

## Narrative Review

# The intricate interplay between acute pancreatitis and small intestinal bacterial overgrowth: Unraveling the unknown



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## ARTICLE INFO

## Article history:

Received 19 March 2025

Accepted 11 June 2025

## Keywords:

Acute pancreatitis

Small intestinal bacterial overgrowth

Gut dysbiosis

Bacterial translocation

## SUMMARY

Small intestinal bacterial overgrowth (SIBO) refers to the overcolonization of bacteria in the small intestine. Multiple studies have shown a correlation between SIBO and the occurrence and development of various diseases. This review focuses on the relationship between SIBO and acute pancreatitis (AP), summarizing the current research on the interaction and development between SIBO, AP, and gut microbiota translocation. It is emphasized that AP may lead to the generation of SIBO by prolonging the migrating motor complex (MMC) time and weakening the intestinal barrier. SIBO also plays a critical role in the development and deterioration of AP, which is related to the poor prognosis of AP through the intermediate factor of bacterial translocation (BT). Dysregulated bacteria and their metabolites can promote the occurrence of inflammatory cytokine storms through a series of immune signaling pathways. Furthermore, we summarize the promising treatments to improve AP by clearing SIBO and form a new therapeutic intervention strategy based on regulating gut microbiota and improving intestinal motility. For AP patients, rifaximin, probiotics, butyrate, and others targeting SIBO may be more effective in reducing the complications of AP and achieving better clinical outcomes, but further research is needed to validate this hypothesis.

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## 1. Introduction

Small intestinal bacterial overgrowth (SIBO) is defined as the presence of an excessive amount of bacteria in the upper gastrointestinal tract [1]. The traditional diagnostic threshold for SIBO is a bacterial concentration of  $\geq 10^5$  colony-forming units (CFU)/mL in jejunal culture [2]. However, this criterion has long been a subject of debate. Recent studies have revealed that the microbial load in the small intestinal fluid of healthy individuals typically remains below  $10^3$  CFU/mL. Clinically significant bacterial overgrowth, reaching concentrations of  $10^6$ – $10^7$  CFU/mL, is generally observed only in post-surgical conditions such as gastrectomy [3]. The conventional diagnostic threshold for SIBO has been reconsidered due to its excessive stringency. Current clinical guidelines,

including both the North American consensus and the American College of Gastroenterology (ACG) recommendations, now define SIBO as a bacterial concentration of  $\geq 10^3$  CFU/mL in jejunal aspirate cultures [4]. An alternative measurement of exhaled hydrogen and methane during the breath test is considered a non-invasive, safe, functional, and cost-efficient method for SIBO. The most used breath test standard for diagnosing SIBO at present is the North American consensus. It recommended that a rise in hydrogen of  $\geq 20$  parts per million (ppm) or methane levels  $\geq 10$  ppm by 90 min during a glucose or lactulose breath test was considered positive [4]. The concept of gut methane-producing microorganism overgrowth has emerged as an important development in gastrointestinal research. Critically, these methane-producing organisms are not true bacteria (which comprise the “B” in SIBO) but rather belong to the domain Archaea, representing a phylogenetically distinct group of prokaryotes. In recognition of this fundamental taxonomic difference, we propose adopting the term intestinal methanogenic overgrowth (IMO) to properly characterize this condition, where methanogenic archaea, particularly *Methanobrevibacter smithii*, predominate instead of

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conventional SIBO-associated bacteria [5,6]. Epidemiological retrospective studies have found that SIBO is more common in the elderly and is a common cause of diarrhea and malnutrition. Abdominal pain, bloating, belching, and diarrhea are the four most common symptoms in SIBO patients. In more severe cases of SIBO, patients may also experience steatorrhea and malabsorption of fat-soluble vitamins. Thus, no single symptom can be attributed explicitly to SIBO [5]. Its diagnosis is prone to confusion with other diseases, such as inflammatory bowel disease (IBD), irritable bowel syndrome (IBS), and functional dyspepsia [7]. Studies have found that the relationship between SIBO and IBD is complex, and many IBD patients may also have SIBO [8]. However, there is currently limited research on the mechanism of action of SIBO in pancreatic diseases, and specific intervention measures still need to be further explored. At present, there is still no clear and unified conclusion about the pathogenesis of SIBO. Myogenic or neurogenic intestinal motility disorders (such as intestinal obstruction, scleroderma, diabetes, hypothyroidism), operations that change the anatomical structure of the gastrointestinal tract (such as diverticulum, gastrectomy), impaired gastrointestinal defense function, and immune deficiency diseases are all susceptible factors of SIBO [9].

Acute pancreatitis (AP) is a common acute abdominal disease, mainly caused by biliary tract disease and excessive alcohol consumption. Other causes may include post-endoscopic retrograde cholangiopancreatography (ERCP), medication, viral infection, metabolic disorders, and abdominal trauma, with some cases being idiopathic [10]. Although most cases have mild and self-limiting conditions, 15–20 % of them will progress to severe acute pancreatitis (SAP), with a mortality rate of up to 30 % [11]. Infectious pancreatic necrosis (IPN) is associated with a higher mortality rate, with over 80 % of SAP deaths associated with enterogenous infections [12]. The translocation of bacteria has been proven to be a significant factor in the secondary acute inflammation and septic shock of AP [13]. Previous studies have found that the acute physiology and chronic health evaluation II (APACHE-II) score of AP patients is positively correlated with the presence or absence of bacteremia, indicating that an increase in the number of bacteria in the patient's circulation can lead to an increase in the severity of AP [14].

The overall balance of the gut microbiota maintains normal physiological functions in the host. Recent studies have confirmed the importance of the human gut microbiota in maintaining health and participating in disease processes. The composition of the gut microbiota plays a crucial role in regulating the immune response to invading pathogens in humans, and it also helps prevent pathogens from crossing the intestinal barrier [15]. The disruption of the intestinal barrier can exacerbate bacterial translocation (BT) and enterogenous infections, leading to the progression of AP [16]. However, only a small portion of research focuses on exploring the correlation between SIBO and AP, as well as how the two interact and influence each other. This review can fill the gap in this field by summarizing the current research on the interaction and development between SIBO, AP, and gut microbiota translocation. We also hope our research can provide prospects for novel treatments for AP patients in the future: improving AP through targeted BT in the intestine.

## 2. Small intestinal bacterial overgrowth attributed to acute pancreatitis

Retrospective studies have shown a higher prevalence of SIBO in patients with AP. Moreover, there are statistically significant differences in the occurrence of SIBO among patients with different severities of AP. Specifically, the incidence of SIBO in mild

acute pancreatitis (MAP), moderate-severe acute pancreatitis (MSAP), and SAP is reported to be 8.42 %, 25.58 %, and 25.92 %, respectively [17]. Additionally, studies have found that AP patients exhibit relatively higher concentrations of exhaled H<sub>2</sub> and CH<sub>4</sub>, indicating a correlation between elevated levels of intestinal bacteria and AP [18].

### 2.1. Acute pancreatitis triggers the occurrence of SIBO through abnormal small intestinal motility

As previously mentioned, myogenic or neurogenic motility disorders are susceptibility factors for SIBO [19]. It has been reported that the average small intestine transit time of SIBO patients is twice that of healthy individuals, indicating that small intestine motility stasis may play an essential role in the occurrence of SIBO. The migrating motor complex (MMC), acting as the “housekeeper” of the gastrointestinal tract and a necessary indicator of gastrointestinal motility, is closely related to the occurrence of SIBO [20,21]. The inappropriate extension of the MMC cycle can impair the ability to clear food residues from the digestive system, which has been reported to be associated with conditions including SIBO, gastroparesis, and intestinal pseudo-obstruction [22]. The pathogenic mechanism may be that prolonged MMC cannot inhibit bacterial attachment to the intestinal wall, and food residues stay in the gut for an extended period, causing the proliferation of aerobic and anaerobic microorganisms [23].

At present, studies from patients with multiple diseases have proved that prolonged MMC can lead to SIBO. For example, the prevalence of SIBO in the population with diabetes is higher than that in the normal control population significantly. Complications such as autonomic neuropathy triggered by poor control of diabetes are just one of the factors that damage gastrointestinal motility, cause gastroparesis, delay gastric emptying, and lengthen MMC [24,25]. It was found that the frequency of phase III MMC decreased in IBS patients with SIBO, indicating that the abnormal hydrogen breath test results in IBS patients may be secondary to gastrointestinal motility defects in the small intestine [26]. Systemic sclerosis, as a multisystem connective tissue lesion, has an impact on the gastrointestinal tract, manifested as gastric paresis or delayed gastric emptying, disrupting the normal cycle of MMC. Retrospective studies have found that the incidence of SIBO in patients with systemic sclerosis is as high as 40 % [27]. Delayed gastric emptying and prolonged gastrointestinal transit time were seen in Parkinson's disease, along with a higher prevalence of SIBO, as high as 25 % [28]. The study from the cohort of advanced radiation-induced enteropathy showed that abnormal colonization of Gram-negative bacteria in the duodenum was associated with the strength of MMC [29]. A meta-analysis revealed that patients with cirrhosis exhibit a significantly higher prevalence of SIBO than healthy controls. The pooled incidence of SIBO was 40.8 % in cirrhotic patients versus 10.7 % in the control group. Notably, decompensated cirrhosis was associated with an even greater likelihood of SIBO than compensated cirrhosis, suggesting a correlation with disease severity. This increased susceptibility may be attributed to delayed small intestinal motility, which is frequently observed in cirrhotic patients with SIBO [30]. And the MMC cycle was significantly prolonged compared to healthy people using an intraluminal pressure measurement to observe the small intestine contraction movement.

A number of evidence from animal experiments support a strong association between SIBO and MMC. A study on the effect of gastrointestinal electromyographic complexes on the gut microbiota of rats found that the use of morphine to destroy MMC promoted excessive growth and translocation of bacteria in the

duodenum [31], especially Gram-negative bacterial colonization in the small intestine, suggesting that MMC is an important regulatory mechanism of the upper gut microbiota [32]. Another study on rats blocked the proximal common bile duct (CBD) showed that the length of the MMC cycle was prolonged compared to before obstruction, and the bacterial levels in the jejunum were higher than those in the control and significantly correlated with the length of the MMC cycle [33].

Similarly, AP can also affect MMC. The interruption of MMC cycle length resulted in a decrease in the dominant frequency and dominant power of slow waves in L-ornithine-induced acute necrotizing pancreatitis (ANP) rats [34]. Some studies have also induced AP in rats through bile duct ligation and found that the MMC interval was significantly prolonged, intestinal motility was damaged, and the intestinal migratory electromyography complex was inhibited after 48 h of bile duct ligation compared to before ligation [17,35]. Therefore, AP may generate SIBO by prolonging MMC time. AP leads to the destruction of MMC; thus, secondary gastrointestinal motility damage and activity reduction may be the main pathogenic factors of SIBO [36].

## 2.2. Acute pancreatitis triggers the occurrence of small intestinal bacterial overgrowth by disrupting the intestinal barrier

The intestinal barrier refers to a significant barrier that can separate the intestinal cavity from the internal environment of the organism, preventing harmful substances and pathogens from entering the internal environment of the organism and maintaining the stability of the internal environment. When the intestinal barrier mechanism fails, the disrupted “geographical distributions” bring about differences in the types and quantities of bacteria colonizing the small intestine [37]. AP can affect the permeability of the intestinal barrier, which is one of the main pathogenic pathways for SIBO.

The mechanical barrier is composed of intestinal mucosal epithelial cells (absorbing goblet cells and Pan cells) and intercellular junctions: tight junctions (TJs), gap junctions, adhesive junctions, and desmosome junctions. Among them, TJs are the most critical link, including occludin, claudin protein, perimembrane protein family (ZO protein), and connecting adhesion molecules [38]. AP can cause mechanical barrier dysfunction in the duodenum. The intestinal mucosal permeability of SAP patients increased due to the detection of ruptured intestinal mucus layer, actin rearrangement, and decreased cell connectivity [39]. Meanwhile, animal experiments verified the down-regulated expression of TJs in the duodenum of MAP and SAP mice in accordance with the severe duodenal pathological damage [40]. The mechanisms by which AP disrupts the intestinal mechanical barrier may be as follows. First, a large amount of fluid replacement leads to intestinal reperfusion, increases the permeability between intestinal epithelial cells, and reduces the function of the intestinal barrier [41]. Second, fasting and, if necessary, performing gastrointestinal decompression leads to a lack of nutrition in the intestinal mucosal epithelium, resulting in epithelial cell atrophy and apoptosis, thinning of villi, and damage to the mechanical barrier of the intestine. Suppose the integrity of the intestinal barrier is compromised. In that case, intestinal barrier leakage can occur, allowing luminal contents to enter the bloodstream, activating immune responses, triggering inflammation, and forming the basis of many diseases, including but not limited to SIBO [42].

The chemical barrier refers to chemical substances secreted by the gastrointestinal tract, such as bile, gastric acid, digestive enzymes, and lysozyme. In AP patients undergoing parenteral nutrition, chemicals are reduced, leading to the breakdown of the intestinal barrier [43].

The biological barrier is a microorganism competitively inhibiting the colonization and growth of pathogenic bacteria in the intestinal epithelium. The disruption of the intestinal barrier promotes the translocation of intestinal bacteria. Studies have observed that in the early stages of SAP, the abundance of beneficial bacteria such as *Bifidobacteria* decreases, weakening their inhibitory effect on pathogenic bacteria, which in turn increases the colonization of pathogenic bacteria such as *Escherichia coli* and *Streptococcus* in the ileum [13,44]. Bacteria are also more likely to infect the abdominal cavity through the bile duct or pancreatic duct, or the outside of the intestine retrogradely [45], indicating that maintaining the stability of the intestinal barrier is an integral part of AP treatment.

Secretory Immunoglobulin A (IgA) and complement are crucial immune defense factors of the intestinal mucosa to exert anti-bacterial effects. Previous studies have found that the levels of endotoxin core antibody Immunoglobulin M (IgM), the plasma levels of tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ), and interleukin (IL)-6/8/10 are higher than those in healthy individuals [46]. The disruption of the intestinal barrier and bacterial translocation (BT) can also have a negative impact on mucosal immune response [38]. The process of pathogenic bacteria crossing the epithelial barrier can activate mucosal immune responses and promote the release of a series of pro-inflammatory cytokines such as interferon- $\gamma$ , TNF- $\alpha$ , IL-1  $\beta$ , and IL-6, further disrupting the function of TJs protein and causing further damage to the mechanical barrier, exacerbating BT and disrupting the normal gut microbiota through a vicious cycle.

## 3. Small intestinal bacterial overgrowth exacerbates the progression of acute pancreatitis

Multiple objective indicators suggest that patients with AP complicated by SIBO show more terrible conditions. Organ failure in patients with AP who develop SIBO is significantly more severe than in those without SIBO [17]. Another study found that higher levels of H<sub>2</sub> and CH<sub>4</sub> in the breath of AP patients are associated with oral glucose intolerance and a higher risk of hyperglycemia, which is one of the indicators of worsening AP [18]. All of these findings indicate that SIBO can exacerbate the progression of AP. However, the occurrence rate of infection or local complications, such as pancreatic necrosis, pseudocysts, or pancreatic abscesses, is not related to the presence of SIBO [17]. Therefore, it is imperative to conduct a deeper exploration of SIBO and the outcome and prognosis of AP.

### 3.1. Small intestinal bacterial overgrowth and acute pancreatitis are both associated with the disruption of gut microbiota

#### 3.1.1. Bacterial and concomitant immunity alterations in small intestinal bacterial overgrowth

The alterations of gut microbiota in SIBO can be summarized as a decrease in beneficial bacteria abundance and an increase in pathogenic bacteria abundance in the small intestine. At the phylum level, the study from duodenal aspirates showed a higher relative abundance of Proteobacteria and a lower relative abundance of Firmicutes in SIBO subjects compared to non-SIBO subjects [47]. Subjects with SIBO exhibited lower microbial diversity in accordance with Proteobacteria abundance, indicating that dysbiosis related to Proteobacteria may serve as a microbial marker for SIBO [48,49]. At the genus level, the small intestinal microbiota of SIBO patients using 16S rRNA sequencing revealed an increased relative abundance of *Escherichia* and *Klebsiella*, members of the Proteobacteria, which was associated with symptoms such as abdominal pain and bloating. Histamine produced by *Klebsiella* has been found to have a significant impact on

visceral hypersensitivity. It is related to the disruption of the regular microbial network in the duodenum [50], with detrimental effects on microbial metabolism pathways [51]. A study using the same 16srRNA method for sequencing fecal samples from subjects found that compared to the healthy control group, the abundance of *Coprococcus* in SIBO increased and showed a positive correlation with the severity of a series of discomfort symptoms in SIBO patients [52]. Studies analyzing bacteria in patients with hydrogen-predominant SIBO and methane-predominant SIBO separately found characteristic bacteria for each subtype. Anaerobic bacteria, such as *Bacteroides*, and facultative anaerobic bacteria, such as *Streptococcus* and *Escherichia coli*, were characteristic bacteria in patients with hydrogen-predominant SIBO [53]. At the same time, *Methanobrevibacter* was characteristic in patients with methane-predominant SIBO [54]. Examination of mucosal-associated microbiota in the upper (duodenum), middle (jejunum), and lower (ileum) gastrointestinal tracts through sequencing analysis revealed a lower Shannon diversity index in the mucosal samples of the jejunum in SIBO-positive subjects compared to SIBO-negative subjects [55]. The composition of mucosal bacteria in the duodenum was significantly different from that in the jejunum and ileum. However, some similar trends were observed across all segments, such as decreased levels of *Rothia*, *Prevotella*, *Lactobacillus*, and *Ruminococcus*, which are beneficial bacteria involved in food digestion, maintaining intestinal barrier integrity, and regulating intestinal immunity [55]. The characteristic alterations in gut microbiota induced by SIBO can also create a pro-inflammatory environment in the duodenum. PCR testing of duodenal fluid in SIBO patients revealed a higher prevalence of elevated levels of three pro-inflammatory cytokines (IL-1 $\beta$ , IL-6, TNF- $\alpha$ ) compared to non-SIBO subjects. Notably, the detection of *Klebsiella pneumoniae* and *Methanobrevibacter*, characteristic bacteria of SIBO, was positively correlated with IL-6 and TNF- $\alpha$  levels and IL-1 $\beta$  levels, respectively [56]. The rearrangement of intestinal microbiota in SIBO patients is summarized in Table 1.

### 3.1.2. Disturbance of gut microbiota and secondary impact on acute pancreatitis

Similarly, patients with AP exhibit reduced gut microbiota diversity, characterized by alterations in the relative abundance of specific bacteria, with a decrease in beneficial bacteria and an increase in pathogenic bacteria. The gut microbiota diversity was lower in AP patients compared to healthy controls from fecal samples using 16S rRNA sequencing [57]. At the phylum level, AP patients had an increased abundance of Proteobacteria and decreased abundances of Firmicutes and Bacteroidetes [58]. At the

genus level, opportunistic pathogens such as *Enterococcus* and *Escherichia-Shigella* were more abundant in AP patients, whereas beneficial bacteria like *Blautia*, *Prevotella*, and *Bifidobacterium* were depleted [59,60]. Recent studies using duodenal mucosal samples also revealed significant enrichment of facultative pathogens such as *Escherichia-Shigella*, *Enterococcus*, and *Staphylococcus* in SAP patients [40]. Animal studies support these findings. Bile acid-induced ANP rats showed a reduced microbial diversity, an increase in the abundance of *Escherichia-Shigella*, and a decrease in beneficial bacteria such as *Prevotella* and *Lactobacillus*, with concomitant changes in clinical outcomes [61]. Microbial composition changes further exacerbate the disease and reflect the severity of AP. Rectal swab sequencing revealed that *Streptococcus*, *Escherichia*, and *Enterococcus* were the most representative gut microbiota in MAP, MSAP, and SAP, respectively [62,63]. Gut microbiota profiles in AP patients are associated with intensive care unit (ICU) stay duration, overall hospital stay, C-reactive protein (CRP) levels, and the duration of organ failure. This suggests that gut microbiota characteristics may serve as predictive markers for disease severity [64]. Above gut dysbiosis indicates that gut microbiota not only suffer during AP but may also play a crucial role in disease progression. The microbial profiles of AP are detailed in Table 2.

The production of short-chain fatty acids (SCFAs) by the primary producers such as *Bifidobacterium*, *Bacteroides*, *Blautia*, and *Gemmiger* is reduced in AP [65–68]. *Eubacterium hallii*, a primary SCFAs-producing bacterium, shows a significant reduction in SAP and MSAP patients. This decrease in SCFAs production in AP patients contributes to the impairment of the gut barrier function and may exacerbate the condition by promoting dysbiosis and inflammation. The diminished SCFAs levels highlight the importance of maintaining a healthy gut microbiota composition to support gut barrier integrity and overall health, particularly in the context of AP [62].

Inflammatory cytokines, along with the changes in gut microbiota, are associated with the severity of AP patients, indicating that gut microbiota plays a crucial role in the progression of AP. Elevated levels of IL-6, IL-1, and TNF- $\alpha$  were observed in patients with SAP and those with systemic complications in later stage [59,69,70]. Serum IL-6 levels were positively correlated with the presence of *Escherichia coli* and *Enterococcus* and negatively correlated with *Bifidobacterium* [57]. Higher plasma endotoxin levels were also positively correlated with *Enterococcus* [71,72]. Animal models with depleted gut microbiota exhibited less pancreatic damage and reduced plasma levels of inflammatory cytokines [59,73]. This evidence indicates that dysbiosis of AP is

**Table 1**  
Summary of gut microbiota alterations in SIBO patients.<sup>a</sup>

Study	Reference	Type of sample	Microbial evaluation	Phylum level	Family level	Genus level
Gabriela Leite	[47]	Duodenal Aspirates	16s rRNA sequencing	NA	Enterobacteriaceae $\uparrow$	<i>Escherichia</i> $\uparrow$ <i>Klebsiella</i> $\uparrow$
Jia Li	[55]	Duodenum Biopsy	16s rRNA sequencing	Firmicutes $\uparrow$ Proteobacteria $\uparrow$ Bacteroidetes $\uparrow$	NA	<i>Bacteroides</i> $\uparrow$ <i>Escherichia-Shigella</i> $\uparrow$ <i>Streptococcus</i> $\uparrow$ <i>Lactobacillus</i> $\downarrow$ <i>Prevotella</i> $\downarrow$ <i>Bifidobacterium</i> $\downarrow$
Gabriela Leite	[51]	Duodenal Aspirates	16s rRNA sequencing	Proteobacteria $\uparrow$ Firmicutes $\downarrow$	Enterobacteriaceae $\uparrow$ Aeromonadaceae $\uparrow$ Moraxellaceae $\uparrow$	<i>Klebsiella</i> $\uparrow$ <i>Escherichia/Shigella</i> $\uparrow$ <i>Acinetobacter</i> $\uparrow$
Andrea S. Shin	[48]	Small bowel aspirate and mucosal samples	16s rRNA sequencing	NA	NA	<i>Clostridium</i> $\uparrow$ <i>Granulicatella</i> $\uparrow$
Guo H	[52]	Feces	16s rRNA sequencing	NA	NA	<i>Bacteroides</i> $\downarrow$ <i>Coprococcus</i> $\uparrow$

<sup>a</sup>  $\uparrow$ , elevated abundance;  $\downarrow$ , reduced abundance; NA, not available.



**Table 2**  
Summary of gut microbiota alterations in AP patients.<sup>a</sup>

Study	Reference	Type of sample	Microbial evaluation	Phylum level	Family level	Genus level
Tan C	[57]	Feces	PCR-DGGE	NA	NA	Enterococcus↑ Enterobacteriaceae↑ Bifidobacterium↓
Zhang XM	[58]	Feces	16s rRNA sequencing	Bacteroidetes↑ Proteobacteria↑ Firmicutes↓ Actinobacteria↓	NA	NA
Zhu Y	[59]	Feces	16s rRNA sequencing	Proteobacteria↑	Enterobacteriaceae↑	Escherichia Shigella↑ Enterococcus↑ Blautia↓ Faecalibacterium↓ Bifidobacterium↓ Bacteroides↑
Yu S	[62]	Rectal swab samples	16s rRNA sequencing	NA	NA	Escherichia-Shigella↑ Enterococcus↑ Eubacterium hallii↓ Blautia↓
Yu S	[63]	Rectal swab samples	Shotgun metagenomic sequencing	NA	NA	Streptococcus↑ Escherichia-coli↑ Enterococcus↑
Zhao MQ	[40]	Duodenal mucosal biopsies	16s rRNA sequencing	Firmicutes↑ Proteobacteria↓ Bacteroidetes↓	Streptococcaceae↑	Streptococcus↑ Neisseria↑

<sup>a</sup> ↑, elevated abundance; ↓, reduced abundance; NA, not available.

linked to inflammatory cytokines and endotoxins, exacerbating systemic inflammatory response syndrome (SIRS) and increasing the risk of organ failure.

Changes in the gut microbiota of AP are associated with various immune pathways. The abundance of pathogenic bacteria such as *Escherichia coli*, *Proteobacteria*, and *Enterococcus* can mediate immune responses through pathogen-associated molecular patterns (PAMPs), which stimulate dendritic cells and macrophages to secrete pro-inflammatory cytokines, leading to the differentiation of immature T cells into Th1/Th17 cells while inhibiting Tregs and B cells. This results in a further decrease in anti-inflammatory cytokines and sIgA [74], pathologically activating the immune response and promoting an “inflammatory storm” through the activation of mitogen-activated protein kinase (MAPK) or nuclear factor kappa B (NF-κB) pathways. It ultimately leads to epithelial cell necrosis and damage to TJs [75]. Pathogenic bacteria enriched in AP rats, such as *Escherichia coli* and *Shigella*, are considered M1 alveolar macrophages (AMs), exacerbating inflammation and promoting the development of pancreatitis-associated lung injury (PALI) [76–80]. This elevates the abundance of Toll-like receptor 4 (TLR4)/MyD88/p38 MAPK and leads to endoplasmic reticulum stress (ERS) signaling, causing intestinal epithelial damage [73]. The lipopolysaccharides of abundant *Escherichia coli* bind to receptors like TLR on intestinal epithelial cells, activating NF-κB signaling and leading to the release of excessive cytokines and inflammatory mediators such as IL-6 [39]. Additionally, the dysbiosis of the gut microbiota during the acute phase of AP stimulates intestinal inflammation through the activation of the nucleotide-binding oligomerization domain-like receptor protein 3(NLRP3), damaging the epithelial barrier and promoting the translocation of intestinal bacteria to distant organs [81].

### 3.2. Bacterial translocation secondary to intestinal microbiota disorder in small intestinal bacterial overgrowth exacerbates the progression of acute pancreatitis

Many studies have indicated the presence of BT during the progression of AP. 39.4 % of surgery samples from ANP patients

could culture gut microbiota [82]. It was found that opportunistic pathogens originating from the gut, including *Escherichia coli*, *Shigella*, *Enterobacter*, and *Enterococcus faecalis*, were likely the main components of translocated bacteria according to peripheral blood samples collected from AP patients [14]. Spearman correlation analysis showed that specific operational taxonomic units (OTUs) such as OTU44 (Muribaculaceae), OTU117 (Halomonas), and OTU27 (Anaeroplasma) had correlated abundances in the pancreas and ileum, which indicates that these bacteria might translocate from the gut to the pancreas by crossing the intestinal barrier [83]. To explore the potential sources of BT in AP, further animal studies verified that the source of pancreatic infection that occurred within 8–16 h post sodium taurocholate induction was likely the colon or terminal ileum [84]. In experiments where the gut bacterial load was reduced via cecostomy formation and colonic lavage in AP-induced rats, there was a significant reduction in serum endotoxin levels and mortality compared to controls [85]. Another study performed gut decontamination of either the small intestine or colon in rats before inducing ANP, and BT was assessed by culturing intestinal mucosa, mesenteric lymph nodes, and pancreas. The results indicated that BT from the colon was less frequent than from the small intestine, suggesting that the small intestine might be the primary source of gut bacteria leading to infective pancreatic necrosis in AP. Infective pancreatic necrosis is currently a significant determinant of prognosis in SAP, and BT from the gut microbiota is considered an important causative factor [13]. The movement of bacteria from the gut to other organs plays a crucial role in the development of systemic infections and complications in SAP, highlighting the importance of maintaining gut barrier integrity and targeting gut microbiota in therapeutic strategies for AP [86].

Researchers have outlined the pathophysiological mechanisms of gut BT in AP. First, the disruption of the normal ecological barrier and the secretion of various gastrointestinal peptides damage the interstitial cells of Cajal, reducing gut motility [87]. Impaired gut motility leads to stasis of intestinal contents, overgrowth of intestinal bacteria, and an increase in pathogenic bacteria such as *Enterobacter* and *Enterococcus*, promoting SIBO [35]. Secondly, the

mechanical barrier of the gut is compromised, increasing intestinal permeability, and the local and systemic bacterial clearance capacity is impaired [88]. Finally, the immune barrier is weakened, as evidenced by a decrease in sIgA [89], which further facilitates bacterial translocation. These findings indicate potential therapeutic strategies for AP that focus on restoring gut barrier function and improving gut microbiota to prevent BT. Such a strategy could better control the progression of AP at an early stage.

In summary, the development of AP is intricately linked to the dysbiosis caused by SIBO. AP facilitates the occurrence of SIBO, which further disrupts gut microbiota homeostasis, exacerbating the condition. Dysbiotic gut microbiota inhibits the secretion of antimicrobial peptides, damages intestinal epithelial cells and TJs, and impairs the gut barrier. This dysbiosis promotes the activation of macrophages and the recruitment of neutrophils through immune and metabolic pathways. While the metabolites of beneficial gut bacteria, such as SCFAs, can suppress inflammatory responses, this beneficial effect is diminished due to microbial homeostasis disruption. Bacteria, pro-inflammatory factors, and endotoxins can translocate through the compromised gut barrier, contributing to the progression of AP.

#### 4. Treatment for small intestinal bacterial overgrowth may improve the prognosis of acute pancreatitis

As summarized earlier, SIBO is one of the risk factors for the progression of AP, and the intermediate factor connecting these two diseases is intestinal BT, which includes disruption of intestinal barrier integrity. Therefore, restoring the stability of the intestinal microbiota and intestinal barrier is of significant value for AP patients. Early treatment targeting SIBO may be more effective in reducing complications of AP, but further research is needed to validate this hypothesis.

##### 4.1. Rifaximin

Currently, Rifaximin is thought effective and safe for the treatment of SIBO, considering its broad spectrum of action and non-absorbed nature in order to achieve low gastrointestinal absorption while retaining good antibacterial activity with low resistance and toxicity [90–92]. A meta-analysis evaluated the efficacy and safety of rifaximin in treating SIBO, concluding that it can safely eradicate SIBO by approximately 64 % and normalize breath test results by 49.5 % [92,93]. Rectal rifaximin administration exhibited a significant reduction in colonic BT to the mesenteric lymph nodes and a decrease in pro-inflammatory cytokines in colonic tissues from colitis mouse models, suggesting that rifaximin may exert immunomodulatory effects by reducing BT, thereby inhibiting the induction of pro-inflammatory cytokines and accelerating the recovery for AP [94].

Several cohort and experimental studies provided clinical evidence for the effect of rifaximin in AP. The results showed that the median length of hospital stay and the number of patients with infected pancreatic necrosis in the rifaximin treatment group were significantly lower than those in the control group, with no difference in mortality rates between the two groups [95]. The research results conducted in experimental AP rats showed that treatment with rifaximin can reduce pancreatic injury and the spread of intestinal bacteria in the abdominal cavity [96]. Rifaximin may also participate in SAP through the regulation of the gut microbiota structure. However, antibiotic use is also associated with risks, including increased incidence of resistant bacteria and

fungal infections [97,98]. Rifaximin appears to be a promising new treatment option for AP.

##### 4.2. Probiotics

Probiotics have been investigated as a treatment for AP. Some randomized controlled trials found that the addition of probiotics to early enteral nutrition brought reduced pancreatic necrosis and the need for surgical intervention, lowered plasma CRP levels, decreased infection complications, and significantly shorter hospital stays [99–102]. Recent animal studies also support the effectiveness of probiotics in AP rats with improved histological scores, reduced edema, parenchymal necrosis, mononuclear cell infiltration, and polymorphonuclear leukocyte infiltration, reducing the incidence of infectious complications and mortality [103–105]. Various probiotics application in experimentally induced AP rats reduced duodenal bacterial overgrowth, notably decreasing the abundance of *Enterococcus* and *Escherichia coli*, subsequently reducing BT in the mesenteric lymph nodes and pancreas of rats [106]. It provides a strategy that probiotics may use to treat SIBO by improving gut microbiota, thereby alleviating AP.

The mechanisms by which probiotics regulate the gut microbiota primarily involve (1) producing bioactive substances, such as organic acids, to inhibit the growth of pathogenic bacteria [107,108]; (2) stimulating mucus secretion in the intestinal mucosa to prevent pathogenic bacteria from adhering to the intestinal epithelium, thereby reducing BT [109]; (3) promoting the biosynthesis of glutathione, which eliminates superoxide and hydroxyl radicals, thus improving intestinal mucosal barrier function and inhibiting BT [110]; (4) upregulating the expression of molecules related to intestinal barrier function, such as tight junction proteins and mucin 2 (MUC2), enhancing intestinal barrier function and inhibiting BT [111–114].

Systematic reviews have demonstrated that probiotic supplementation significantly benefits patients with SIBO. Clinical evidence indicates probiotics effectively reduce hydrogen concentrations and alleviate abdominal pain symptoms [115]. Furthermore, probiotics serve as a valuable adjunct to established SIBO treatments, as shown in multiple clinical investigations. In a 90-day real-world observational study to evaluate the therapeutic approach combining rifaximin, low-FODMAP (fermentable, oligo-, di-, mono-saccharides and polyols) diet, Chinese herbal medicine, and probiotics for hydrogen-dominant and IMO subtypes. While the experimental group (additional herbal supplements, probiotics, prebiotics, and glutamine) showed similar breath test normalization rates compared to the control group (antibiotics + low-FODMAP diet), they demonstrated superior gastrointestinal symptom relief [116]. This benefit was especially pronounced in IMO patients [117]. Among various probiotic strains investigated for SIBO management, *Saccharomyces boulardii* currently represents the most extensively studied and clinically applied option, with substantial evidence supporting its therapeutic role [118,119]. However, some researchers are skeptical on account of the fact that double-blind trials and meta-analyses have not demonstrated improvements in intestinal permeability, mortality, or ICU stay duration for SAP patients treated with probiotics [120,121]. A multicenter, randomized, double-blind trial even found increased mortality in AP patients treated with probiotics [122]. This indicates potential variability in probiotic efficacy among different patients, underscoring the need for further multicenter, large-scale, randomized controlled trials. Such studies should consider the etiology of AP, specific probiotic strains, timing of intervention, dosage, and individual patient differences [123–128].

#### 4.3. Fecal microbiota transplantation

As previously mentioned, dysbiosis of intestinal microbiota exacerbates pancreatic injury and inflammatory responses in AP. By improving gut microbiota and reducing BT, fecal microbiota transplantation (FMT) has shown potential in treating AP. Studies have demonstrated that FMT treatment in mice models with gut microbiota dysbiosis led to the alleviation of intestinal mucosal barrier damage and increased levels of sIgA, indicating the restoration of intestinal mucosal barrier integrity and reduction of BT, thus rebuilding the gut ecosystem [129]. Further research on the impact of FMT on gut microbiota in AP mice revealed an increased microbial diversity index, accompanied by reduced pancreatic tissue damage and decreased serum markers of AP. However, the exact role of FMT in AP still requires further investigation. Experimental studies on animal models of AP have not demonstrated a beneficial effect of FMT. Instead, significant pancreatic damage and increased mortality rates were observed after FMT treatment [59,130].

FMT can also be effective in SIBO with reduced gastrointestinal symptoms, increased rates of negative breath tests, and enhanced diversity of gut microbiota [131]. A case study investigated FMT as a therapeutic intervention for a patient with SIBO. Post-FMT evaluation revealed significant improvements in several key parameters: (1) enhanced intestinal barrier function, (2) increased bacterial species richness and microbiome evenness, (3) reduced fungal  $\alpha$ -diversity, and (4) progressively elevated SCFAs levels. These findings suggest that FMT may exert its therapeutic effects through a dual mechanism: first by restoring eubiosis of the gut microbiota, and subsequently by preserving intestinal barrier integrity. This restoration process appears to prevent the translocation of pathogenic microorganisms and their metabolic byproducts from the intestinal lumen into the systemic circulation [132]. Although FMT is considered a promising therapeutic approach for gut microbiota restoration, the potential risks are not yet fully understood and require further research [133].

#### 4.4. Enteral nutrition

The latest guidelines for managing SAP recommend the early use of enteral nutrition over parenteral nutrition for patients [134]. Enteral nutrition in AP had a reduced risk of postoperative sepsis, improving the acute-phase response and severity scores of AP [135–137]. Animal experiments have reported that short-peptide enteral nutrition (SPEN) can improve intestinal microcirculation in SAP mice, thereby preventing intestinal BT that may occur later in SAP [138]. Thus, the main reason enteral nutrition is recommended in the treatment of AP patients is its advantage in protecting mucosal barriers.

Studies have shown that enteral nutrition supplements rich in glutamine, dietary fiber, and oligosaccharides can improve intestinal damage caused by bacterial overgrowth models and prevent bacterial overgrowth caused by intestinal BT [139]. Therefore, enteral nutrition may alleviate the severity of AP by improving impaired intestinal barrier permeability owing to SIBO.

#### 4.5. Octreotide

Octreotide can reduce mortality and the incidence rate of complications in AP [140]. Octreotide can stimulate intestinal motility and induce migrating motor complex-like movements in the small intestine. The clinical study supported an increased frequency of intestinal migrating complexes and a significant reduction in hydrogen excretion in the glucose hydrogen breath test after octreotide treatment [141]. The improvement in

intestinal motility disorder is accompanied by a decrease in bacterial overgrowth, indicating that the improvement of SIBO by octreotide may be one of the mechanisms inhibiting the worsening of AP.

#### 4.6. Butyrate

Butyrate, as one of the SCFAs, possesses beneficial effects such as stabilizing the intestinal barrier, enhancing mucosal immune function, and restoring intestinal microbial balance [60,142–145]. A diet rich in fiber has been proven effective for many patients with concurrent SIBO symptoms, as this type of diet can increase SCFAs production and inhibit the growth of harmful bacteria [146]. Butyrate may improve SIBO by protecting the intestinal barrier and regulating the stability of the intestinal microbiota, thereby further inhibiting BT and alleviating the severity of AP. Therefore, butyrate is a promising therapeutic approach as a protective measure against intestinal damage during AP progression [147].

Oral administration of butyrate salts resulted in a significant reduction in serum endotoxin levels and mortality in ANP mice [130]. Additionally, butyrate-treated SAP mice revealed improved pancreatic tissue pathology and lower levels of inflammatory factors [148]. A study analyzing the fecal microbiota of SAP rats found that butyrate restored the intestinal microbiota of SAP rats, manifested by increased microbial diversity, increased beneficial bacteria such as *Lactobacilli* and *Fecalococci*, and decreased pathogenic bacteria such as *Pseudomonads* and *Escherichia coli* [149]. Butyrate can also upregulate tight junction proteins in SAP rats and restore goblet cell secretion of mucin, thereby protecting the intestinal barrier, reducing intestinal BT, and lowering the mortality rate of AP [150–152]. Therefore, supplementing SCFAs substrates such as butyrate can be one of the treatment strategies for AP.

### 5. Conclusions

Current evidence has shown the etiology of SIBO, including small intestinal motility and dysfunction of the intestinal barrier. The increased incidence of SIBO in AP patients indicates that AP is one of the causes of SIBO. AP can promote the occurrence of SIBO by prolonging MMC duration and weakening the intestinal barrier function. On the other hand, SIBO can exacerbate AP mainly due to dysbiosis caused by BT, characterized by a decrease in beneficial bacteria and an increase in pathogenic bacteria. The relationship between AP, SIBO, and intestinal microbiota is illustrated in Fig. 1. Recent research has also considered interventions such as antibiotics, primarily with rifaximin, probiotics, FMT, enteral nutrition, octreotide, and SCFAs in clinical practice.

### 6. Perspectives

Currently, there are some limitations in the research between SIBO and AP. First of all, most studies on the microbiota of AP patients currently rely on fecal samples, which, despite their convenience, non-invasiveness, ample biomass, and low cost, may not fully reflect the actual members of the mucosal microbiota, thus failing to reveal changes in the gut microbiota accurately. Subsequently, although duodenal aspirate culture has long been considered the gold standard for diagnosing SIBO, its clinical application is limited due to its invasive nature and potential for contamination. Additionally, there is limited research describing the characteristics of the mucosal microbiota. Mucosal microbiota and luminal microbiota represent two functionally distinct ecosystems. The former may be more critical in terms of direct microbiota-mucosa interactions. At the same time, luminal bacteria are involved in digestion and interact with the host indirectly

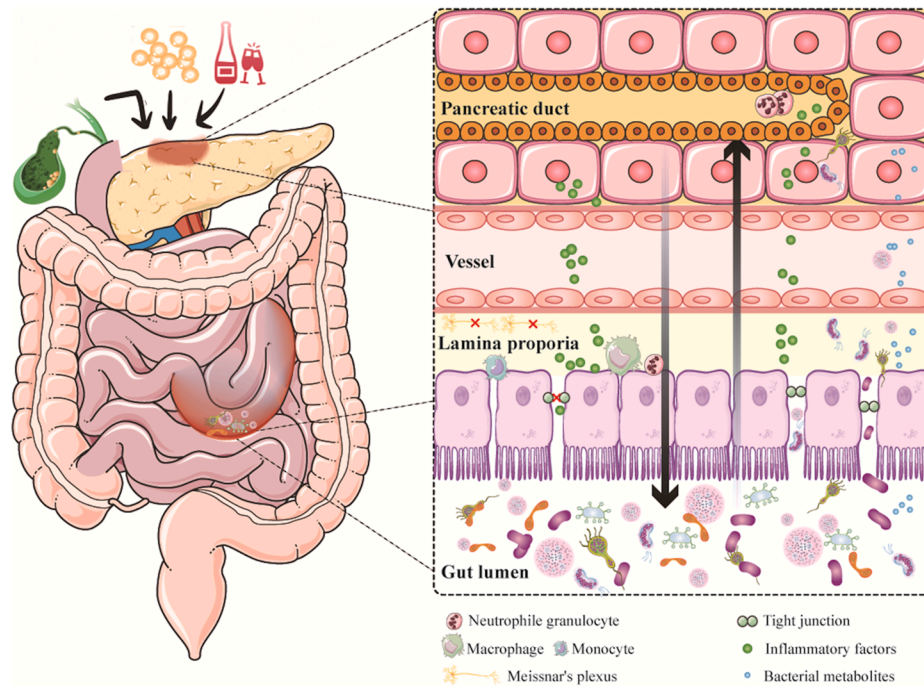


Fig. 1. A diagram of the relationship between AP, SIBO, and gut microbiota.

through the production of metabolites and toxins. Therefore, simultaneous analysis and comparison of the microbial characteristics of both could better enhance our overall understanding of the gut microbiota. After that, there is currently only research on the correlation between SIBO and the severity of AP, without further analysis of the specific impact of SIBO on the microbial characteristics of AP patients. Additional prospective studies are needed to examine the correlation between symptom spectrum and small intestinal aspirate and mucosal microbiota, combined with deep sequencing technology and consideration of functional and metabolic omics analyses, to characterize the microbial communities associated with the progression of AP and analyze the role of specific bacterial species in improving the diagnosis and management of AP. Finally, the development of techniques such as metagenomics, metabolomics, metatranscriptomics, and culturomics will bring breakthroughs in microbial research and microbiota-based therapies. In the future, we will further utilize animal studies and human trials better to validate the mechanisms of gut dysfunction in AP. While some results suggest that these therapies may represent promising new treatment options for AP and SIBO, conflicting evidence from studies also highlights the need for further large-scale research to understand the impact and risks better, enhancing the benefits of precise treatment for AP.

**Ethics approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable.

**Author contributions**

Xiaorui Cui: Investigation, Data curation, Methodology, Formal analysis, Writing—original draft. Huaizhu Guo: Conceptualization,

Data curation, Formal analysis, Writing—original draft, Visualization. Zhen Liu, Yuanyuan Lei, and Yunxiong Wei: Data curation, Validation, Visualization, Writing—review & editing. Guangyong Sun and Dong Zhang: Conceptualization, Validation, Visualization, Writing—review & editing. Jianyu Hao: Resources; Supervision; Conceptualization, Writing—review & editing. Donglei Zhang: Conceptualization, Methodology, Visualization, Writing—review & editing, Supervision. Xinjuan Liu: Resources, Conceptualization, Methodology, Visualization, Writing—review & editing, Supervision.

**Availability of data and materials**

Not applicable.

**Funding**

This research was supported by the Beijing Key Clinical Specialty Project.

**Conflict of interest**

The authors declare that there is no conflict of interest.

**Acknowledgments**

The correspondence author discloses receipt of the following financial support for the research, authorship, and publication of this article: Beijing Key Clinical Specialty Project.

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