



Research Progress of Intestinal Flora and Related Diseases

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Abstract

Keywords

- intestinal flora
- metabolic diseases
- bowel diseases
- mental system diseases
- immune diseases
- tumors

The intestinal tract is an important digestive organ and detoxification organ of the human body, and its circling structure is vividly called the “second brain” of the human body. There are hundreds of millions of bacterium in the intestinal tract. These bacteria live in mutual benefit with the body, provide energy and nutrients for the host and themselves through fermented food, participate in the metabolism of the body, and form a metabolic mode of cometabolism between the host and the symbiotic flora. In addition, intestinal flora can also help the body resist the invasion of pathogens, promote human health, and resist diseases. More and more studies have shown that when the body is subjected to exogenous or endogenous stimuli, the microbial flora in the intestinal will change, and the disturbance of intestinal flora is closely related to the occurrence and development of inflammatory bowel diseases, metabolic diseases, immune system diseases, mental system diseases, and tumors. This article reviews the research progress of the intestinal flora affecting the pathogenesis of various diseases, aiming to provide new references and ideas for the clinical treatment of diseases.

Introduction

In recent years, with the increasing number of research on the composition and function of intestinal microbiota, it has become increasingly clear that microorganisms play a very important role in the maintenance of health and the occurrence and development of diseases. Microbes are important in a wide range of physiological processes, from the digestion of complex polysaccharides to the regulation of neural signaling.¹ The total number of parasitic microorganisms in the human intestinal tract exceeds hundreds of trillions, which is 10 times the number of human cells.² Each individual's microbiome is unique like people's fingerprints, and they are closely related to intestinal metabolic and immune functions. The biological function of the body needs energy

as the basis. However, the carbohydrates in the food cannot be completely digested, absorbed, and utilized by themselves. A large part needs to be fermented and decomposed with the help of intestinal flora and then absorbed and utilized by the body. The metabolic pattern is called “host-intestinal flora cometabolism” metabolic pattern, and different intestinal bacteria have different metabolites. The composition and metabolism of the intestinal microbial community are affected by many factors, such as poor eating habits and lifestyles, overuse of antibiotics, etc., which seriously endanger the ecological balance of the intestinal flora, resulting in a decrease in the diversity of the microbiome in the body and the abundance of some bacteria. The change in this abundance will change the metabolites of the

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flora and threaten the health.³ Studies have shown that the imbalance of intestinal flora is closely related to the occurrence and development of various diseases, such as irritable bowel syndrome,⁴ acute anterior uveitis,⁵ rheumatoid arthritis,⁶ diabetes,⁷ hypertension,⁸ autism,⁹ and colorectal cancer.¹⁰ This article reviews the research on the correlation between intestinal flora and diseases in recent years, in order to provide new references and strategies for clinical treatment.

Intestinal Flora and Inflammatory Bowel Disease

Inflammatory bowel disease (IBD) is an intestinal immune response caused by the interaction of multiple factors such as environment, genetics, infection, and immunity, which then causes tissue damage. Two disease subtypes of Crohn's disease (CD),¹¹ which often occurs in children and young adults, are incurable and associated with complications, such as infection, hospitalization, surgery, and cancer,^{12,13} seriously affecting the patient's mental health and increasing the risk of depression and anxiety.^{14,15} Studies based on 16S rRNA gene sequencing have revealed significant differences between the microbiota of IBD patients and healthy individuals, suggesting a potential role of the intestinal flora not only in development but also in determining prognosis and disease progression,¹⁶ and common changes in the intestinal flora of patients with IBD include increases in facultative anaerobes such as *Escherichia coli*¹⁷ and reduced obligate anaerobic producers of short-chain fatty acids, such as Firmicutes.¹⁸ The study found that the intestinal flora of healthy people had abundance of *Akkermansia muciniphila* and *Coproccoccus regularis*, while ulcerative colitis (UC) patients had abundance of *Bifidobacterium adolescentis* and *Haemophilus parainfluenzae*¹⁹; intestinal flora was decreased in CD patients, there was a scarcity of Firmicutes, *Bacteroides*, *Rhodesia*, and *Clostridium praesens*, while there was abundance of *Proteus*, *Actinomyces*, *Escherichia coli*, and sulfate-reducing bacteria.^{20–23} As an important part of Chinese medicine, acupuncture and moxibustion have dual benefits. The study of acupuncture and moxibustion treatment of CD patients found that the clinical remission rate of the acupuncture group was significantly increased, the CD activity index and C-reactive protein levels were significantly reduced, and the CD severity degree index, histopathological score, and recurrence rate were all significantly reduced, the intestinal flora increased, *Faecalibacterium prausnitzii* and *Roseburia faecis* and *Rhodesia* in feces relatively increased, and relevant cytokines of plasma diamine oxidase, lipopolysaccharide, and Th1/Th17 decreased.²⁴ Studies have found that Gegen Qinlian decoction can improve the metabolism of fatty acids, bile acids, and amino acids by regulating the composition of intestinal flora, enhancing intestinal barrier function, repairing intestinal ultrastructural damage, relieving oxidative stress, promoting antioxidant activity, reducing the expression of inflammatory factors and chemokines, and up-regulating anti-inflammatory factors, thereby alleviating colitis in rats.^{25–27}

Intestinal Flora and Metabolic Diseases

Obesity

With the continuous improvement of living standards, people's eating habits have undergone tremendous changes. The number of obese people in the world is increasing, and their age is getting younger and younger, which seriously threatens human's health.²⁸ The root cause of obesity is an imbalance between energy intake and expenditure, but changes in genetics, epigenetics, and intestinal microbial composition all contribute to obesity,^{29–31} which in turn increase the risk of diseases such as cancer, atherosclerosis, and diabetes.^{32–34} The study found that after feeding resveratrol to mice for 16 weeks, fecal bacteria were transplanted to mice that had been fed a high-fat diet (HFD), and it was found that the obesity of the high-fat-fed mice was significantly improved and insulin sensitivity was significantly increased. Alcohol-induced intestinal flora can regulate lipid metabolism in white adipose tissue and brown adipose tissue, reduce inflammation and improve intestinal barrier function.³⁵ Huanglian (*Coptidis Rhizoma*) and berberine were administered to C57BL/6J mice fed a HFD, and both Huanglian (*Coptidis rhizoma*) and berberine were found to significantly reduce the levels of Firmicutes and *Bacteroidetes* in the feces of HFD mice, decrease body and visceral fat mass, decrease blood glucose and blood lipid levels, and degrade dietary polysaccharides in HFD mice.³⁶ The researchers used genetic and diet-induced two obese mouse models, orally administered *Parabacteroides distasonis* (PD), and found that PD can improve the metabolism of obese mice, control the weight of obese mice, reduce hyperglycemia and lead to fatty liver.³⁷ After taking *Bifidobacterium animalis* milk subsp. *CECT 8145* (Ba8145) and heat-inactivated Ba8145 for obese patients for three consecutive months, the patients' waist circumference, waist circumference/height ratio, taper index, body mass index, and visceral fat area were significantly reduced, and AKK bacteria in intestinal flora increased.³⁸ Through the above studies, it is found that the intestinal flora is closely related to the occurrence and development of obesity disease, and the intestinal flora may be a potential target for the treatment of obesity.

Diabetes

Diabetes mellitus (DM) refers to a metabolic disorder syndrome dominated by sugar and lipids caused by insulin deficiency or insulin resistance and is characterized by elevated blood sugar. The main feature of diabetes is elevated fasting blood sugar, which is mainly divided into diabetes mellitus type 1 (T1D) and DM type 2 (T2D), etc. T1D is insulin-dependent DM, which is an autoimmune disease. Due to the destruction of pancreatic islet B cells, insulin secretion is absolutely insufficient, and patients need to use insulin to maintain blood sugar levels. In recent years, the incidence of T1D in children has been increasing year by year, and it has become a major basic disease affecting the health of children and adults in China. Studies have shown that the structure and function of intestinal flora in T1D children are disordered, and the transplantation of flora in T1D children can

increase fasting blood sugar and reduce insulin sensitivity in antibiotic model mice.³⁹ Human milk oligosaccharides and prebiotics can inhibit the occurrence and development of T1D by regulating intestinal flora and controlling blood sugar.^{40,41} T2D is noninsulin-dependent diabetes. The ability of the patient to produce insulin is not completely lost, but the patient is resistant to the action of insulin. Therefore, insulin in the patient's body is in a state of relative deficiency, which is the most common type of diabetes, accounting for more than 90% of diabetes, and most patients develop it after the age of 35 to 40. Microorganisms in the intestine can inhibit the levels of proinflammatory cytokines and chemokines and inflammatory proteins, regulate intestinal permeability, affect glucose homeostasis and insulin resistance in major metabolic organs such as liver, muscle, and fat, and increase fatty acid oxidation and energy consumption and reduction of fatty acid synthesis and other effects regulate glucose metabolism in T2D patients.⁴² The study found that after probiotic treatment in T2D patients, the weight, body mass index, and waist circumference of the patients were significantly improved, and the fasting blood glucose, insulin concentration, and insulin resistance were significantly reduced.^{42–44} In addition, Huangqi (*Astragalus Radix*) polysaccharides and bitter melon polysaccharides reduce blood sugar in T2D mice by regulating the intestinal environment and improving intestinal flora disorder.^{45,46}

Hypertension

Hypertension is a chronic noncommunicable disease and an important risk factor for the occurrence of cardiovascular diseases. The incidence is increasing. Because of long-medication cycle and poor clinical outcomes, it seriously affects the life of patients. Recent studies have shown that hypertension is closely related to changes in the composition and function of intestinal flora,⁴⁷ the feces of hypertensive patients were transplanted into germ-free mice and the blood pressure of the transplanted mice increased.⁴⁸ High-salt diet seriously affects people's health and is one of the important factors inducing high blood pressure. It can affect the body's immune system by changing the intestinal flora, thereby changing the body's blood pressure.^{49,50} High-fiber and cellulose acetate diet, supplementation of specific microorganisms, etc. can improve hypertension by regulating the structure of intestinal microorganisms.^{51,52}

Nonalcoholic Fatty Liver

Nonalcoholic fatty liver disease (NAFLD) is a clinicopathological syndrome characterized by diffuse macrovesicular steatosis of liver cells without alcohol and other clear pathogenic factors, including simple fatty liver, nonalcoholic steatohepatitis, and nonalcoholic cirrhosis. NAFLD is the most common chronic liver disease worldwide, affecting about a quarter of the adult population,⁵³ and the prevalence is increasing, and currently, there is no NAFLD drug with significant curative effect.⁵⁴ There is an urgent need to identify modifiable risk factors that may prevent or delay its development, as well as new clinical treatment strategies. Studies have shown that intestinal microbiota imbalance is

also an important factor in the development of NAFLD, playing an important role in regulating energy balance and fat deposition.⁵⁵ Intestinal bacteria were stimulated by feeding mice the fermentable dietary fiber guar gum and suppressed by long-term oral administration of antibiotics. It was found that guar gum can significantly alter intestinal microbiota composition in mice while reducing dietary obesity induced and improving glucose tolerance, but it enhanced liver inflammation and fibrosis, with significantly elevated plasma and hepatic bile acid levels. This result suggested a causal relationship between changes in the intestinal microbiota and hepatic inflammation and fibrosis in a mouse model of NAFLD and that this change may be related to the regulation of bile acids.⁵⁶ Further studies also found that the intestinal flora of NAFLD patients was significantly changed, and the level of serum fibroblast growth factor 21 (FGF21) was increased, and FGF21 can regulate bile acid metabolism by targeting intestinal flora to improve NAFLD.⁵⁷ The above studies indicate that intestinal flora and their metabolites may be new targets for the treatment or prevention of NAFLD. In addition, Chinese medicine ingredients and preparations of resveratrol, phytosterol esters, black fungus polysaccharides, Fuzhuan tea, Simiao prescription, and Jiangnan Jiangzhi pills can improve NAFLD by regulating intestinal flora disorder.^{58–63}

Intestinal Flora and Immune System Diseases

Asthma

Asthma is a type I hypersensitivity disease. After exposure to allergens, atopic individuals induce mast cells and basophils to degranulate, causing them to release active mediators such as prostaglandins, histamine, and leukotrienes, triggering bronchospasm and impaired pulmonary ventilation. The intestinal flora is an important risk factor for asthma and has become a widespread concern in the pathogenesis of asthma.⁶⁴ Compared with healthy people, the levels of *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* in fecal samples of asthmatic patients are reduced, and both of them can induce anti-inflammatory cytokine IL-10 and prevent the secretion of proinflammatory cytokine IL-12, further promoting the occurrence and development of inflammation.⁶⁵ Colonization of the intestine by the environmental fungus *Wallemia mellicola* exacerbated dust mite-induced asthma-like inflammation and exacerbated asthma in mice.⁶⁶ Studies showed that nasal inoculation of mice with *Lactobacillus rhamnosus* could prevent birch pollen-induced allergic asthma in mice.⁶⁷ Similarly, after oral administration of specific *Lactobacillus* in severe asthma model mice, it can significantly reduce the infiltration of neutrophils and eosinophils in alveolar lavage fluid, decrease inflammatory factors in lung tissue, and have obvious protective effects for asthmatic mice.^{68–70} Chinese medicine prescriptions, Chinese medicine extracts, and monomeric compounds such as Shaoyao Gancao decoction, Tingli Dazao Xiefei decoction, Sijunzi decoction, Yangfei decoction, Pipaye (*Eriobotryae Folium*) water extract can inhibit intestinal

inflammation by regulating intestinal flora disorder, repair intestinal mucosal barrier, and improve asthma.^{71–75}

Rheumatoid Arthritis

Rheumatoid arthritis (RA) is a chronic systemic autoimmune disease characterized by chronic joint inflammation, bone erosion, and cartilage destruction.⁷⁶ Multiple studies suggest that intestinal flora plays a significant role in the etiology of RA.^{77,78} The fecal microbial diversity of RA high-risk individuals was reduced, and the structure and function of bacterial communities were significantly altered. The intestinal permeability and expression of ZO-2 in the small intestine and Caco-1 cells of mice transplanted with intestinal flora from high-risk RA patients were increased. Th17 cells in mesenteric lymph nodes and Peyer's plaques increased, which further contributed to the development of arthritis,⁶ and structurally and functionally altered gut microbiota in RA patients,⁷⁹ and the gut microbiota structure was altered after oral administration of *Porphyromonas gingivalis* in mice, aggravating collagen-induced arthritis.⁸⁰ And RA model mice can exert its protective effect on RA mice by maintaining the normal intestinal microbiota of arthritis mice after taking tufts-in-phosphocholine.⁸¹ Intervention of Ershiwu (25) Wei Lyuxue pills, extract of Jishiteng (Chinese fever-vine), and Sinomenine can significantly relieve the symptoms of arthritis in the RA model, reduce the score of arthritis, inhibit arthritis, and restore the homeostasis of intestinal flora.^{82–84}

Intestinal Flora and Neurological Disease

Depression

Depression is a relatively common mental illness at present. Patients with severe depression are accompanied by severe self-harm and suicidal tendencies. Chronic stress is the main risk factor for the development of depression, with a prevalence rate of 11 to 15%. During the coronavirus 2019 pandemic, its incidence has doubled and in some countries even tripled.⁸⁵ More and more research works suggest that the intestinal microbiota may affect brain activity and behavior through neural and humoral pathways, possibly involved in causal pathways leading to depression.⁸⁶ In patients with depression, the abundance of *Bacteroides* was negatively correlated with brain depression characteristics, and potential neurotransmitter GABA-producing or metabolic bacteria in the intestine may inhibit the development of depression.⁸⁷ After transplanting fecal microbiota from patients with depression into rats, it was found that the rats exhibited behavioral and physiological characteristics of depression.⁸⁸ With probiotic supplementation in patients with severe depression, the concentration of kynurenine in plasma was significantly reduced, the ratio of 3-hydroxyanthranilic acid/kynurenine was significantly increased, and the cognitive function of patients with depression was significantly improved.⁸⁹ Extracts of *Cistanche Tubulosa* and Xiaoyao powder can relieve anxiety and depression by regulating intestinal flora, reducing LPS levels, and inhibiting the excessive activation of NLRP3 inflammasome in the colon.^{90,91}

Autism

Autism, also known as autism spectrum disorder (ASD), is characterized by impaired communication skills and often accompanied by stereotyped behaviors, interests and activities, and abnormal living abilities. Autism has become one of the global problems. Since its pathogenesis is not entirely clear, the clinical effect is very little. The intestine microbiota plays a part not only in the development of parenchymal organ diseases but also in the development of mental disorders. Children with ASD have altered intestinal microbiota with higher levels of Proteobacteria, Actinomycetes, and Sutterella.^{92,93} Intestinal bacterial metabolites can activate the atypical immune response of lymphoblastoid cell lines in autistic patients with abnormal metabolism, which has a potential protective effect on the treatment of autism.⁹⁴ Taking prebiotics or specific microbial strains can significantly improve intestinal flora, metabolism, and psychological status and alleviate the antisocial behavior of autistic children.⁹⁵ Palmitoylethanolamine can reduce the stereotyped and repetitive autism-like behaviors of autism model mice, increase their social activities, reduce intestinal permeability, change the structure of intestinal flora, and have protective effects on autism mice.⁹⁶ In addition, studies have found that fecal transplants can significantly improve the symptoms of autistic patients and have a potential therapeutic effect on autism.⁹⁷

Alzheimer's Disease

Alzheimer's disease (AD), also known as senile dementia, is a neurodegenerative disease related to age and cognition. The main pathological manifestations include amyloid β -protein ($A\beta$) abnormal deposition to form senile plaques and hyperphosphorylation of tau protein in neurons to form fibrillary tangles. Studies have shown that increased intestinal and blood-brain barrier permeability caused by intestinal microbiota disturbance will increase the incidence of neurodegenerative diseases, and intestinal microbial metabolites and their impact on host neurochemical changes may increase or decrease the risk of AD.⁹⁸ Intestinal flora changes in Alzheimer's patients,⁹⁹ and the regulation of microorganisms can affect the occurrence and development of AD.¹⁰⁰ Daily probiotic supplementation for 12 weeks in patients with Alzheimer's disease can effectively improve cognitive and metabolic function, and the results of mental state examination were significantly improved.^{101,102} Studies have shown that probiotic preparations SLAB51 and *Lactobacillus plantarum* MTCC1325 exert antioxidant and neuroprotective effects on AD mice.^{103,104}

Intestinal Flora and Tumors

Colorectal Cancer

Colorectal cancer is an epithelial tumor of the colon or rectum that is considered malignant only when it penetrates the muscularis mucosae to the submucosa. Clinically, it can be manifested as blood in the stool, changes in bowel habits, abdominal mass, anemia, intestinal obstruction, etc. Malignant epithelial tumors above the dentate line to the

recto-sigmoid junction are rectal cancers, and malignant epithelial tumors from the recto-sigmoid junction to the ileocecal junction are colon cancers. Studies suggest a possible link between dysbiosis in intestinal microbiota and colorectal cancer.¹⁰⁵ The host can affect the structure of intestinal flora through miRNA, and colorectal cancer inducers can also change the structure of intestinal flora, and intestinal flora metabolites, especially butyrate, can affect gene transcription activity and the pathogenesis of colorectal cancer.¹⁰⁶ Studies have shown that *Salmonella* colonization in the intestinal tract significantly reduces the expression level of Wnt1 in intestinal epithelial cells and inhibits the invasion and migration of cancer cells.¹⁰⁷ Continuous preoperative administration of synbiotics (Simbioflora) can significantly reduce the inflammatory indicators of patients with colorectal cancer, and the incidence of post-operative infectious complications is also significantly reduced.¹⁰⁸ Olive oil and its metabolites, *Ganoderma lucidum* polysaccharides, etc., can change the structure and function of the flora, help maintain a healthy flora, and alleviate colorectal cancer.^{109,110}

Liver Cancer

The liver is an important metabolic and detoxification organ of the human body and participates in the biotransformation and metabolism of the body. According to incomplete statistics from 1999 to 2016, the number of deaths from liver cirrhosis in the United States increased by 65%, the number of deaths from hepatocellular carcinoma doubled, and the mortality rate increased by 2.1%, which seriously threatened human health.¹¹¹ The liver is profoundly influenced by the intestinal microbiota and its metabolites, and leaky gut and microbiota imbalance are triggers for liver pathological reactions.¹¹² The intestine–liver axis is a two-way communication pathway composed of intestinal flora, hepatic portal system, and biliary system, which is the physiological basis for the interaction between intestinal flora and liver.¹¹³ The disordered intestinal flora can promote the progression of liver disease and the development of hepatocellular carcinoma, and regulating the intestinal flora to restore it to normal can improve liver cancer, intestinal leakage, etc. Therefore, the intestine–liver–intestinal flora becomes an ideal target to prevent chronic liver disease from developing into advanced liver disease and liver cancer. Intestinal commensal *Clostridium* bacteria suppress immune responses to liver cancer by metabolizing host-generated primary bile acids to secondary bile acids.¹¹⁴ After certain probiotic combinations were administered to mice with liver cancer, anti-inflammatory bacteria such as intestinal *Prevotella* and *Fibrobacillus* increased, hepatoma decreased, IL-17 expression and the number of Th17 cells decreased, and Th17 cells migrated to the tumor from the intestinal tract and peripheral blood cell decrease.¹¹⁵ Shaoyao Ruangan mixture and Supplemented Xiaoyao powder can effectively inhibit the progression of liver cancer by changing the intestinal flora composition of the incidence of liver cancer, increasing the proportion of beneficial bacteria and reducing the proportion of harmful bacteria.^{116,117}

Lung Cancer

Lung cancer is a type of cancer with the highest mortality rate. In addition to genetic and environmental factors, the microbiota plays a vital role in the development of lung cancer.¹¹⁸ Intestinal microbiome composition altered in lung cancer patients with lower levels of *Kluyvera*, *Escherichia-Shigella*, *Dialister*, *Faecalibacterium*, and *Enterobacter* and increased levels of *Veillonella*, *Fusobacterium*, and *Bacteroides*,¹¹⁹ and some studies suggest that *Enterococcus* and *Bifidobacterium* are potential biomarkers for lung cancer.¹²⁰ The administration of *Lactobacillus acidophilus* to lung cancer mice can enhance the anti-tumor effect of cisplatin, reduce the tumor size, and improve the survival rate, suggesting that probiotics can improve the effect of cisplatin on tumor cells.¹²¹ In addition, Bufeixiao decoction can improve the NLRP3 inflammatory response and intestinal flora in mice with lung cancer complicated with qi and yin deficiency¹²²; combined treatment of Xihuang pills and Anlotinib can significantly inhibit tumor growth in mice with Lewis lung cancer and increase the ratio of beneficial bacteria *Bacteroides* and *g_norank_f_Muribaculaceae*.¹²³

Conclusion

The microbial genome is called the “second genome” of the human body, and the intestinal flora is also regarded as a new “organ” of the body to participate in the life process of the body. From the above explanations, we know that the homeostasis of the intestinal flora is crucial to the maintenance of health. Once the intestinal flora is disturbed, it can regulate the body's metabolism and immunity through metabolites and cause varying degrees of damage to the body and lead to a series of diseases. Probiotics can maintain the intestinal homeostasis of the body and the development of normal physiological functions of the intestinal tract and also play a crucial role in the clinical treatment of diseases. Chinese materia medica and its preparations can be used as probiotics to regulate the structure and metabolic phenotype of host intestinal microbiota and further act as a new source of leading drugs for the treatment of intestinal microbiota-targeted diseases. With the continuous development of science and technology, people will gradually explore the relationship between intestinal flora and diseases. The analysis of intestinal flora will provide a certain basis for the clinical diagnosis of the disease and provide new targets for the clinical treatment of diseases.

CRediT Authorship Contribution Statement

Y.S. was responsible for conceptualization, funding acquisition, and writing-review & editing. X.Z. was responsible for investigation, and writing—original draft. Y.Z. was responsible for supervision. Y.S., B.C. and Z.S. were responsible for investigation.

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Conflict of Interest

The authors declare no conflict of interest.

References

- 1 Sekirov I, Russell SL, Antunes LC, Finlay BB. Gut microbiota in health and disease. *Physiol Rev* 2010;90(03):859–904
- 2 Qin J, Li R, Raes J, et al; MetaHIT Consortium. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 2010;464(7285):59–65
- 3 Campbell EL, Colgan SP. Control and dysregulation of redox signalling in the gastrointestinal tract. *Nat Rev Gastroenterol Hepatol* 2019;16(02):106–120
- 4 Kim GH, Lee K, Shim JO. Gut bacterial dysbiosis in irritable bowel syndrome: a case-control study and a cross-cohort analysis using publicly available data sets. *Microbiol Spectr* 2023;11(01):e0212522
- 5 Rosenbaum JT, Asquith M. The microbiome and HLA-B27-associated acute anterior uveitis. *Nat Rev Rheumatol* 2018;14(12):704–713
- 6 Luo Y, Tong Y, Wu L, et al. Alteration of gut microbiota in high-risk individuals for rheumatoid arthritis is associated with disturbed metabolome and initiates arthritis by triggering mucosal immunity imbalance. *Arthritis Rheumatol* 2023 (e-pub ahead of print). Doi: 10.1002/art.42616
- 7 Funsten MC, Yurkovetskiy LA, Kuznetsov A, et al. Microbiota-dependent proteolysis of gluten subverts diet-mediated protection against type 1 diabetes. *Cell Host Microbe* 2023;31(02):213–227.e9
- 8 O'Donnell JA, Zheng T, Meric G, Marques FZ. The gut microbiome and hypertension. *Nat Rev Nephrol* 2023;19(03):153–167
- 9 Fattorusso A, Di Genova L, Dell'Isola GB, Mencaroni E, Esposito S. Autism spectrum disorders and the gut microbiota. *Nutrients* 2019;11(03):521
- 10 Wong CC, Yu J. Gut microbiota in colorectal cancer development and therapy. *Nat Rev Clin Oncol* 2023;20(07):429–452
- 11 Liu D, Saikam V, Skrada KA, Merlin D, Iyer SS. Inflammatory bowel disease biomarkers. *Med Res Rev* 2022;42(05):1856–1887
- 12 Torres J, Mehandru S, Colombel JF, Peyrin-Biroulet L. Crohn's disease. *Lancet* 2017;389(10080):1741–1755
- 13 Ungaro R, Mehandru S, Allen PB, Peyrin-Biroulet L, Colombel JF. Ulcerative colitis. *Lancet* 2017;389(10080):1756–1770
- 14 Bisgaard TH, Allin KH, Keefer L, Ananthakrishnan AN, Jess T. Depression and anxiety in inflammatory bowel disease: epidemiology, mechanisms and treatment. *Nat Rev Gastroenterol Hepatol* 2022;19(11):717–726
- 15 Bisgaard TH, Poulsen G, Allin KH, Keefer L, Ananthakrishnan AN, Jess T. Longitudinal trajectories of anxiety, depression, and bipolar disorder in inflammatory bowel disease: a population-based cohort study. *EClinicalMedicine* 2023;59:101986
- 16 Varela E, Manichanh C, Gallart M, et al. Colonisation by *Faecalibacterium prausnitzii* and maintenance of clinical remission in patients with ulcerative colitis. *Aliment Pharmacol Ther* 2013;38(02):151–161
- 17 Knights D, Silverberg MS, Weersma RK, et al. Complex host genetics influence the microbiome in inflammatory bowel disease. *Genome Med* 2014;6(12):107
- 18 Morgan XC, Tickle TL, Sokol H, et al. Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment. *Genome Biol* 2012;13(09):R79
- 19 Barberio B, Facchin S, Patuzzi I, et al. A specific microbiota signature is associated to various degrees of ulcerative colitis as assessed by a machine learning approach. *Gut Microbes* 2022;14(01):2028366
- 20 Martinez-Medina M, Garcia-Gil LJ. *Escherichia coli* in chronic inflammatory bowel diseases: an update on adherent invasive *Escherichia coli* pathogenicity. *World J Gastrointest Pathophysiol* 2014;5(03):213–227
- 21 Lopez-Siles M, Martinez-Medina M, Busquets D, et al. Mucosa-associated *Faecalibacterium prausnitzii* and *Escherichia coli* co-abundance can distinguish irritable bowel syndrome and inflammatory bowel disease phenotypes. *Int J Med Microbiol* 2014;304(3–4):464–475
- 22 Imhann F, Vich Vila A, Bonder MJ, et al. Interplay of host genetics and gut microbiota underlying the onset and clinical presentation of inflammatory bowel disease. *Gut* 2018;67(01):108–119
- 23 Lewis K, Lutgendorff F, Phan V, Söderholm JD, Sherman PM, McKay DM. Enhanced translocation of bacteria across metabolically stressed epithelia is reduced by butyrate. *Inflamm Bowel Dis* 2010;16(07):1138–1148
- 24 Bao C, Wu L, Wang D, et al. Acupuncture improves the symptoms, intestinal microbiota, and inflammation of patients with mild to moderate Crohn's disease: a randomized controlled trial. *EClinicalMedicine* 2022;45:101300
- 25 Li Q, Cui Y, Xu B, et al. Main active components of Jiawei Gegen Qinlian decoction protects against ulcerative colitis under different dietary environments in a gut microbiota-dependent manner. *Pharmacol Res* 2021;170:105694
- 26 Wang Y, Zhang J, Zhang B, et al. Modified Gegen Qinlian decoction ameliorated ulcerative colitis by attenuating inflammation and oxidative stress and enhancing intestinal barrier function in vivo and in vitro. *J Ethnopharmacol* 2023;313:116538
- 27 Wang X, Huang S, Zhang M, et al. Gegen Qinlian decoction activates AhR/IL-22 to repair intestinal barrier by modulating gut microbiota-related tryptophan metabolism in ulcerative colitis mice. *J Ethnopharmacol* 2023;302(Pt B):115919
- 28 Swinburn BA, Kraak VI, Allender S, et al. The global syndemic of obesity, undernutrition, and climate change: the lancet commission report. *Lancet* 2019;393(10173):791–846
- 29 Lu Y, Loos RJ. Obesity genomics: assessing the transferability of susceptibility loci across diverse populations. *Genome Med* 2013;5(06):55
- 30 Waterland RA. Epigenetic mechanisms affecting regulation of energy balance: many questions, few answers. *Annu Rev Nutr* 2014;34:337–355
- 31 Ley RE. Obesity and the human microbiome. *Curr Opin Gastroenterol* 2010;26(01):5–11
- 32 Guh DP, Zhang W, Bansback N, Amarsi Z, Birmingham CL, Anis AH. The incidence of co-morbidities related to obesity and overweight: a systematic review and meta-analysis. *BMC Public Health* 2009;9:88
- 33 Renehan AG, Tyson M, Egger M, Heller RF, Zwahlen M. Body-mass index and incidence of cancer: a systematic review and meta-analysis of prospective observational studies. *Lancet* 2008;371(9612):569–578
- 34 Bogers RP, Bemelmans WJ, Hoogenveen RT, et al; BMI-CHD Collaboration Investigators. Association of overweight with increased risk of coronary heart disease partly independent of blood pressure and cholesterol levels: a meta-analysis of 21 cohort studies including more than 300 000 persons. *Arch Intern Med* 2007;167(16):1720–1728
- 35 Wang P, Li D, Ke W, Liang D, Hu X, Chen F. Resveratrol-induced gut microbiota reduces obesity in high-fat diet-fed mice. *Int J Obes* 2020;44(01):213–225
- 36 Xie W, Gu D, Li J, Cui K, Zhang Y. Effects and action mechanisms of berberine and *Rhizoma coptidis* on gut microbes and obesity in high-fat diet-fed C57BL/6J mice. *PLoS One* 2011;6(09):e24520
- 37 Wang K, Liao M, Zhou N, et al. *Parabacteroides distasonis* alleviates obesity and metabolic dysfunctions via production of succinate and secondary bile acids. *Cell Rep* 2019;26(01):222–235.e5
- 38 Pedret A, Valls RM, Calderón-Pérez L, et al. Effects of daily consumption of the probiotic *Bifidobacterium animalis* subsp.

- lactis CECT 8145 on anthropometric adiposity biomarkers in abdominally obese subjects: a randomized controlled trial. *Int J Obes* 2019;43(09):1863–1868
- 39 Yuan X, Wang R, Han B, et al. Functional and metabolic alterations of gut microbiota in children with new-onset type 1 diabetes. *Nat Commun* 2022;13(01):6356
 - 40 Xiao L, Van't Land B, Engen PA, et al. Human milk oligosaccharides protect against the development of autoimmune diabetes in NOD-mice. *Sci Rep* 2018;8(01):3829
 - 41 Ho J, Reimer RA, Doulla M, Huang C. Effect of prebiotic intake on gut microbiota, intestinal permeability and glycemic control in children with type 1 diabetes: study protocol for a randomized controlled trial. *Trials* 2016;17(01):347
 - 42 Gurung M, Li Z, You H, et al. Role of gut microbiota in type 2 diabetes pathophysiology. *EBioMedicine* 2020;51:102590
 - 43 Khalili L, Alipour B, Jafarabadi MA, Hassanilou T, Abbasi MM, Faraji I. Retraction Note: probiotic assisted weight management as a main factor for glycemic control in patients with type 2 diabetes: a randomized controlled trial. *Diabetol Metab Syndr* 2023;15(01):109
 - 44 Abbasi B, Mirlohi M, Daniali M, et al. Effects of probiotic soy milk on lipid panel in type 2 diabetic patients with nephropathy: a double-blind randomized clinical trial. *Prog Nutr* 2018;20:70–78
 - 45 Babadi M, Khorshidi A, Aghadavood E, et al. The effects of probiotic supplementation on genetic and metabolic profiles in patients with gestational diabetes mellitus: a randomized, double-blind, placebo-controlled trial. *Probiotics Antimicrob Proteins* 2019;11(04):1227–1235
 - 46 Liu Y, Liu W, Li J, et al. A polysaccharide extracted from *Astragalus membranaceus* residue improves cognitive dysfunction by altering gut microbiota in diabetic mice. *Carbohydr Polym* 2019;205:500–512
 - 47 Kim S, Goel R, Kumar A, et al. Imbalance of gut microbiome and intestinal epithelial barrier dysfunction in patients with high blood pressure. *Clin Sci (Lond)* 2018;132(06):701–718
 - 48 Li J, Zhao F, Wang Y, et al. Gut microbiota dysbiosis contributes to the development of hypertension. *Microbiome* 2017;5(01):14
 - 49 Wilck N, Matus MG, Kearney SM, et al. Salt-responsive gut commensal modulates T_H17 axis and disease. *Nature* 2017;551(7682):585–589
 - 50 Allison SJ. Hypertension: salt: the microbiome, immune function and hypertension. *Nat Rev Nephrol* 2018;14(02):71
 - 51 Ellison DH, Welling P. Insights into salt handling and blood pressure. *N Engl J Med* 2021;385(21):1981–1993
 - 52 Sircana A, De Michieli F, Parente R, et al. Gut microbiota, hypertension and chronic kidney disease: recent advances. *Pharmacol Res* 2019;144:390–408
 - 53 Huang DQ, El-Serag HB, Loomba R. Global epidemiology of NAFLD-related HCC: trends, predictions, risk factors and prevention. *Nat Rev Gastroenterol Hepatol* 2021;18(04):223–238
 - 54 Sberna AL, Bouillet B, Rouland A, et al. European Association for the Study of the Liver (EASL), European Association for the Study of Diabetes (EASD) and European Association for the Study of Obesity (EASO) clinical practice recommendations for the management of non-alcoholic fatty liver disease: evaluation of their application in people with Type 2 diabetes. *Diabet Med* 2018;35(03):368–375
 - 55 Anstee QM, Daly AK, Day CP. Genetics of alcoholic and nonalcoholic fatty liver disease. *Semin Liver Dis* 2011;31(02):128–146
 - 56 Janssen AWF, Houben T, Katiraei S, et al. Modulation of the gut microbiota impacts nonalcoholic fatty liver disease: a potential role for bile acids. *J Lipid Res* 2017;58(07):1399–1416
 - 57 Lin D, Sun Q, Liu Z, et al. Gut microbiota and bile acids partially mediate the improvement of fibroblast growth factor 21 on methionine-choline-deficient diet-induced non-alcoholic fatty liver disease mice. *Free Radic Biol Med* 2023;195:199–218
 - 58 Du F, Huang R, Lin D, et al. Resveratrol improves liver steatosis and insulin resistance in non-alcoholic fatty liver disease in association with the gut microbiota. *Front Microbiol* 2021;12:611323
 - 59 Song L, Li Y, Qu D, et al. The regulatory effects of phytosterol esters (PSEs) on gut flora and faecal metabolites in rats with NAFLD. *Food Funct* 2020;11(01):977–991
 - 60 Shu Y, Huang Y, Dong W, et al. The polysaccharides from *Auricularia auricula* alleviate non-alcoholic fatty liver disease via modulating gut microbiota and bile acids metabolism. *Int J Biol Macromol* 2023;246:125662
 - 61 Tang Y, Chen B, Huang X, et al. Fu brick tea alleviates high fat induced non-alcoholic fatty liver disease by remodeling the gut microbiota and liver metabolism. *Front Nutr* 2022;9:1062323
 - 62 Han R, Qiu H, Zhong J, et al. Si Miao Formula attenuates non-alcoholic fatty liver disease by modulating hepatic lipid metabolism and gut microbiota. *Phytomedicine* 2021;85:153544
 - 63 Zhao Z, Wang J, Ren W, et al. Effect of Jiangnan-Jiangzhi pill on gut microbiota and chronic inflammatory response in rats with non-alcoholic fatty liver. *Chem Biodivers* 2022;19(05):e202100987
 - 64 Zheng H, Dai H, Yan X, Xiang Q. Study on intestinal flora and asthma: knowledge graph analysis based on CiteSpace (2001–2021). *J Asthma Allergy* 2023;16:355–364
 - 65 Demirci M, Tokman HB, Uysal HK, et al. Reduced *Akkermansia muciniphila* and *Faecalibacterium prausnitzii* levels in the gut microbiota of children with allergic asthma. *Allergol Immunopathol (Madr)* 2019;47(04):365–371
 - 66 Skalski JH, Limon JJ, Sharma P, et al. Expansion of commensal fungus *Wallersteina mellicola* in the gastrointestinal mycobiota enhances the severity of allergic airway disease in mice. *PLoS Pathog* 2018;14(09):e1007260
 - 67 Spacova I, Petrova MI, Fremau A, et al. Intranasal administration of probiotic *Lactobacillus rhamnosus* GG prevents birch pollen-induced allergic asthma in a murine model. *Allergy* 2019;74(01):100–110
 - 68 Raftis EJ, Delday MI, Cowie P, et al. *Bifidobacterium breve* MRx0004 protects against airway inflammation in a severe asthma model by suppressing both neutrophil and eosinophil lung infiltration. *Sci Rep* 2018;8(01):12024
 - 69 Huang C-F, Chie W-C, Wang I-J. Efficacy of *Lactobacillus* administration in school-age children with asthma: a randomized, placebo-controlled trial. *Nutrients* 2018;10(11):1678
 - 70 Kepert I, Fonseca J, Müller C, et al. D-tryptophan from probiotic bacteria influences the gut microbiome and allergic airway disease. *J Allergy Clin Immunol* 2017;139(05):1525–1535
 - 71 Chen SM, Wu XY, Peng GY, et al. Based on 16S rRNA sequencing to study the effect of Shaoyao Gancan Decoction on the intestinal flora of bronchial asthma mice. *J Beijing Univ Tradit Chin Med* 2022;45(05):492–499
 - 72 Zhang BB, Zeng MN, Zhang QQ, et al. Effects of Tingli Dazao Xiefei Decoction on the immune inflammation and intestinal flora in asthmatic rats. *Yao Xue Xue Bao* 2022;57(08):2364–2377
 - 73 Jia W, Xu C, Zhao T, et al. Integrated network pharmacology and gut microbiota analysis to explore the mechanism of Sijunzi decoction involved in alleviating airway inflammation in a mouse model of asthma. *Evid Based Complement Alternat Med* 2023;2023:1130893
 - 74 Kong YH, Shi Q, Han N, et al. Structural modulation of gut microbiota in rats with allergic bronchial asthma treated with recuperating lung decoction. *Biomed Environ Sci* 2016;29(08):574–583
 - 75 He Q, Liu C, Shen L, et al. Theory of the exterior-interior relationship between the lungs and the large intestine to explore the mechanism of *Eriobotrya japonica* leaf water extract in the treatment of cough variant asthma. *J Ethnopharmacol* 2021;281:114482
 - 76 de Oliveira GLV, Leite AZ, Higuchi BS, Gonzaga MI, Mariano VS. Intestinal dysbiosis and probiotic applications in autoimmune diseases. *Immunology* 2017;152(01):1–12

- 77 Wu X, He B, Liu J, et al. Molecular insight into gut microbiota and rheumatoid arthritis. *Int J Mol Sci* 2016;17(03):431
- 78 Horta-Baas G, Romero-Figueroa MDS, Montiel-Jarquín AJ, Pizano-Zárate ML, García-Mena J, Ramírez-Durán N. Intestinal dysbiosis and rheumatoid arthritis: a link between gut microbiota and the pathogenesis of rheumatoid arthritis. *J Immunol Res* 2017;2017:4835189
- 79 Maeda Y, Kumanogoh A, Takeda K. [Altered composition of gut microbiota in rheumatoid arthritis patients]. *Nihon Rinsho Meneki Gakkai Kaishi* 2016;39(01):59–63
- 80 Sato K, Takahashi N, Kato T, et al. Aggravation of collagen-induced arthritis by orally administered *Porphyromonas gingivalis* through modulation of the gut microbiota and gut immune system. *Sci Rep* 2017;7(01):6955
- 81 Ben-Amram H, Bashi T, Werbner N, et al. Tuftsin-phosphorylcholine maintains normal gut microbiota in collagen induced arthritic mice. *Front Microbiol* 2017;8:1222
- 82 Li Y, Liu C, Luo J, et al. Ershiwuwei Lvxue Pill alleviates rheumatoid arthritis by different pathways and produces changes in the gut microbiota. *Phytomedicine* 2022;107:154462
- 83 Xiao M, Fu X, Ni Y, et al. Protective effects of *Paederia scandens* extract on rheumatoid arthritis mouse model by modulating gut microbiota. *J Ethnopharmacol* 2018;226:97–104
- 84 Jiang ZM, Zeng SL, Huang TQ, et al. Sinomenine ameliorates rheumatoid arthritis by modulating tryptophan metabolism and activating aryl hydrocarbon receptor via gut microbiota regulation. *Sci Bull (Beijing)* 2023;68(14):1540–1555
- 85 Salari N, Hosseini-Far A, Jalali R, et al. Prevalence of stress, anxiety, depression among the general population during the COVID-19 pandemic: a systematic review and meta-analysis. *Global Health* 2020;16(01):57
- 86 Radjabzadeh D, Bosch JA, Uitterlinden AG, et al. Gut microbiome-wide association study of depressive symptoms. *Nat Commun* 2022;13(01):7128
- 87 Strandwitz P, Kim KH, Terekhova D, et al. GABA-modulating bacteria of the human gut microbiota. *Nat Microbiol* 2019;4(03):396–403
- 88 Kelly JR, Borre Y, O' Brien C, et al. Transferring the blues: Depression-associated gut microbiota induces neurobehavioural changes in the rat. *J Psychiatr Res* 2016;82:109–118
- 89 Rudzki L, Ostrowska L, Pawlak D, et al. Probiotic *Lactobacillus Plantarum* 299v decreases kynurenine concentration and improves cognitive functions in patients with major depression: a double-blind, randomized, placebo controlled study. *Psychoneuroendocrinology* 2019;100:213–222
- 90 Li Y, Peng Y, Ma P, et al. Antidepressant-like effects of *Cistanche tubulosa* extract on chronic unpredictable stress rats through restoration of gut microbiota homeostasis. *Front Pharmacol* 2018;9:967
- 91 Hao W, Wu J, Yuan N, et al. Xiaoyaosan improves antibiotic-induced depressive-like and anxiety-like behavior in mice through modulating the gut microbiota and regulating the NLRP3 inflammasome in the colon. *Front Pharmacol* 2021;12:619103
- 92 Kortenien J, Karlsson L, Aatsinki A. Systematic review: autism spectrum disorder and the gut microbiota. *Acta Psychiatr Scand* 2023;148(03):242–254
- 93 Strati F, Cavalieri D, Albanese D, et al. New evidences on the altered gut microbiota in autism spectrum disorders. *Microbiome* 2017;5(01):24
- 94 Tabouy L, Getselter D, Ziv O, et al. Dysbiosis of microbiome and probiotic treatment in a genetic model of autism spectrum disorders. *Brain Behav Immun* 2018;73:310–319
- 95 Grimaldi R, Gibson GR, Vulevic J, et al. A prebiotic intervention study in children with autism spectrum disorders (ASDs). *Microbiome* 2018;6(01):133
- 96 Cristiano C, Pirozzi C, Coretti L, et al. Palmitoylethanolamide counteracts autistic-like behaviours in BTBR T+tf/J mice: contribution of central and peripheral mechanisms. *Brain Behav Immun* 2018;74:166–175
- 97 Kang DW, Adams JB, Gregory AC, et al. Microbiota transfer therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. *Microbiome* 2017;5(01):10
- 98 Jiang C, Li G, Huang P, Liu Z, Zhao B. The gut microbiota and Alzheimer's disease. *J Alzheimers Dis* 2017;58(01):1–15
- 99 Zhang L, Wang Y, Xiayu X, et al. Altered gut microbiota in a mouse model of Alzheimer's disease. *J Alzheimers Dis* 2017;60(04):1241–1257
- 100 Bonfili L, Cecarini V, Berardi S, et al. Microbiota modulation counteracts Alzheimer's disease progression influencing neuronal proteolysis and gut hormones plasma levels. *Sci Rep* 2017;7(01):2426
- 101 Leblhuber F, Egger M, Schuetz B, Fuchs D. Commentary: effect of probiotic supplementation on cognitive function and metabolic status in Alzheimer's disease: a randomized, double-blind and controlled trial. *Front Aging Neurosci* 2018;10:54
- 102 Akbari E, Asemi Z, Daneshvar Kakhaki R, et al. Effect of probiotic supplementation on cognitive function and metabolic status in Alzheimer's disease: a randomized, double-blind and controlled trial. *Front Aging Neurosci* 2016;8:256
- 103 Bonfili L, Cecarini V, Cuccioloni M, et al. SLAB51 probiotic formulation activates SIRT1 pathway promoting antioxidant and neuroprotective effects in an AD mouse model. *Mol Neurobiol* 2018;55(10):7987–8000
- 104 Nimgampalle M, Kuna Y. Anti-Alzheimer properties of probiotic, *Lactobacillus plantarum* MTCC 1325 in Alzheimer's disease induced albino rats. *J Clin Diagn Res* 2017;11(08):KC01–KC05
- 105 Song M, Chan AT. Environmental factors, gut microbiota, and colorectal cancer prevention. *Clin Gastroenterol Hepatol* 2019;17(02):275–289
- 106 Bultman SJ. Interplay between diet, gut microbiota, epigenetic events, and colorectal cancer. *Mol Nutr Food Res* 2017;61(01):10
- 107 Wang J, Lu R, Fu X, et al. Novel regulatory roles of Wnt1 in infection-associated colorectal cancer. *Neoplasia* 2018;20(05):499–509
- 108 Polakowski CB, Kato M, Preti VB, Schieferdecker MEM, Ligocki Campos AC. Impact of the preoperative use of synbiotics in colorectal cancer patients: A prospective, randomized, double-blind, placebo-controlled study. *Nutrition* 2019;58:40–46
- 109 Borzi AM, Biondi A, Basile F, Luca S, Vicari ESD, Vacante M. Olive oil effects on colorectal cancer. *Nutrients* 2018;11(01):32
- 110 Luo JM, Zhang C, Liu R, et al. *Ganoderma lucidum* polysaccharide alleviating colorectal cancer by alteration of special gut bacteria and regulation of gene expression of colonic epithelial cells. *J Funct Foods* 2018;47:127–135
- 111 Tapper EB, Parikh ND. Mortality due to cirrhosis and liver cancer in the United States, 1999–2016: observational study. *BMJ* 2018;362:k2817
- 112 Liu S, Yang X. Intestinal flora plays a role in the progression of hepatitis-cirrhosis-liver cancer. *Front Cell Infect Microbiol* 2023;13:1140126
- 113 Yang X, Lu D, Zhuo J, Lin Z, Yang M, Xu X. The gut-liver axis in immune remodeling: new insight into liver diseases. *Int J Biol Sci* 2020;16(13):2357–2366
- 114 Hartmann N, Kronenberg M. Cancer immunity thwarted by the microbiome. *Science* 2018;360(6391):858–859
- 115 Li J, Sung CYJ, Lee N, et al. Probiotics modulated gut microbiota suppresses hepatocellular carcinoma growth in mice. *Proc Natl Acad Sci U S A* 2016;113(09):E1306–E1315
- 116 Zhen H, Qian X, Fu X, Chen Z, Zhang A, Shi L. Regulation of Shaoyao Ruangan mixture on intestinal flora in mice with primary liver cancer. *Integr Cancer Ther* 2019;18:1534735419843178
- 117 Li Z, Zhao Y, Cheng J, et al. Integrated plasma metabolomics and gut microbiota analysis: the intervention effect of Jiawei Xiaoyao San on liver depression and spleen deficiency liver cancer rats. *Front Pharmacol* 2022;13:906256

- 118 Zhao Y, Liu Y, Li S, et al. Role of lung and gut microbiota on lung cancer pathogenesis. *J Cancer Res Clin Oncol* 2021;147(08): 2177–2186
- 119 Zhang WQ, Zhao SK, Luo JW, et al. Alterations of fecal bacterial communities in patients with lung cancer. *Am J Transl Res* 2018; 10(10):3171–3185
- 120 Zhuang H, Cheng L, Wang Y, et al. Dysbiosis of the gut microbiome in lung cancer. *Front Cell Infect Microbiol* 2019;9:112
- 121 Gui QF, Lu HF, Zhang CX, Xu ZR, Yang YH. Well-balanced commensal microbiota contributes to anti-cancer response in a lung cancer mouse model. *Genet Mol Res* 2015;14(02): 5642–5651
- 122 Jiang RY, Wang T, Lan QY, et al. BuFeiXiaoJiYin ameliorates the NLRP3 inflammation response and gut microbiota in mice with lung cancer companied with Qi-yin deficiency. *Cancer Cell Int* 2022;22(01):121
- 123 Cao B, Wang S, Li R, et al. Xihuang Pill enhances anticancer effect of anlotinib by regulating gut microbiota composition and tumor angiogenesis pathway. *Biomed Pharmacother* 2022; 151:113081