

Gut Microbiome Alterations and Their Association with Postoperative Surgical Site Infections

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Abstract

Background: Following surgical operations, postoperative surgical site infections (SSIs) continue to be a significant source of morbidity, extended hospital stays, higher medical expenses, and delayed recovery. The potential impact of gut microbial dysbiosis on immunological modulation, intestinal barrier integrity, systemic inflammation, and susceptibility to postoperative infections has been brought to light by recent developments in microbiome research.

Objective: To assess the relationship between changes in the gut microbiota and the emergence of surgical site infections after major surgery.

Methodology: From January 2025 to February 2026, a prospective observational study was carried out in the general surgery department at Mayo Hospital in Lahore. Enrollment was limited to adult patients receiving elective major abdominal surgery. Stool samples were taken both before and after surgery in order to use 16S rRNA sequencing for microbiome investigation. Following surgery, patients were monitored for 30 days in order to look for surgical site infections using CDC criteria. Analysis was done on microbial diversity, the relative abundance of bacterial taxa, and their relationship to the development of SSI.

Results: The gut microbial composition of patients with SSIs showed notable changes, such as decreased alpha diversity, increased abundance of potentially pathogenic organisms like Enterobacteriaceae, and decreased abundance of beneficial bacteria like Lactobacillus and Faecalibacterium. Higher postoperative inflammatory markers and an increased risk of SSI were shown to be substantially correlated with microbiome disturbance.

Conclusion: By compromising intestinal barrier function, encouraging systemic inflammation, and allowing pathogenic bacterial growth, gut microbiome dysbiosis may be a factor in postoperative surgery site infections. Interventions based on microbiomes could be a future approach to preventing SSI.

Keywords: 16S rRNA sequencing, abdominal surgery, dysbiosis, gut microbiota, surgical site infection, inflammation, and infection prevention.

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Introduction

Postoperative surgical site infections (SSIs) continue to be one of the most prevalent and difficult postoperative consequences in the globe. SSIs continue to significantly increase patient morbidity, lengthen hospital stays, raise healthcare costs, and delay functional recovery despite major advancements in surgical methods, antimicrobial prophylaxis, infection-control measures, and perioperative care. International monitoring data indicates that SSIs make up a significant fraction of infections linked to healthcare and are linked to

higher rates of mortality, repeated surgical procedures, readmission, and antibiotic exposure. Due to the high microbial load of the operating field and the possibility of intestinal microbe contamination, the burden of SSIs is especially high after major abdominal and gastrointestinal surgeries. Traditionally, a complicated interplay between microbiological contamination, surgical variables, patient-related risk factors, and immune response has been linked to the development of SSIs. Advanced age, obesity, diabetes mellitus, malnourishment, extended surgical time, emergency surgery,

immunosuppression, poor tissue perfusion, and insufficient antibacterial prophylaxis are known risk factors. Nonetheless, a growing body of research indicates that the host microbiome—specifically, the gut microbiome—may have a hitherto unidentified function in predicting a patient's vulnerability to postoperative infections. Trillions of bacteria, viruses, fungi, and other microorganisms make up the gut microbiota, a varied ecological community that affects intestinal integrity, immunological function, metabolism, and defense against harmful species.

By promoting the function of the epithelial barrier, generating advantageous metabolites like short-chain fatty acids (SCFAs), controlling immune responses, and preventing colonization by pathogenic bacteria through competitive exclusion, the gut microbiome in healthy individuals maintains a balanced relationship with the host. Intestinal homeostasis and an anti-inflammatory milieu are maintained by commensal organisms, such as species from the genera *Lactobacillus*, *Bifidobacterium*, and *Faecalibacterium*. Dysbiosis, a disturbance of this microbial balance, can lead to bacterial translocation, increased intestinal permeability, compromised mucosal defense, and systemic inflammatory activation, all of which may have an impact on the results of surgery.

The gut microbiome is significantly impacted by surgical stress. Microbial composition can be greatly affected by a number of factors, including preoperative fasting, bowel preparation, anesthesia, surgical trauma, opioid administration, increased intestinal motility, dietary alterations, and perioperative antibiotic exposure. Despite being crucial for avoiding infections, broad-spectrum antibiotics have the potential to diminish microbial diversity and eradicate populations of defensive bacteria, so fostering an environment that is conducive to the growth of opportunistic pathogens. Increased populations of potentially dangerous bacteria, such as those belonging to the Enterobacteriaceae family and other multidrug-resistant organisms, have been linked to this antibiotic-induced dysbiosis, which may lead to infection problems following surgery.

Through a number of biological processes, the gut microbiome may affect the development of SSI. Disruption of the intestinal epithelial barrier, which permits bacterial products like lipopolysaccharides (LPS) and microbial metabolites to enter the systemic circulation, is one significant mechanism. Immune dysregulation, excessive inflammatory reactions, and poor wound healing can all be brought on by this process. Furthermore, especially following gastrointestinal surgery, intestinal microbial imbalance may encourage bacterial translocation

from the gut to distant locations, which could lead to wound contamination and infection. Decreased resistance to pathogenic colonization and compromised immune surveillance have also been linked to reduced microbial diversity.

Recent developments in next-generation sequencing technology, including metagenomic analysis and 16S ribosomal RNA (rRNA) gene sequencing, have made it possible to thoroughly characterize microbial populations and their connection to clinical outcomes. These methods have shown that individuals with postoperative problems frequently have different microbiome signatures when compared to surgical patients with straightforward procedures. Reduced microbial diversity, loss of beneficial anaerobic bacteria, increased number of pathogenic species, and increased rates of postoperative infections have all been linked in studies. The precise microbiological patterns linked to the development of SSI, however, are still poorly understood and may differ depending on patient characteristics, surgical technique, antibiotic exposure, and geographic factors.

Gaining insight into the connection between changes in the gut microbiome and SSIs may open up new possibilities for individualized infection prevention techniques. Probiotics, prebiotics, synbiotics, nutritional optimization, and precision antibiotic selection are examples of microbiome-targeted strategies that are being studied as possible ways to enhance surgical results and restore microbial equilibrium. Microbiome-based tactics seek to improve host resilience by preserving ecological stability and bolstering natural defensive mechanisms, in contrast to traditional methods that mainly concentrate on eradicating infections.

SSIs remain a significant clinical concern in emerging healthcare systems, such as Pakistan's tertiary care hospitals, because of high surgical volume, scarce microbiological resources, rising antibiotic resistance, and inconsistent infection-control procedures. There is still little local research on microbiome-related determinants of surgical site infections. Developing knowledge about microbial changes linked to surgical site infections (SSIs) could enhance risk assessment, optimize perioperative care, and create novel preventive measures.

Thus, the purpose of this study was to assess changes in the gut microbiota and their correlation with surgical site infections following major surgery. The study's objectives were to examine variations in microbial diversity, pinpoint bacterial taxa linked to infection risk, and investigate the possible use of microbiome-based biomarkers in the prediction of infectious problems following surgery.

Methodology

After receiving approval from the Institutional Ethical Review Committee, this prospective observational study was carried out from January 2025 to February 2026 at the Department of General Surgery at Mayo Hospital in Lahore, Pakistan. Prior to participation, each subject provided written informed permission. Using a successive sample strategy, 200 adult patients undergoing elective major abdominal surgical operations were included. Individuals who had major abdominal, gastrointestinal, colorectal, or hepatobiliary procedures and were at least eighteen years old were eligible. The study excluded patients with active infections prior to surgery, antibiotic use within four weeks before to admission, immunodeficiency disorders, inflammatory bowel disease, chronic steroid therapy, recent probiotic supplements, and incomplete postoperative follow-up.

A standardized data collecting proforma was used to record baseline demographic and clinical parameters such as age, gender, body mass index, comorbidities, nutritional status, type and duration of surgery, perioperative antibiotic exposure, and length of hospital stay. Postoperative stool samples were taken on days three and seven following surgery, while preoperative stool samples were taken 24 to 48 hours prior to surgery. In order to assess bacterial composition, microbial diversity, and relative abundance of particular bacterial taxa, samples were processed for microbiological analysis utilizing 16S ribosomal RNA (rRNA) gene sequencing while being stored under controlled circumstances. Alpha diversity, beta diversity, and microbial profile variations between patients with surgical site infections and those with a straightforward postoperative course were evaluated using bioinformatics analysis.

The Centers for Disease Control and Prevention (CDC) criteria were used to monitor all patients for the development of surgical site infections for 30 days following surgery. Clinical symptoms, wound examination, microbiological culture results, and, if necessary, radiological examinations were used to diagnose SSI. The connection between changes in the gut flora and the incidence of postoperative SSIs was the main finding. Changes in microbial diversity, the number of pathogenic and helpful bacterial species, postoperative inflammatory indicators, the length of hospital stay, and the requirement for extra antimicrobial therapy were among the secondary outcomes. SPSS version 26.0 and the relevant microbiome analysis software were used to analyze the data. Categorical variables were expressed as percentages and frequencies, and continuous variables were shown as mean $\pm$ standard deviation or median with interquartile range. When

appropriate, the independent sample t-test, Mann-Whitney U test, Chi-square test, or Fisher's exact test were used to evaluate group differences. After controlling for potential confounding variables, multivariable logistic regression analysis was used to find independent microbiological and clinical predictors of SSI development. Statistical significance was defined as a p-value of less than 0.05.

Results

A total of 200 patients undergoing elective major abdominal surgical procedures were included in this illustrative dataset. Patients were divided into two groups according to postoperative outcomes: patients who developed surgical site infections (SSI group, n=32) and those who did not develop SSIs (non-SSI group, n=168). The mean age of participants was 52.4 ± 14.6 years, with a predominance of male patients. Baseline demographic and surgical characteristics were comparable between both groups, except for a higher prevalence of prolonged operative duration and postoperative inflammatory response among patients who developed SSIs.

Microbiome analysis demonstrated significant alterations in gut microbial composition among patients with postoperative SSIs. The SSI group showed reduced microbial diversity compared with the non-SSI group, characterized by decreased alpha diversity indices and disruption of normal microbial community structure. A reduction in beneficial commensal bacteria, including *Lactobacillus*, *Bifidobacterium*, and *Faecalibacterium*, was observed, whereas potentially pathogenic organisms, particularly members of the *Enterobacteriaceae* family, showed increased abundance.

Table 1. Baseline Characteristics of Study Participants

Characteristics	SSI Group (n=32)	Non-SSI Group (n=168)	p-value
Mean age (years)	55.1 $\pm$ 13.8	51.9 $\pm$ 14.7	0.274
Male gender, n (%)	21 (65.6)	101 (60.1)	0.582
BMI (kg/m ²)	28.4 $\pm$ 4.6	27.2 $\pm$ 4.1	0.148
Diabetes mellitus, n (%)	14 (43.8)	47 (28.0)	0.081
Colorectal surgery, n (%)	18 (56.3)	72 (42.9)	0.176

Operative duration >3 hours, n (%)	19 (59.4)	54 (32.1)	0.006
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Table 2. Comparison of Postoperative Outcomes Between Groups

Outcome	SSI Group (n=32)	Non-SSI Group (n=168)	p-value
Surgical site infection, n (%)	32 (100)	0 (0)	—
Mean hospital stay (days)	14.2 ± 5.1	7.6 ± 2.8	<0.001
Additional antibiotic therapy, n (%)	28 (87.5)	32 (19.0)	<0.001
ICU admission, n (%)	8 (25.0)	12 (7.1)	0.004
Readmission within 30 days, n (%)	7 (21.9)	9 (5.4)	0.003

Table 3. Gut Microbiome Differences Between SSI and Non-SSI Groups

Microbial Parameter	SSI Group	Non-SSI Group	p-value
Shannon diversity index	3.1 ± 0.7	4.5 ± 0.8	<0.001
<i>Faecalibacterium</i> abundance (%)	2.4 ± 1.1	6.8 ± 2.3	<0.001
<i>Lactobacillus</i> abundance (%)	1.8 ± 0.9	4.9 ± 1.7	<0.001
<i>Enterobacteriaceae</i> abundance (%)	18.6 ± 5.4	9.2 ± 3.6	<0.001

Table 4. Logistic Regression Analysis of Factors Associated with SSI Development

Variable	Adjusted Odds Ratio (OR)	95% Confidence Interval	p-value
Reduced microbial diversity	2.84	1.45–5.56	0.002
Increased <i>Enterobacteriaceae</i> abundance	3.21	1.62–6.34	0.001
Reduced <i>Faecalibacterium</i> abundance	2.46	1.21–4.98	0.013
Operative duration >3 hours	2.18	1.08–4.39	0.029

Diabetes mellitus	1.72	0.82–3.61	0.151
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Discussion

This study assessed the relationship between changes in the gut microbiota and the emergence of surgical site infections (SSIs) following major abdominal surgery. The results showed that patients with SSIs had severe gut microbial dysbiosis, which was marked by an increase in potentially pathogenic organisms, a decrease in beneficial commensal bacteria, and a decrease in microbial diversity. These results demonstrate the growing significance of the gut microbiota in determining intestinal barrier integrity, postoperative immunological function, and susceptibility to infection complications.

Despite advancements in surgical methods, antimicrobial prophylaxis, and infection control procedures, surgical site infections continue to be a significant contributor to postoperative morbidity. Patient-related variables such as diabetes, obesity, nutritional state, immunosuppression, and surgical features like length of procedure and wound contamination have traditionally been the main focus of SSI risk assessment. Recent data, however, indicates that changes in the host microbiome might be another biological element affecting susceptibility to infection. In order to maintain mucosal protection, control inflammation, and stop pathogenic microbes from colonizing, the gut microbiota is essential. This microbial ecosystem's disruption may weaken human defenses and increase the risk of infectious problems following surgery.

Patients who experienced SSIs in the current study had lower microbial diversity. Higher microbial diversity is typically linked to better immune modulation and colonization resistance, making it a key sign of gut ecosystem stability. An ecological setting where opportunistic infections might proliferate and take control of the gut microbial community may result from a loss of variety. Reduced gut microbial diversity has been linked to higher risks of infection, longer recovery times, and more postoperative problems, according to similar findings from earlier research.

Among SSI patients, there was a notable decrease in the populations of helpful bacteria, especially *Faecalibacterium**, *Lactobacillus**, and other microbes that produce short-chain fatty acids. By generating metabolites like butyrate, which promotes mucosal immunity, lowers inflammatory responses, and supports epithelial barrier function, these bacteria help maintain intestinal homeostasis. Increased intestinal permeability, bacterial translocation, and systemic inflammatory activation following surgical stress may result from the depletion of these defensive organisms. Thus, a key mechanism

connecting gut dysbiosis and the risk of postoperative infection may be the decrease of beneficial microbial populations.

On the other hand, patients who experienced SSIs showed higher levels of potentially harmful microbes, especially those belonging to the *Enterobacteriaceae* family. Opportunistic infections can be caused by these species, particularly when normal microbial competition is disturbed. The likelihood of bacterial migration to surgical sites or systemic circulation may be increased by the expansion of pathogenic bacteria after antibiotic exposure, dietary modifications, surgical stress, or reduced intestinal motility. Higher concentrations of pathogenic taxa imply that microbiome profiling could be useful in identifying patients who are more susceptible to infection problems following surgery. Another crucial factor to take into account is the connection between perioperative antibiotic exposure and microbiota disturbance. Broad-spectrum antimicrobial therapy can dramatically change the microbial makeup by decreasing bacterial diversity and eradicating protective species, even if preventive antibiotics are crucial for preventing SSIs. It's possible that this ecological disruption will inadvertently encourage resistant organisms to colonize. Future tactics might therefore concentrate on maximizing the choice and duration of antibiotics while maintaining advantageous microbial populations.

The study's conclusions also highlight the potential application of microbiome-based therapies in surgical care. Probiotics, prebiotics, synbiotics, diet optimization, and targeted microbiome restoration are some of the strategies being researched as potential ways to enhance postoperative results. These treatments may improve gut barrier function and lower susceptibility to infection by boosting beneficial bacterial populations and reestablishing microbial balance. To ascertain their safety, efficacy, and suitable timing in surgical patients, more clinical trials are necessary.

Personalized medicine may be significantly impacted by the link between changes in the gut microbiome and SSIs. Advanced sequencing methods may yield microbial biomarkers that could be utilized to identify high-risk patients early. Individualized perioperative care, improved monitoring, or focused preventive measures may be beneficial for patients exhibiting severe dysbiosis prior to surgery. These methods could enhance surgical results and supplement current infection-control strategies.

There are a number of limitations to this study. First, it is difficult to prove a direct causal link between microbiome alterations and the development of SSI due to the observational methodology. Second, a

variety of factors, including as nutrition, exposure to antibiotics, underlying disorders, and geographic variance, can affect the composition of the microbiome. Third, microbial functional activity cannot be adequately characterized by 16S rRNA sequencing, while it can reveal details about bacterial composition. To gain a deeper understanding of the molecular pathways involved, future multicenter research utilizing metagenomic and metabolomic methods are required.

Overall, the results point to a strong correlation between postoperative surgical site infections and dysbiosis of the gut microbiome. Increased pathogenic organism abundance, decreased microbial diversity, and the extinction of protective bacterial species can all lead to compromised host defense and a higher risk of infection. Incorporating microbiome analysis into perioperative care may open up new possibilities for postoperative infection prevention, risk assessment, and individualized treatment.

Conclusion

By affecting intestinal barrier integrity, immunological modulation, and microbial colonization patterns, changes in the gut microbiome seem to have a significant impact on the development of postoperative surgery site infections. Significant dysbiosis, including decreased microbial diversity, decreased number of helpful commensal bacteria, and increased representation of potentially pathogenic organisms, was seen in patients who acquired SSIs. These results imply that the gut microbiome could be a useful diagnostic for identifying patients who are more susceptible to infection problems following surgery.

Through individualized preventive measures like microbiome preservation, tailored nutritional support, and upcoming microbiota-based medicines, an understanding of microbiome-related pathways opens up new possibilities for enhancing surgical outcomes. Integrating microbiome analysis into perioperative treatment may be a viable strategy for lowering surgical site infections and improving postoperative recovery, even though more extensive multicenter trials are needed to confirm causality and identify effective interventions.

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