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Bile acids and their receptors: Potential therapeutic targets in inflammatory bowel disease

Long XQ *et al.* Bile acids in inflammatory bowel disease

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Abstract

Chronic and recurrent inflammatory disorders of the gastrointestinal tract caused by a complex interplay between genetic and intestinal dysbiosis are called inflammatory bowel disease. As a result of the interaction between the liver and the gut microbiota, bile acids are an atypical class of steroids produced in mammals and traditionally known for their function in food absorption. With the development of genomics and metabolomics, more and more data suggest that the pathophysiological mechanisms of inflammatory bowel disease are regulated by bile acids and their receptors. Bile acids operate as signalling molecules by activating a variety of bile acid receptors that impact intestinal flora, epithelial barrier function, and intestinal immunology. Inflammatory bowel disease can be treated in new ways by using these potential molecules. This study mainly discussed the increasing function of bile acids and their receptors in inflammatory bowel disease and their prospective therapeutic applications. In addition, we explored bile acid metabolism and the interaction of bile acids and gut microbiota.

Key Words: Bile acids; Inflammatory bowel disease; Intestinal immunology; Bile acid receptors; Bile acid metabolism; Gut microbiota

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Core Tip: Chronic and recurrent inflammatory disorders of the gastrointestinal tract caused by a complex interplay between genetic and intestinal dysbiosis are called inflammatory bowel disease. With the development of genomics and metabolomics, more and more data suggest that bile acids operate as signalling molecules by activating a variety of bile acid receptors that regulate pathophysiological mechanisms of inflammatory bowel disease. Inflammatory bowel disease can be treated in new ways by using these potential molecules.

INTRODUCTION

Inflammatory bowel disease (IBD) are chronic and recurrent inflammatory diseases of the gastrointestinal tract, including two main subtypes: Ulcerative colitis (UC) and Crohn's disease (CD). Globally, the prevalence of IBD is increasing, especially in newly industrialized countries, with a prevalence of 0.5% in 2010, 0.75% in 2020, and a projected 1% in 2030, increasing the burden on health care systems around the world^[1,2]. The etiology and pathogenesis of IBD are not well understood. However, it is generally accepted that it is a persistent and excessive immune inflammatory response in people with genetic susceptibility when exposed to environmental factors^[3]. Immune homeostasis in the intestine involves the coordinated action of epithelial cells and innate and adaptive immune cells. As a result of impaired intestinal epithelial barrier function in IBD, commensal microorganisms are translocated into the intestinal wall. The innate immune cells then take up the microbes and their mediators and respond, which activates immune cells and produces cytokines and chemokines. This process, in turn, upsets the homeostasis of the intestine, recruiting more immune cells to the intestinal wall and activating adaptive immunity^[4,5]. IBD usually presents with chronic recurrent abdominal pain, diarrhea, mucus, and bloody stools and can also present with serious complications such as anal fistula, intestinal obstruction, and intestinal perforation^[6]. Additionally, IBD patients frequently experience symptoms outside of the digestive system, such as joint, eye, or skin inflammation^[7]. With the introduction of new biological and small molecule therapies, such as anti-TNF- α biologic agents, anti-interleukin-12/23 biologic agents, and anti-integrin biologic agents, significant progress has been made in the pharmacological treatment of IBD, but at a high financial and physical cost to patients. Moreover, these therapies can potentially produce life-threatening side effects and cannot cure IBD, and a significant proportion of patients still require surgical treatment. This underscores the need for new treatment strategies for IBD^[8,9].

As a result of the interaction between the liver and gut bacteria, bile acids are a class of atypical steroids produced in mammals. Bile acid receptors are a type of cell membrane and nuclear receptor that is found in several digestive and immune system cells. The majority of bile acid biological effects are mediated by serving as ligands for specific bile acid receptors. In the past, bile acids were widely assumed to aid in intestinal nutrition absorption and biliary transport of lipids, toxic metabolites, and foreign substances. However, it is now well established that bile acids can act as multidirectional signaling metabolites, modulating physiopathological processes associated with a variety of digestive diseases *via* dynamic interactions with germline-encoded host receptors and microbiota^[10-12]. In particular, in IBD, bile acids can modulate IBD pathophysiological pathways by acting on several bile acid receptors, including the farnesol X receptor (FXR), the retinoid-related orphan receptor γ (ROR γ t), the G protein-coupled bile acid receptor 1 (GPABR1), vitamin D receptor (VDR), pregnane X receptor (PXR), constitutive androstane receptor (CAR), sphingosine-1-phosphate receptor 2 (S1PR2)^[13] (Table 1). This review primarily outlined the growing function of bile acids and their receptors in IBD, as well as their prospective therapeutic applications. Furthermore, we explored bile acid metabolism and the interaction of bile acids and microbiota to present fresh perspectives and molecular targets for diagnosing and treating IBD.

BILE ACID METABOLISM

Bile acids are the end product of cholesterol metabolism. Bile acids are composed mainly of cholesterol, and unlike other steroid hormones, bile acids are amphiphilic molecules with a hydrophobic (beta side) and a hydrophilic (alpha side) surface. They have detergent properties due to their amphiphilic nature, which helps to solubilize lipids in micelles, facilitating emulsification and absorption of dietary fatty acids and cholesterol^[14,15]. Mammals have two main types of bile acids: Primary bile acids (PBAs) and secondary bile acids (SBAs). PBAs are formed by cholesterol catabolism in hepatocytes, whereas SBAs are derivatives of PBAs and are generated by the gut

microbiome. The bile acid pool is maintained in balance by their hepatic synthesis, enterohepatic circulation, and microbial metabolism^[16] (Figure 1).

Bile acid metabolism in the liver

In the liver, cholesterol is generated in the central hepatocyte in several steps to produce PBAs of 24 carbons. In humans, cholic acid (CA) and chenodeoxycholic acid (CDCA) are the most prevalent PBAs, while rats create the 6-hydroxylated versions of CA and CDCA, named muricholic acid (MCA)^[17]. The conventional or alternative/acidic pathways are both possible for this process to take place in the human liver. The first limiting step in the conventional route is the 7-hydroxylation of cholesterol catalysed by cholesterol-7-hydroxylase (CYP7A1), which irreversibly transforms cholesterol to 7-hydroxycholesterol. This intermediate is then converted to 7 α -hydroxy-4-cholesten-3-one by 3 β -hydroxy- Δ 5-C27-steroid oxidoreductase, which can be used for generating both CA and CDCA in the classic pathway. In contrast, the alternative/acidic pathway begins with the conversion of cholesterol by sterol 27-hydroxylase (CYP27A1) to 27-hydroxycholesterol, followed by B-ring hydroxylation and metabolic side chain modification by oxysterol 7-hydroxylase (CYP7B) to create CDCA. The alternate pathway generates solely CDCA, which accounts for 10% of the liver's total bile acids^[18-20]. Subsequently, PBAs are converted to tauro-CA (TCA) and tauro-CDCA (TCDCA) and glyco-CA (GCA) and glyco-CDCA (GCDCA), respectively, by the actions of BA-CoA synthase and BA-CoA amino acid N-acetyltransferase. Conjugation turns bile acids into stronger acids and increases their aqueous solubility at acidic pH and the retention of their amphiphilic structure. This limits their passive reabsorption and is essential for their lipid emulsification activity in the acidic environment of the duodenum^[21,22]. Notably, conjugation with glycine is common in the human liver, accounting for 90% of the bile acid pool. However, approximately 95% of PBAs in mice are taurine-conjugated^[23]. Conjugated bile acids will be stored in the gallbladder, forming bile with phospholipids, cholesterol and other components. Finally, the gallbladder releases bile acids into the duodenum after each meal^[24].

Bile acid metabolism in the intestine

Upon release into the small intestine, bile acids form micelles with cholesterol and dietary fats to facilitate their dissolution and absorption^[25,26]. However, conjugated bile acids are not absorbed and are instead retained in the small intestine. At the end of the ileum, ²⁴ approximately 95% of the conjugated bile acids are reabsorbed via the apical sodium-dependent bile acid transporter (ASBT) and enter the liver via the portal vein^[27]. It is estimated that humans complete the enterohepatic circulation of bile acids between six and eight times a day, depending on their dietary habits. The bile acid pool in healthy persons remains between 4 and 6 g. In contrast, changes in the intestinal epithelium of individuals with IBD decrease ⁴ the reabsorption of bile acids by ASBT and increase the number of bile acids discharged in the feces^[28]. It's important to note that the bile acid pool that is returned from the ileum to the liver directly suppresses the production of new bile acids in hepatocytes through the FXR, FXRibid-dependent transactivation of the small isomeric partner (SHP), and SHP-mediated suppression of CYP7A1 and CYP8B1 expression^[17,29,30]. In addition, bile acid-activated FXR drives ⁶ fibroblast growth factor (FGF-15/19, FGF-15 in mice; FGF-19 in humans) expression in intestinal epithelial cells (IECs). Subsequently, FGF-15/19 ⁶ is secreted into the portal circulation, translocated to the liver, binds to heterodimeric receptors on hepatocytes, and reduces hepatic bile acid synthesis by inhibiting CYP7A1 expression^[26,31].

The intestinal microbiota can be directly involved in the biotransformation of bile acids through microbial enzymes. The five known mechanisms of bile acid metabolism by the intestinal microbiota are dehydroxylation, ²² dehydration, exo-embedding of the cholesterol backbone, depolymerization of amino acids (glycine or taurine), and amide conjugation of the bile acid backbone with the amino acids phenylalanine, tyrosine and leucine. Many potential mechanisms still exist to be discovered and explored^[32]. Approximately 5% of bile acids are retained in the intestinal lumen for further metabolism by the intestinal microbiota to generate SBAs via the aforementioned processes^[33]. In particular, the depolymerization reaction of bile acid metabolism is first

carried out by the gut bacteria (enzymatic hydrolysis of the C-24N-acylamide bond). Bile salt hydrolases (BSHs), which are extensively found in both Gram-positive and Gram-negative bacteria in the gut, including *Clostridium*, *Bifidobacterium*, *Lactobacillus*, *Bacteroides*, and *Enterococcus*, mediate this process^[34]. It eliminates the glycine or taurine conjugates and stops the small intestine's active reabsorption. The depolymerized PBAs are then converted to SBAs in the colon by dehydroxylation at the carbon-7 position. Bacteria that express 7-dehydroxylases, such as *Clostridium* and *Eubacterium*, play a major role in mediating this process. The two SBAs that are most frequently produced by these reactions are lithocholic acid (LCA from CDCA) and deoxycholic acid (DCA from CA). Additionally, a variety of oxo-, iso- and epi-derivatives of bile acids can also arise in the colon as a result of different intestinal microbiota dehydrogenation and exo-embedding processes^[35]. For example, *Escherichia*, *Clostridium*, *Bacteroides*, and *Eubacterium* can undergo C7 β exochimerization of CDCA to produce the 7 β exochimer, 3 α -, 7 β -dihydroxy-5 β -cholic acid, also known as ursodeoxycholic acid (UDCA)^[36]. The complete metabolic pathway for the conversion of PBAs (CA and CDCA) to the two major SBAs (DCA and LCA) has been identified^[37]. It is still unclear how the gut microbiota converts PBAs into other bile acid derivatives. Moreover, it is not clear which exact bacterial species or strains are required for these processes. Furthermore, it is noteworthy that the gut microbiota can also regulate the hepatic enzymes CYP7A1 and CYP27A1, thus affecting the synthesis of bile acids in the liver^[38].

The intestines of IBD patients have been found to have dysbiosis of the intestinal bacterial flora and a considerable loss in microbial diversity. Most importantly, the abundance of bacteria containing BSH and bile acid-inducible enzymes (BAIs), such as Firmicutes, Ruminococcaceae, Lachnospiraceae, and *Eubacterium*, was decreased. This alteration reduces depolymerization and 7 α -dehydroxylation, strongly decreasing the conversion capacity of the microbiota, resulting in a decrease in SBAs (DCA, LCA) and an elevation in primary and conjugated bile acids (CA, CDCA, TCA, GCA)^[39-41]. Multiple risk factors (genetics, psychological factors, Western food, and antibiotics) may lead to intestinal flora dysbiosis and bile acid abnormalities, which are linked to the

pathophysiology of IBD^[42]. Notably, it has been reported that disturbances in bile acid metabolism will, in turn, exacerbate IBD damage, affect intestinal stem cell differentiation and renewal, and impair intestinal mucosal barrier function^[30].

Notably, the composition of the microbiota is directly or indirectly affected by bile acids in several studies. It has been shown that bile acids inhibit bacteria by increasing cell membrane permeability and causing cell damage, as well as causing oxidative DNA damage in bacteria. Alternatively, bile acids can indirectly influence bacterial growth through FXR and VDR receptors^[40]. The overall number of bacteria in rats' feces reduced with increased CA concentration in their meal, as determined by DAPI staining, sequencing of 16S rRNA gene clone libraries, and FISH analysis. The proportion of Bacteroidetes and Actinobacteria reduced dramatically in the CA-fed group, whereas the proportion of Firmicutes increased significantly^[43]. Considered together, bile acids and gut microbiota have a bidirectional effect on each other, and this balance is critical for human health and disease.

THE IMPACT OF BILE ACIDS AND THEIR RECEPTORS IN IBD

FXR

FXR is a nuclear receptor belonging to a subclass of metabolic receptors, first described by Forman *et al*^[44] in 1995. FXR is predominantly found in intestinal epithelial cells, hepatocytes, and some immune cells (such as macrophages and dendritic cells) of the colon and liver^[45]. Its main endogenous ligand is bile acids, in the order of FXR activation potency: CDCA > DCA > LCA > CA. Numerous studies demonstrate that through modulating bile acid metabolism, FXR can improve the pathogenesis of IBD. The enzyme CYP8B1, which synthesises CA, was increased in the livers of mice with colitis. Chen *et al*^[30] found that mucosal barrier repair was impaired in CYP8B1 overexpressing mice, which developed into more severe colitis. The specific mechanism was shown that CA leads to impaired fatty acid oxidation (FAO) and LGR5+ intestinal stem cell (ISC) renewal through inhibition of peroxisome proliferator-activated receptor alpha (PPARα). Surprisingly, they found that activation of FXR inhibited hepatic

CYP8B1 expression and ameliorated colitis in mice. FGF19-M52, an analog of FGF19, has been reported to inhibit bile acid synthesis, modulate bile acid pool composition, and inhibit intestinal inflammation in mice. The particular mechanisms underlying these processes are associated with maintaining intestinal epithelial barrier integrity, suppressing inflammatory immune responses, and controlling microbial composition. However, the FGF19-M52-induced anti-inflammatory effect was completely abolished in FXR-deficient animals^[46]. In addition, in UC mouse models, dextran sodium sulfate (DSS)-induced colitis activates the intestinal PPAR α -UDP-glucuronosyltransferases (UGTs) axis, which inhibits downstream FXR-FGF15 signaling, resulting in upregulation of hepatic CYP7A1 and promotion of hepatic bile acids synthesis. Both inhibition of PPAR α and stimulation of the FXR-FGF15 axis greatly decreased colitis produced by DSS^[47]. As a result, intestinal FXR-FGF15 signaling may play a key role in controlling bile acid homeostasis and colitis development.

Mammalian innate lymphocyte type 3 (ILC3) is important in IBD, especially in innate intestinal immunity and mucosal barrier function^[48]. Activation of FXR has been reported to block the production of interleukin (IL)-17A and IL-17F in ILC3, thereby eliminating ILC3-dependent intestinal inflammation and attenuating IBD injury. Interestingly, they also found that activation of FXR reduced characteristic transcription factors (including Batf3, Tcf7)^[49]. ¹⁸ Transforming growth factor-beta (TGF- β) belongs to a family of multifunctional polypeptides produced by non-lymphoid cells and various lymphocytes. Previous studies have shown that TGF- β is essential for regulating immune cells and that TGF- β production is also associated with the pathogenesis of colitis. This implies that the pathological changes in UC may be caused by disorders of the TGF- β pathway^[50]. A recent study revealed that a high-fat diet accelerated the course of DSS-induced UC and led to the downregulation of FXR target genes (FXR, Shp, and Ibabp). The addition of the FXR agonist FexD repaired the high-fat diet-induced phenotype, whereas the TGF- β inhibitor SB431542 prevented FexD's restorative activity in DSS-induced UC mice^[51]. This study showed that FXR alleviates

inflammation in UC through a TGF- β -dependent pathway. In conclusion, these findings suggest that FXR can improve IBD by modulating intestinal immunity.

Western diets have high levels of fecal DCA, a substance that can cause inflammation in the intestines. The researchers discovered that mice fed a DCA-supplemented diet showed localised ileal and colonic inflammation, as well as changes in gut microbiota composition and faecal bile acid buildup. Dysregulation of gut microbiota homeostasis induced by DCA reduced bile acid depolymerization. This regulation was associated with the repressed expression of target genes in the FXR-FGF15 axis, leading to increased hepatic *ad libitum* bile acid synthesis. These results suggest that DCA-induced intestinal dysbiosis may be a key etiology of intestinal inflammation associated with disturbed bile acid metabolism and downregulation of the FXR-FGF15 axis^[52]. Subsequently, Xu *et al*^[53] used the FXR agonist fexaramine to restore intestinal FXR activity. Activating FXR increased the abundance of bacteria producing short-chain fatty acids and normalized bile acid metabolism. DCA-induced intestinal inflammation can be reduced by targeting the FXR-gut microbiota signaling pathway.

In addition, FXR may ameliorate IBD through modifying the function of the intestinal mucosal barrier. By blocking lipopolysaccharide (LPS)-induced activation of the myosin light chain kinase (MLCK) pathway in an FXR-dependent manner, Song *et al*^[54] showed that CDCA reversed LPS-induced decreases in intestinal permeability and tight junction protein expression and mitigated LPS-induced intestinal barrier breakdown. In another study, using the FXR agonist GW4064 to restore FXR activity, Liu *et al*^[55] discovered that activation of FXR attenuates intestinal tight junction damage by inhibiting the LPS-induced TLR4/MyD88 signaling pathway. In summary, these recent findings suggest that FXR can influence the pathophysiological processes of IBD by regulating bile acid metabolism, intestinal immunity, intestinal flora, and intestinal mucosal barrier function (Figure 2). Activation of FXR may be considered a new therapeutic strategy for IBD.

ROR γ t

ROR γ is one of three retinoid-related orphan nuclear receptors with two main isoforms: The ROR γ 1 and ROR γ t (or ROR γ 2), encoded by the RORC gene. ROR γ 1 is normally involved in the regulation of transcription of metabolic genes and some circadian rhythms in the liver and adipose tissue. However, the expression of ROR γ t is restricted to specific subpopulations of lymphoid spectrum immune cells, namely T helper 17 (Th17) cells, ILC3, and $\gamma\delta$ T cells^[19,56]. Recently, increasing attention has turned to ROR γ t, as it acts as a key transcription factor for Th17 cells and regulatory T(Treg) cell differentiation in IBD (Figure 2). Moreover, ROR- γ t can depend on ILC3 to provide protective immunity^[23,48]. Hang *et al*^[57] discovered that 3-oxolithocholic acid (3-oxoLCA) decreased Th17 cells differentiation by directly interacting with the important transcription factor ROR γ t by giving mice 3-oxoLCA and isoallothocholic acid (isoalloLCA). In contrast, isoalloLCA decreases intestinal inflammation by increasing Treg cell differentiation by generating mitochondrial reactive oxygen species (mitoROS), which enhances the expression of Forkhead box P3 (Foxp3). Interestingly, similar to 3-oxoLCA, isolithocholic acid (isoLCA) can also de-suppress Th17 cells differentiation by inhibiting ROR γ t^[58]. In vivo models, another study demonstrated that the secondary bile acid 3 β -hydroxydeoxycholic acid (isoDCA) promotes Treg cells differentiation by increasing the induction of Foxp3 through its action on dendritic cells (DCs). Surprisingly, the researchers found that disruption of FXR in DCs enhanced Treg cell generation^[59]. In addition, taurohyodeoxycholic acid (THDCA) was reported to not only inhibit ROR γ t-mediated Th17 cell differentiation, but also trigger Foxp3 expression and promote Treg cell differentiation^[60]. These recent findings demonstrate the potential of bile acid derivatives to improve IBD prognosis by acting on ROR γ t. Kathania *et al*^[61] identified a serine/threonine kinase, Pak2, directly associated with ROR γ t. Pak2 recognizes the conserved KRLS motif within ROR γ t and phosphorylates S-316 within this motif. Genetic deletion of Pak2 in Th17 cells decreases ROR γ t phosphorylation, increases IL-17 expression, and induces severe colitis after transfer to Rag1-/- mice. This suggests that other biological molecules *in vivo* can also

regulate the developmental process of IBD by acting on ROR γ t and are potential targets for the treatment of IBD to be explored further.

ROR γ t⁺ immune cells are generally thought to coordinate immunity, inflammation, or tolerance in the gut. In IBD, the function of ROR γ t⁺ immune cells can be significantly altered^[62-64]. According to a recent study, ILC3 in intestinal draining lymph nodes expressed numerous significant class II histocompatibility complexes (MHCII). To increase microbiota-specific ROR γ t⁺ Treg cells and prevent them from proliferating into inflammatory Th17 cells, ILC3 is both essential and sufficient. AlphaV integrin, competing IL-2, and ILC3-mediated antigen presentation all contributes to this impact. Single cell analysis indicated that IBD impaired the interaction between ILC3 and ROR γ t⁺ Treg cells^[65]. It is interesting to note that Akagbosu *et al*^[66] described a class of ROR γ t⁺ antigen-presenting cells dubbed Thetis cells. These cells had dendritic cell and medullary thymic epithelial cell (mTEC) transcriptional signatures. Colitis results from the loss of MHCII or ITGB8 by Thetis cells, which severely impairs peripheral Treg (pTreg) cells differentiation in the intestine. MHCII expression by ROR γ t⁺ ILC3 and classic dendritic cells, in contrast, is neither sufficient nor essential for pTreg cells formation. In a colitis model, Liu *et al*^[67] demonstrated that *Akkermansia muciniphila* improves colitis by upregulating the ROR γ t⁺ Treg cell-mediated immune response, and this process is regulated by Toll-like receptor 4 (TLR4). ROR γ t is a main transcription factor for Th17 cells. However, in the intestine, ROR γ t is co-expressed in peripherally induced pTreg cells together with Foxp3. Surprisingly, Bhaumik *et al*^[68] observed that ROR γ t-mediated T-bet inhibition is essential for regulating the immunosuppressive function of pTreg cells in inflammatory states, restoring Foxp3 expression, and preventing the onset of severe colitis. ⁶ Despite these advancements, the full-spectrum cellular heterogeneity of ROR γ t⁺ immune cells, the potential for functional interactions between subpopulations, and the specific mechanisms influencing the pathophysiological processes of IBD in the context of complex microbiota remain unknown and require further investigation.

GPABR1

Kawamata *et al*^[69] first described GPABR1 (TGR5 or M-BAR) in 2003 as a receptor for bile acids in the membrane. GPCRs are mainly found in epithelial cells, immune cells, and intestinal nerves in the gut and biliary tract and belong to the superfamily of G protein-coupled receptors. Bile acids agonistically affect GPABR1 in different ways: LCA > DCA > CDCA > UDCA > CA^[20]. ¹⁸ The adaptor-apoptosis-associated speck-like protein with a caspase recruitment domain, sensor NLRP3, and procaspase-1 form the cytosolic polyprotein complex NLRP3 inflammasome. The pathogenesis of IBD is closely linked to the NLRP3 inflammasome^[70,71]. An *in vivo* experimental study showed ³⁴ that bile acids could inhibit NLRP3 inflammasome-dependent inflammation via the GPABR1-cAMP-PKA axis, suggesting GPABR1 as a potential target for alleviating intestinal inflammation in IBD^[72]. Biagioli *et al*^[73] found that activation of GPBAR1 can lower macrophage inflammatory gene expression (mRNA for TNF- α , IL-1, IL-6, and CCL 2), hence reducing inflammation in animal models of IBD. The anti-inflammatory gene angiotensin-converting enzyme 2 (ACE2) is deleted from mice with colitis, resulting in worse inflammation^[74]. Biagioli *et al*^[75] further discovered that activation of GPBAR1 could regulate ACE2 colonic expression through a glucagon-promoting factor glucagon-like peptide (GLP)-1-dependent mechanism. Furthermore, the regulation of ACE2 mRNA in the colitis setting may contribute to the anti-inflammatory effects of GPBAR1. A recent study showed that supplementation with LCA and DCA reduced intestinal inflammation in three mouse models of colitis. This anti-inflammatory effect partially depends on GPABR1 bile acid receptors^[76].

AKT, a serine/threonine kinase, is crucial for the differentiation, proliferation, survival, and metabolism of cells. In a mouse model of DSS-induced colitis and the colonic epithelium of UC patients, Azuma *et al*^[77] showed that DCA could slow wound healing in the colonic epithelial cell environment by acting as a ligand for GPABR1 to activate the AKT signaling pathway. Interestingly, another recent study showed that in a Caco-2 cell model, GPABR1 activation ameliorated LPS-induced reduction in trans-epithelial electrical resistance (TEER) and upregulated tight junction protein expression,

thereby enhancing mucosal barrier function to alleviate the progression of IBD^[78]. However, inhibition of GPABR1 expression in the porcine jejunal epithelial cell line IPEC-J2 did not affect the function of the intestinal barrier^[54]. This may be due to the different expression levels of GPABR1 in different intestinal slices. In conclusion, these findings suggest that GPABR1 plays different roles in the gastrointestinal tract of IBD (Figure 2). Moreover, the functions of GPABR1 may also differ due to differences in species and cell types. Therefore, the role of GPABR1 on the pathophysiological mechanisms of IBD deserves further investigation.

VDR

A nuclear receptor activated by 1,25-dihydroxyvitamin D is the VDR. The human metabolism, immunity, and cancer are all regulated by this gene, which is widely expressed in a range of tissues. Additionally, secondary bile acid LCA and its metabolites (3-oxoLCA and isoalloLCA) can activate VDR^[79,80]. LCA was reported to ameliorate the TNF- α -induced decrease in the expression and distribution of tight junction proteins (ZO-1, Occludin, and Claudin-1) through activation of VDR. Furthermore, it significantly blocked TNF- α -mediated downregulation of the oxidative stress-related genes silent information regulator 1 (SIRT1), nuclear factor erythroid 2-related factor 2 (Nrf2), and heme oxygenase-1. In addition, the TNF- α -induced increase in NF- κ B p-p65 and p-I κ B- α were significantly suppressed by LCA^[81]. This study reveals that LCA strongly protects against TNF- α -induced intestinal barrier degradation *via* VDR. Activation of hypoxia-inducible factor 1 α (HIF-1 α) as a heterodimeric transcription factor has been shown in previous research to accelerate the course of DSS-induced colitis in mice^[82,83]. However, the association of VDR signaling and HIF-1 α in the development of IBD has been enigmatic. A recent study showed that in an animal model of colitis, VDR signaling suppressed the overexpression of HIF-1 α in colonic epithelial cells by regulating the NF- κ B pathway, thereby inhibiting the overproduction of interferon-gamma (IFN- γ) and IL-1 β in these cells and attenuating the development of colitis in the animal model^[84]. Another study showed that VDR

could physically bind to Y box binding protein 1 (YBX-1), blocking its nuclear translocation, thus ameliorating the death of colonic epithelial cells in the presence of inflammation^[85]. Furthermore, Fernández-Barral *et al*^[86] demonstrated for the first time that activation of VDR can regulate stemness-related genes, including LGR5, SMOC2, LRIG1, MSI1, PTK7, and MEXA, and decrease cell proliferation in LGR5+ human colonic stem cells. This function is essential for maintaining colonic epithelial homeostasis in IBD.

Paneth cells, which are positioned at the base of small intestinal crypts, release defensins and play a crucial role in regulating intestinal flora and preserving intestinal homeostasis^[87]. Paneth cells showed a significant decrease in lysozyme, a diminished inhibition of pathogenic bacterial growth, and a reduced autophagic response in a Paneth cell-specific VDR knockout mouse model, resulting in an increased inflammatory response. These findings suggest the importance of VDR on Pan cells in IBD in preventing intestinal inflammation^[88]. Claudin-2 is a linker protein that mediates water transport between epithelial cells, and elevated Claudin-2 has been reported to be associated with active human IBD^[89]. Another study showed that ²⁸ in a *Salmonella colitis* model and a DSS-induced colitis model, VDR deficiency may lead to Claudin-2 hyperfunction and increased permeability in an inflammatory state, resulting in more severe intestinal leakage and intestinal inflammation in mice^[90]. This study highlights the importance of VDR in intestinal mucosal barrier function. In addition, intestinal fibrosis is a common complication of CD. The ²⁹ epithelial-mesenchymal transition (EMT) describes the process by which epithelial cells change from epithelial to mesenchymal cells, a crucial component of fibrogenesis. In addition to inhibiting fibroblast activation and epithelial mitochondria-mediated EMT, Yu *et al*^[91] revealed that VDR activation attenuates intestinal fibrosis.

Several recent studies have shown that colonic mucosal VDR expression is reduced in patients with IBD and that VDR transcript expression negatively correlates with IBD inflammation^[92,93]. Yang *et al*^[94] found that dysbiosis of the gut microbiota and altered fecal bile acids could regulate the immune response in UC patients. VDR may alleviate

40 intestinal inflammation by downregulating NF- κ B signaling and activating autophagy. These findings suggest restoring intestinal VDR expression in IBD may be a viable therapeutic strategy. In conclusion, 12 these findings contribute to a better understanding of the role of VDR in the etiology of IBD and serve as a significant reference for future research aimed at developing more effective therapeutic options (Figure 2).

PXR and CAR

8 PXR and CAR are members 2 and 3 of nuclear receptor subfamily 1, group I, NR1I2, and NR1I3, respectively. PXR was first described as a major regulator of CYP family 3 subfamily A (CYP3A) transcription by Kliewer *et al*^[95] and Lehmann *et al*^[96] in 1998. In contrast, CAR was first reported by Baes *et al*^[97] in 1994 and was later found to be a transcriptional regulator of CYP2B6. 8 PXR and CAR have the typical modular nuclear receptor structure, which consists of a hinge, a DNA-binding domain, a ligand-binding domain, activation function 1, and activation function 2. In addition to many endogenous and exogenous complex ligands, several subsequent studies have shown that PXR and CAR are hybrid receptors that can also accommodate LCA and CDCA and function as sensors for LCA and CDCA^[98]. PXR and CAR are key transcription factors that regulate intestinal homeostasis. Uehara *et al*^[99] demonstrated that PXR might reduce apoptosis in a mouse model of DSS-induced colitis by lowering the 9 mRNA expression of pro-inflammatory cytokines (TNF- and IL-1b). CAR inhibits apoptosis by inducing Gadd45b. Both of them protected mice from DSS-induced colitis. Interestingly, they also observed that the protective effect of FXR activation on CAR knockout mice and the protective effect of CAR activation on PXR knockout mice was reduced. CAR and PXR can synergistically ameliorate DSS-induced colitis. Another study showed that PXR and CAR deficiency synergistically increased the pro-inflammatory bacteria Helicobacteraceae and Helicobacter and the relative abundance of Lactobacillus. Lactobacillus has BSHs activity, corresponding to a decrease in primary taurine-bound bile acids in feces. This may lead to an increased internal burden

of taurine and unbound bile acids, which are associated with inflammation, oxidative stress, and cytotoxicity^[100].

The metabolism of tryptophan produces indole-3-propionic acid (IPA) in the intestine *via* *Clostridium perfringens*. Previous studies have shown that it can affect mucosal barrier function and inflammation through interaction with PXR^[101]. Flannigan *et al*^[102] found that PXR-deficient myofibroblasts overreact to stimuli and produce higher inflammatory mediators. In addition, biopsies from CD and UC patients revealed a correlation between decreased PXR expression and increased expression of fibrosis and innate immune genes. Intriguingly, they discovered that IPA decreased intestinal inflammation and fibrosis in mice with DSS-induced colitis *via* activating PXR, whereas microbiota removal increased intestinal inflammation and fibrosis^[102]. These findings suggest that the interaction of the microbiota metabolite IPA with PXR may be an important determinant of the progression of fibrotic complications in IBD. In addition, Deuring *et al*^[103] found a strict negative association between colonic epithelial PXR levels and NF- κ B target gene expression in CD patient colon biopsy tissue. During IBD, their findings show that PXR is a substantial and clinically relevant antagonist of NF- κ B activity in the intestinal epithelium^[103].

MDR1 is a membrane-associated, ATP-dependent efflux pump preferentially expressed in intestinal and circulating human CD4⁺ effector T cells^[104]. Chen *et al*^[105] discovered CAR as a regulator of MDR1 expression in T cells that prevents bile acid toxicity and inflammation in the mouse small intestine. Activation of CAR induces not only the expression of detoxifying enzymes and transporters in CD4⁺ T effector cells in the lamina propria of the small intestine, but also the expression of the key anti-inflammatory cytokine IL-10. The activation of these programs provides an unexpected strategy for treating IBD and defines the subspecialization of lymphocytes in the small intestine.

S1PR2

⁴ The S1PR2 is highly expressed in the ileum and colon, and it can be activated by the conjugated main bile acids GCA and TCA as well as GCDCA and TCA^[23]. Vascular and immune dysfunction are thought to be involved in the pathogenesis of IBD, but the exact mechanisms of mucosal vascular endothelial barrier dysfunction and macrophage phenotypic transformation are not fully clarified. Wang *et al*^[106] discovered that S1PR2 expression was considerably enhanced in intestinal mucosal vascular endothelium cells and macrophages from IBD patients and animals with DSS-induced colitis, as well as in vascular endothelial cells and macrophages treated with LPS *in vitro*. Knockdown or inhibition of S1PR2 expression significantly reduced the expression of RhoA and ROCK1 in vascular endothelial cells and macrophages. Furthermore, they discovered that inhibiting S1PR2 and ROCK1 reversed impaired vascular barrier function and M1 macrophage polarisation *in vivo* and *in vitro*, while decreasing endoplasmic reticulum stress and macrophage glycolysis in vascular endothelial cells, reversing LPS-induced impairment of M1 macrophage polarisation and vascular endothelial cell barrier dysfunction. The results imply that ³² the S1PR2/RhoA/ROCK1 signalling pathway, which regulates vascular endothelial cell barrier function and M1 macrophage polarisation, may have a role in the aetiology of IBD^[106]. Chen *et al*^[107] previously demonstrated that S1PR2 is abundantly expressed in intestinal epithelial cells and stimulates IEC proliferation and migration. However, the precise role of S1PR2 in UC is unknown. They recently discovered that S1PR2 may play a significant role in intestinal epithelial cell proliferation and barrier maintenance by influencing the expression levels of SphK2, HDAC1, HDAC2, and ERK1/2 signaling pathways. Surprisingly, they discovered that inhibiting S1PR2 in the UC mouse model might also reduce the severity of colonic pathological injury in mice, which was followed by a drop in TNF- α and IL-18 Levels in their serum^[107]. These findings reveal that S1PR2, despite its beneficial effects on intestinal epithelial cell proliferation and barrier maintenance, maybe a key pathogenic factor in UC. In addition, researchers discovered that DCA dose-dependently increased S1PR2 expression in a mouse model of colitis. Meanwhile, at least in part, DCA-induced NLRP3 inflammasome activation was achieved by

stimulating the ERK1/2 signaling pathway downstream of S1PR2 to promote cathepsin B release. S1PR2/ERK1/2/cathepsin B signaling is key in triggering DCA activation of inflammatory vesicles^[108]. The results of this study suggest that S1PR2 should be investigated further as a possible treatment for IBD.

THE POTENTIAL THERAPEUTIC TARGETS OF BILE ACIDS AND THEIR RECEPTORS IN IBD

Bile acid receptor agonists or inhibitors

Based on growing knowledge and understanding of the mechanism of action of bile acid receptors, the development of medications targeting the bile acid receptor activity that changes considerably during the progression of IBD may give a more specific therapeutic effect. The development of bile acid receptor agonists or antagonists is widely recognized as a promising therapeutic avenue for treating IBD and is a hot area of research (Table 2). Recently, Miyazaki *et al*^[109] showed that administration of the novel FXR agonist nelumal A induced the expression of FXR target genes and tight junction proteins in the intestine while decreasing the expression of hepatic bile acid synthesis genes, effectively reducing colitis and inhibiting colitis-related carcinogenesis. Another study found that the FXR agonist ¹⁹ nigakinone alleviates DSS-induced experimental colitis *via* regulating bile acid profile and FXR/NLRP3 signaling pathways. inhibited inflammatory cytokine production by activating the FXR/NLRP3 signaling pathway and regulated bile acid metabolism by controlling cholesterol hydroxylase and FXR-mediated transporter proteins, reducing bile acid accumulation in the colon and thereby reducing colitis^[110]. Although FXR agonists exhibit very positive effects, they are also commonly associated with many side effects. Its most common side effects are dose-dependent pruritus and an increased LDL: HDL ratio, which may increase the risk of atherosclerosis. Its long-term efficacy remains to be determined^[111]. ¹⁰ Qi *et al*^[112] used structure-based virtual screening to identify 2',4'-dihydroxy-2,3-dimethoxychalcone (DDC). This is a chalcone derivative enriched in plants and food, located in the binding pocket of ROR γ t, which can target and inhibit ROR γ t activity,

thereby indirectly stabilizing Foxp 3 expression, achieving regulation of Th17/Treg homeostasis and improving Th17-mediated inflammation. In another study, Chen *et al*^[113] proposed a dual-targeting approach for treating IBD using ROR γ t and dihydroorotic dehydrogenase (DHODH). Dual ROR γ t/DHODH inhibitors are expected to reduce ROR γ t-driven Th17 cell differentiation and attenuate T cell expansion and activation, which may enhance anti-inflammatory effects. They found that the 2-aminotetrahydrobenzothiazole compound 14d could act as a potent dual ROR γ t/DHODH inhibitor, exhibiting significant *in vivo* anti-inflammatory activity and dose-dependently reducing the severity of DSS-induced acute colitis in mice. Furthermore, by screening a large combinatorial library of 1,5-disubstituted acylated 2-amino-4,5-dihydroimidazoles and using a positional scanning library strategy to rapidly identify a novel class of ROR γ inhibitors, Ortiz *et al*^[113] found that compound 1295-273 had the highest activity against ROR γ in this series, with almost twofold selectivity for this receptor isoenzyme. However, they did not further validate it *in vivo* or *in vitro* experiments.

Genistein, a key isoflavone, stimulates GPABR1 receptors in a DSS-induced mouse colitis model, dramatically lowering inflammatory cell infiltration and generation of pro-inflammatory mediators in the blood and colon and reducing weight loss and increasing colon length in mice^[114,115]. In another study, Nakhi *et al*^[116] observed that the acid group of CDCA can be replaced by a wide range of chemical groups that can simultaneously maintain or significantly increase its agonistic potency against GPABR1. In particular, pyrrolidinamide 9 and 1,3,4-oxadiazole analog 23 were 10- and 70-fold more potent than CDCA. There is a slight loss of potency when the hydroxyl group at position 3 of the bile acid scaffold is methylated. Surprisingly, however, a more than 100-fold increase in potency was observed upon methylation of the 7-hydroxyl group of pyrrolidinamide 9. Based on these observations, they synthesized the 7-methylated oxadiazole analogue 17, which proved to be a highly potent agonist at the GPABR1 receptor. However, the specific efficacy has to be further de-validated in IBD models^[116]. However, most of the GPABR1 agonists studied are unrestricted GPABR1

agonists, and the pharmacological application would be limited by the systemic targeting effect, with associated side effects such as gallbladder overfilling and gallbladder emptying block. Recently, researchers are exploring a series of intestinal-restricted GPABR1 agonists in an attempt to avoid these side effects. Dipeptidyl peptidase IV (DPP4) is a serine exopeptidase, and DPP4 inhibitors have been reported to reduce colitis *via* the GLP pathway after colonic administration in mice^[117]. Recently, Han *et al*^[118] identified a series of highly potent intestine-restricted GPABR1-DPP4 bifunctional molecules for the first time by integrating GPABR1 agonistic and DPP4 inhibitory efficacy into a single molecule. The effects of GPABR1 and DPP4 on UC were exploited and made to act locally in the gut to avoid unwanted systemic effects. In particular, racemic compound 15, a highly potent GPABR1-DPP4 bifunctional molecule, showed good intestinal distribution, efficacy, and gallbladder safety in a mouse model of colitis^[118]. Chen *et al*^[119] also described the discovery and optimization of a series of intestinal-restricted selective thiazolidine-type GPABR1 agonists that elicit a potent response with minimal effects on the gallbladder. They mainly explored this series of drug compounds No. 12, with minimal systemic availability, which stimulates prolonged and potent GLP-1 (7-36) amide (tGLP-1) secretion and may have significant therapeutic value in IBD^[119].

Dvořák *et al*^[120] proposed microbial metabolite mimicry as a new strategy for drug discovery based on the effect of microbial metabolites on PXR and reported the functionalized indole derivative lead compound Felix Kopp Kortagere 6 (FKK6) as the first class of non-cytotoxic PXR agonists as a proof of concept for microbial metabolite mimicry. In cells, human organs, and animals, FKK6 can directly bind PXR and stimulate PXR-specific target gene expression. In mice expressing human PXR genes, FKK6 dramatically suppressed the production of pro-inflammatory cytokines and prevented inflammation^[120]. The development of FKK 6 provided the first evidence that microbial metabolite mimicry is a viable drug discovery strategy and opened the door to an underutilized chemical space for IBD drug development.

In conclusion, the research and development of bile acid receptors and their agonist or inhibitor medicines is a viable treatment method for IBD. However, there are still numerous issues, such as the increased adverse effects of non-selective agonists and activators. Increasing the intestinal restriction of agonists by identifying modifications that block the active transport of ASBT while reducing passive absorption by increasing the compounds' size and polar surface area is a feasible solution to their side effects. However, the synthesis of existing intestinal restriction activators or inhibitors is very complex and expensive, and further research is needed to explore.

Traditional Chinese medicine

Chinese medicine is garnering more attention as the global pharmaceutical industry develops, and herbal medicine has distinct advantages in treating IBD due to allopathic treatment^[121]. Many academics have recently conducted basic research on traditional Chinese medicine for the treatment of IBD from various angles, and they discovered that traditional Chinese medicine may benefit the treatment of IBD by affecting bile acids and their receptors, which support intestinal mucosal barrier function, regulate intestinal immunity, and influence bile acid metabolism (Table 2). In China, Baitouweng Tang (BTWT) is a commonly prescribed drug for the treatment of UC. In a DSS-induced mouse model of UC, mice were given BTWT for 7 d. Surprisingly, the researchers found that BTWT treatment reduced the increased UDCA, HDCA, MCA, CA, and GLCA in UC and normalized the levels of some bile acids, especially CA and MCA. Moreover, BTWT increased the expression of FXR and GPBAR1 in the liver. In addition, they found that the relative species abundance and gut microbiota diversity were significantly higher in the BTWT-exposed group. BTWT significantly ameliorated colonic inflammation and clinical signs, such as histological damage and colonic shortening, in mice. This result may be achieved by affecting the intestinal microbiota, bile acid metabolism^[122]. Gualou Xiebai Decoction (GXD) is a classic formula used in China for thousands of years to treat inflammatory diseases. A recent study showed that GXD significantly improved intestinal barrier dysfunction caused by abnormal bile

acid metabolism in IBD by regulating tight junction protein expression levels, inhibiting oxidative stress, and reducing apoptosis^[123].

“Kushen”, the dried root of the *Sophora flavescens* Aiton, is a classical drug widely used in China to treat UC in ancient and modern times, with alkaloids and flavonoids as the main components. Previous studies have shown that *Sophora flavescens* Aiton total flavonoids extracts (SFE) exhibits anti-UC effects by restoring the balance of the "host-microbe" co-metabolic network and modulating the intestinal microbial structure in UC mice^[124]. A recent study further found that SFE, especially the flavonoid component represented by Kurarinone, had a significant protective effect against UC by regulating the transcriptional levels of ROR γ T and Foxp 3 in the colon and down-regulating the expression of the pro-inflammatory factor IL-17 A in colon tissue^[125]. In addition, Chingchang Wenzhong Decoction (QCWZD) and licorice water extraction (LWE) also inhibited the transcriptional activation of ROR γ T and IL-17A, thereby suppressing the differentiation of Th17 Lymphocytes and reducing colonic inflammation^[126,127]. Huanglian Ganjiang Tang (HGT) is the classic formula in Danxi Xinfu, used to relieve diarrhea, abdominal pain, and blood in the stool, it is currently used clinically for the treatment of UC with remarkable efficacy, but its mechanism of action needs to be further elucidated. Xiong *et al*^[128] recently showed that HGT could reduce DSS-induced colitis in mice by inhibiting DSS-induced necrotizing lesions in the colon through upregulation VDR levels. Furthermore, in animal models of IBD, researchers found that patchouli alcohol (PA) and alpinetin from ginger plants could activate PXR signaling and inhibit NF- κ B signaling, thereby ameliorating inflammation^[129,130]. In conclusion, the results of these herbal studies provide new options for treating IBD and provide a theoretical basis for pharmacological studies of herbal medicines, which are beneficial for their application.

UDCA

UDCA is a secondary bile acid generated from CDCA, which is found in low concentrations in humans and was initially licensed by the FDA to treat cholestatic liver

disease. However, several studies have shown that UDCA may play an important role in IBD by acting on bile acid receptors. For example, a previous study showed that DCA could inhibit the expression of CFTR Cl channels by activating FXR, thereby delaying the repair of the intestinal mucosal barrier. Interestingly, UDCA inhibits this process and promotes epithelial cell migration and recovery^[131]. In a recent study, UDCA was shown to reduce inflammatory cytokine production by activating FXR while inhibiting NF- κ B activation in macrophages in a piglet model of intestinal inflammation^[132]. These findings suggest a protective role for UDCA in IBD and support its use as a novel approach to treat IBD. In addition, UDCA can improve IBD injury through a few other potential mechanisms. MAdCAM-1 binds to $\alpha 4\beta 7$ integrin on circulating T cells and recruits intestinal homing lymphocytes to intestinal damage sites during inflammation^[133]. A recent study showed that by inhibiting NF κ B signaling, UDCA could directly attenuate the endothelial expression of MAdCAM-1 and other adhesion molecules, leading to a decrease in the accumulation of $\alpha 4\beta 7$ + lymphocytes in the colon, thereby reducing the severity of colitis^[134]. Another study showed that in a DSS-induced mouse model, UDCA and LCA prevented intestinal inflammation *in vivo*, at least in part by inhibiting epithelial cell apoptosis and promoting barrier function. Interestingly, LCA was more effective than UDCA in inhibiting epithelial cytokine release and preventing DSS-induced mucosal inflammation^[135,136]. Mesalazine is the main drug used clinically for the treatment of UC and has been shown to induce remission of IBD and prevent IBD recurrence^[137]. UDCA + mesalazine has been reported to have a better therapeutic effect than mesalazine alone, which may be related to the significant reduction of IL-23 and IL-17 and the altered distribution ratio of intestinal flora^[138]. Tauroursodeoxycholic acid, a taurine conjugated UDCA, has been shown to reduce the accumulation of MPO activity, decrease colonic tissue levels of IL-1 β , IFN- γ , and TNF- α , and also down-regulate nuclear receptor and bile acid transporter protein levels^[139,140]. Hyodeoxycholic acid, glycine ursodeoxycholic acid, and taurocholate have similarly reduced colitis severity in mice in an IBD model^[141-143]. However, it has also been shown that long-term use of high-dose UDCA increases the risk of colorectal

neoplasia in patients with IBD, suggesting that we need to control the course and dose of the drug rationally^[144]. In conclusion, secondary bile acids such as UDCA may be promising therapeutic agents for reducing ecological dysregulation and improving inflammation in human IBD and are attractive candidates for treating IBD.

Probiotics and fecal microbiota transplantation

Probiotic therapy introduces specific bacteria that have a recognized advantage in competitively suppressing pathogens and normalizing intestinal microbiota composition. ²³ Probiotics are classified by the World Health Organization as live microorganisms that, when consumed in sufficient quantities, can help the host's health. The probiotics *Bifidobacterium*, *Lactobacillus*, and *Lactococcus* are the most frequently utilized. One adjuvant therapy for addressing the functional symptoms of IBD, probiotics have shown promise in numerous human and animal studies^[145-147]. Wong *et al*^[148] recently demonstrated that *Lactobacillus casei* strain Shirota (LcS) not only increased beneficial bacterial species but also modified the circulating bile acid profile in mice with colitis in a mouse model of DSS-induced acute colitis. Furthermore, LcS treatment increased mucin-2 and occludin expression in the colon while improving intestinal integrity. It was also shown that LcS therapy ¹² decreased the expression of pro-inflammatory mediators IFN- and NO and raised the expression of anti-inflammatory mediator in colonic tissue, possibly due to an altered bile acid profile^[148]. Another study showed that probiotic mixtures containing *Lactobacillus rhamnosus* and *Lactococcus lactis* ²¹ reduced the expression levels of IFN- γ , IL-17F, IL-1 α , and IL-25 also reduced the levels of the main NLRP3 inflammasome components (NLRP3, ASC, caspase-1 and IL-1 β) and NOD2 in IBD mice. Probiotics have also increased FXR, GPABR1, vitamin D, and CAR expression in IBD mice^[149]. Furthermore, the probiotic *Lactobacillus* has anti-inflammatory activity and induces cellular autophagy, and these effects are achieved by increasing VDR expression^[150]. Recently, Zhou *et al*^[151] designed a bile acid consortium (BAC) composed of three species of *Bacteroides ovatus*, *Clostridium* AP sp000509125, and *Eubacterium limosum*. They observed that BAC restored secondary bile acid metabolism

in DSS-treated mice, thereby increasing the levels of UDCA and LCA, which induced activation of GPABR1 to improve the integrity of the intestinal barrier and reduce inflammation^[151]. In addition, the probiotic strain *Bifidobacterium longum* CECT 7894 could improve the efficacy of infliximab against DSS-induced colitis by modulating intestinal flora composition and bile acid metabolism^[152]. Probiotics may increase the risk of bacteremia, adverse effects, and the spread of antibiotic resistance in IBD patients because of their bioactivity and other characteristics. In addition, probiotics used for adjuvant therapy may be unsuccessful in some patients due to strain specificity or individual differences, in which case they should be discontinued. Therefore, the duration of probiotics should be dependent on various therapeutic benefits, objectives, and practical circumstances. Future clinical and animal investigations are required to study the direct effects and specific mechanisms of probiotics on bile acids and their receptors in IBD patients.

Fecal microbiota transplantation (FMT) is a novel and appropriate route to modify the microbial ecosystem in the host gastrointestinal tract. In recent decades, FMT has improved diseases such as *Clostridioides difficile* infections, IBD, and irritable bowel syndrome. However, the exact mechanisms still need to be better understood^[153,154]. Several recent studies have found that FMT may improve IBD by acting on bile acids and their receptors. Lima *et al*^[155] showed that FMT induced the production of ROR γ t+ regulatory T cells, IL-10, and short-chain fatty acids by macrogenomic analysis and strain tracing in 60 donor and recipient samples of active UC treated with FMT, thus protecting patients from colitis^[155]. Another study showed that the long-term Faecalibacterium colonization following FMT could reduce intestinal inflammation by regulating the expression of ROR γ t and Foxp3 in UC, thereby ameliorating the imbalance in Th 17/Treg levels^[156]. In addition, a mouse model of colitis was shown to be significantly inhibited by the intestinal fungus *C. metapsilosis* M2006 B, which was isolated from human feces. Moreover, the researchers identified two acyclic sesquiterpenoids (F4 and F5) as the main active metabolites of M2006 B. Surprisingly, in an animal model, these metabolites were able to effectively ameliorate colitis by

16
selectively activating FXR. These findings suggest that M2006 B in human feces may be a beneficial intestinal fungus for treating and preventing IBD^[157]. Interestingly, another recent study found that administering antibiotic pretreatment to IBD patients contributed to microbial implantation and possible clinical effectiveness^[158]. In conclusion, these findings support the use of FMT in treating IBD, but the safety and efficacy of FMT remain to be investigated.

Bile acid sequestrants

A bile acid sequestrant is a positively charged indigestible resin that binds to bile acids in the intestine and forms insoluble compounds in the feces. They are mainly used in treating primary hypercholesterolemia and hypercholesterolemia with mild hypertriglyceridemia^[159,160]. Currently, there are three major medications available for purchase: cholestyramine, colestipol, and, more recently, colesevelam. 37
Bile acid malabsorption (BAM), also known as bile acid diarrhea (BAD), is a prevalent, underappreciated, and frequently missed indicator of IBD. Clinically relevant BAM is most commonly seen in patients with IBD, especially in ileal resected CD patients.

In most cases, BAM in IBD is caused by impaired reabsorption of conjugated bile acids^[161]. CD patients with BAM treated with bile acid sequestrants achieved a good response in 72.2% of cases. Researchers also analyzed the relationship between the degree of BAM (moderate or severe), intestinal surgery, and response to bile acid chelation therapy, but unfortunately, they were not statistically significant^[162]. Another study showed a significant improvement in the quality of life of CD patients after terminal ileal resection when molecular treatment was given to them^[163]. Although some research progress has been made, the specific mechanisms of bile acid chelators in treating BAM caused by IBD need to be further explained.

CONCLUSION

The data suggested that bile acid metabolism and receptor signaling play a key role in regulating dysregulated gut homeostasis in IBD. Changing bile acid metabolism and

bile acid receptor signalling has been found to influence the pathogenesis of IBD *via* modulation of immunology, intestinal epithelial barrier function, and the gut microbiome. It is an attractive and highly promising therapeutic target for IBD. Many therapeutic strategies have shown positive effects, such as bile acid receptor agonists or inhibitors, traditional Chinese medicine, UDCA, probiotics, FMT, and bile acid sequestrants. However, due to the differences between species and cell types (IBD is exclusively a human disease), valuable preclinical mechanistic studies must be performed to elucidate the function of bile acids and their receptors in human intestinal models. In this regard, human organoid technologies and bioinformatics approaches may be good tools to address this issue. In addition, the current therapeutic strategies described above have yet to be widely validated in clinical trials in patients with IBD, despite the promising results documented in cellular and animal studies. Future research efforts should focus on clinical trial data collection in IBD patients.

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