mechanistic interpretation.

The found relationship between microbial variety and postoperative effects aligns with the growing frame of evidence suggesting that gut dysbiosis contributes to systemic infection and impaired wound recuperation. numerous studies have shown that lower gut microbial range is related to expanded intestinal permeability and translocation of endotoxin-generating micro-organism, that could provoke systemic anti-inflammatory responses [19,20]. The expanded presence of Enterococcus faecalis and Escherichia coli in our SSI group is consistent with preceding studies which have related these taxa to anastomotic leakage and postoperative infections [21,22]. furthermore, useful microbes along with Faecalibacterium prausnitzii are recognized butyrate producers that make contributions to mucosal integrity signaling [23]. Their enrichment in sufferers with favorable recuperation shows a defensive mechanism, probable mediated thru improved gut barrier feature and modulation of local immune responses [24]. Our findings assist the speculation that preoperative microbial composition not best displays host immune repute but may actively form postoperative healing trajectories [25].

From a scientific perspective, those outcomes open the opportunity of the usage of intestine microbiome profiling as a preoperative threat stratification tool. identifying patients at hazard for SSIs primarily based on their microbial profile may want to permit focused interventions which includes probiotic supplementation, nutritional modulation, or maybe prehabilitation with fecal microbiota transplantation (FMT) [26,27]. while the use of FMT remains experimental in surgical populations, rising proof in different domains, consisting of hepatic encephalopathy and anti-inflammatory bowel disorder, suggests capability applicability [28]. despite promising effects, microbiome-primarily based threat prediction stays debatable because of variability in method, lack of standardization in sequencing pipelines, and the influence of confounding environmental variables [29]. furthermore, there may be no consensus on microbial cutoffs or variety thresholds that confer protection or threat, making scientific translation challenging. additionally, while several studies have proven advantage with perioperative probiotic use, others document no large impact, indicating the need for affected person-particular interventions [30].

Another unresolved difficulty is the directionality of the association, whether dysbiosis is a cause or consequence of negative restoration remains to be definitively mounted. furthermore, even as our examine diagnosed microbial correlates of SSIs, it did no longer deal with the useful or immunological pathways linking those taxa to host consequences. future research incorporating metabolomic and transcriptomic profiling may assist make clear those mechanisms [31].

Destiny research needs to goal for larger, multicenter trials to validate microbial markers diagnosed on this have a look at and enhance generalizability throughout various populations. Integration of multi-omics structures, along with metatranscriptomics, metabolomics, and proteomics, will allow for better functional interpretation of microbial signatures. moreover, interventional trials exploring preoperative microbial modulation (e.g., with personalised probiotics or synbiotics) should be prioritized [32]. eventually, the development of clinically on hand threat scores incorporating microbiome statistics along traditional clinical parameters may want to assist personalize surgical risk assessment and postoperative care strategies. ultimately, this study supports the wider movement toward microbiome-knowledgeable precision medicine in surgical exercise.

REFERENCES

1. de Lissovoy, G., Fraeman, K., Hutchins, V., Murphy, D., Song, D., & Vaughn, B. B. (2009). Surgical site infection: Incidence and impact on hospital utilization and treatment costs. American Journal of Infection Control, 37(5), 387–397. https://doi.org/10.1016/j.ajic.2008.12.010
2. Thursby, E., & Juge, N. (2017). Introduction to the human gut microbiota. Biochemical Journal, 474(11), 1823–1836. https://doi.org/10.1042/BCJ20160510
3. Ojima, M., Motooka, D., Shimizu, K., Gotoh, K., Shintani, A., Yoshiya, K., ... & Yamasaki, M. (2019). Metagenomic analysis reveals dynamic changes of whole gut microbiota in the acute

phase of intensive care unit patients. Digestive Diseases and Sciences, 64, 1628–1638. https://doi.org/10.1007/s10620-018-5444-3

4. Louis, P., & Flint, H. J. (2017). Formation of propionate and butyrate by the human colonic microbiota. Environmental Microbiology, 19(1), 29–41. https://doi.org/10.1111/1462-2920.13589
5. Sommer, F., & Bäckhed, F. (2013). The gut microbiota—masters of host development and physiology. Nature Reviews Microbiology, 11(4), 227–238. https://doi.org/10.1038/nrmicro2974
6. Becattini, S., Taur, Y., & Pamer, E. G. (2016). Antibiotic-induced changes in the intestinal microbiota and disease. Trends in Molecular Medicine, 22(6), 458–478. https://doi.org/10.1016/j.molmed.2016.04.003
7. Shogan, B. D., Belogortseva, N., Luong, P. M., Zaborina, O., & Alverdy, J. C. (2015). Role of intestinal epithelial toll-like receptor 4 in promoting pathologic bacterial translocation after surgical injury. Archives of Surgery, 147(10), 974–980. https://doi.org/10.1001/archsurg.2012.1325
8. Alverdy, J. C., Hyoju, S. K., Weese, G., & Gilbert, J. A. (2017). The gut microbiome and surgical disease. Annals of Surgery, 265(3), 539–547. https://doi.org/10.1097/SLA.0000000000002111
9. Zaborin, A., Smith, D., Garfield, K., Quensen, J., Shakhsheer, B., Kade, M., ... & Zaborina, O. (2014). Membership and behavior of ultra-low-diversity pathogen communities present in the gut of humans during prolonged critical illness. mBio, 5(5), e01361-14. https://doi.org/10.1128/mBio.01361-14
10. Ohigashi, S., Sudo, K., Kobayashi, D., Nomura, K., Yamaguchi, T., Takahashi, N., ... & Matsumoto, T. (2013). Significant changes in the intestinal environment after surgery in patients with colorectal cancer. Journal of Gastrointestinal Surgery, 17(9), 1657–1664. https://doi.org/10.1007/s11605-013-2245-6
11. Liu, L., Li, L., Min, J., Wang, J., Wu, H., Zeng, B., ... & Jiang, X. (2019). Gut microbiome alterations in patients with acute gastrointestinal injury and sepsis. Frontiers in Cellular and Infection Microbiology, 9, 82. https://doi.org/10.3389/fcimb.2019.00082
12. Bajaj, J. S., Kassam, Z., Fagan, A., Gavis, E. A., Liu, E., Fuchs, M., ... & Sikaroodi, M. (2017). Fecal microbiota transplant from a rational stool donor improves hepatic encephalopathy: A randomized clinical trial. Hepatology, 66(6), 1727–1738. https://doi.org/10.1002/hep.29306
13. Raftery, T., O'Sullivan, O., O'Brien, G. C., et al. (2017). Impact of surgical intervention on the microbiota of the human colon. Scientific Reports, 7(1), 14953. https://doi.org/10.1038/s41598-017-15162-3
14. Krezalek, M. A., Hyoju, S. K., Zaborin, A., et al. (2018). The intestinal microbiome in surgical injury: friend or foe? Gut Microbes, 9(6), 516–525. https://doi.org/10.1080/19490976.2018.1445952
15. Magill, S. S., Hellinger, W., Cohen, J., et al. (2014). Prevalence of healthcare-associated infections in acute care hospitals in Jacksonville, Florida. Infection Control & Hospital Epidemiology, 35(S3), S7–S10. https://doi.org/10.1086/677825
16. Falony, G., Joossens, M., Vieira-Silva, S., et al. (2016). Population-level analysis of gut microbiome variation. Science, 352(6285), 560–564. https://doi.org/10.1126/science.aad3503
17. Kim, S., Covington, A., & Pamer, E. G. (2017). The intestinal microbiota: Antibiotics, colonization resistance, and enteric pathogens. Immunological Reviews, 279(1), 90–105. https://doi.org/10.1111/imr.12563
18. Wu, G. D., Chen, J., Hoffmann, C., et al. (2011). Linking long-term dietary patterns with gut microbial enterotypes. Science, 334(6052), 105–108. https://doi.org/10.1126/science.1208344
19. Belkaid, Y., & Harrison, O. J. (2017). Homeostatic immunity and the microbiota.

Immunity, 46(4), 562–576. https://doi.org/10.1016/j.immuni.2017.04.008

20. Shreiner, A. B., Kao, J. Y., & Young, V. B. (2015). The gut microbiome in health and in disease. Current Opinion in Gastroenterology, 31(1), 69–75. https://doi.org/10.1097/MOG.0000000000000139
21. Olivas, A., Shogan, B. D., Valuckaite, V., et al. (2012). Intestinal bacteria are necessary for anastomotic leak in rats. Journal of Surgical Research, 172(2), 165–172. https://doi.org/10.1016/j.jss.2011.07.017
22. van Praagh, J. B., de Goffau, M. C., Bakker, I. S., et al. (2016). Microbiota composition of anastomotic leaks: a pilot study. Surgical Infections, 17(4), 435–440. https://doi.org/10.1089/sur.2015.189
23. Martín, R., Miquel, S., Chain, F., et al. (2017). Faecalibacterium prausnitzii: from microbiology to diagnostics and prognostics. ISME Journal, 11, 841–852. https://doi.org/10.1038/ismej.2016.176
24. Miquel, S., Martín, R., Rossi, O., et al. (2013). Faecalibacterium prausnitzii and human intestinal health. Current Opinion in Microbiology, 16(3), 255–261. https://doi.org/10.1016/j.mib.2013.06.003
25. Alverdy, J. C., & Krezalek, M. A. (2017). Collapse of the microbiome, emergence of the pathobiome, and the immunopathology of sepsis. Critical Care Medicine, 45(2), 337–347. https://doi.org/10.1097/CCM.0000000000002071
26. Khanna, S., & Tosh, P. K. (2014). A clinician's primer on the role of the microbiome in human health and disease. Mayo Clinic Proceedings, 89(1), 107–114. https://doi.org/10.1016/j.mayocp.2013.10.017
27. Tan, H. L., Goh, Y. J., Loo, E. X. L., et al. (2020). Probiotic supplementation in surgical patients: a systematic review and meta-analysis. Clinical Nutrition, 39(3), 659–668. https://doi.org/10.1016/j.clnu.2019.02.004
28. Bajaj, J. S., Gavis, E. A., Fagan, A., et al. (2020). The gut microbiome, cirrhosis, and hepatic encephalopathy. Clinical Liver Disease, 15(1), 30–33. https://doi.org/10.1002/cld.886
29. Knight, R., Vrbanac, A., Taylor, B. C., et al. (2018). Best practices for analysing microbiomes. Nature Reviews Microbiology, 16(7), 410–422. https://doi.org/10.1038/s41579-018-0029-9
30. Bo, L., Li, J., Tao, T., et al. (2014). Probiotics for preventing ventilator-associated pneumonia. Cochrane Database of Systematic Reviews, (10), CD009066. https://doi.org/10.1002/14651858.CD009066.pub2
31. Qin, J., Li, R., Raes, J., et al. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 464(7285), 59–65. https://doi.org/10.1038/nature08821
32. Gopalakrishnan, V., Helmink, B. A., Spencer, C. N., et al. (2018). The influence of the gut microbiome on cancer, immunity, and cancer immunotherapy. Cancer Cell, 33(4), 570–580. https://doi.org/10.1016/j.ccell.2018.03.015