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Challenges in Nutrition

Role of the gut microbiome in chronic diseases: a narrative review

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European Journal of Clinical Nutrition (2022) 76:489–501; <https://doi.org/10.1038/s41430-021-00991-6>**WHAT IS CURRENTLY KNOWN ON THE TOPIC**

The gut microbiome, i.e., the community of bacteria and other microorganisms living in the human gut, has been implicated both directly and indirectly (mediating the effects of diet) on human health [1, 2]. The associations between gut microbiome composition and disease status have been widely reported, while recent studies have demonstrated a role for the gut microbiome in influencing remote organs, mucosal, and immune function [3, 4]. Considerable effort is currently focused on understanding the natural history of microbiome development in humans in the context of health outcomes, in parallel with improving our knowledge of microbiome–host molecular interactions. These efforts ultimately aim to develop effective approaches to rehabilitate perturbed human microbial ecosystems as a means to restore health and prevent disease. This review details the role of the gut microbiome in chronic diseases (Fig. 1) and ways it can be modulated for the management or prevention of chronic conditions.

Differences in gut microbiome composition and function have been associated with a variety of chronic diseases ranging from gastrointestinal inflammatory and metabolic conditions to neurological, cardiovascular, and respiratory illnesses.

The aim of this narrative review is to describe the associations between gut microbiome composition and various types of chronic diseases and to discuss the links to habitual diet and dietary components (Table 1).

Gut microbiome and autoimmune disease

The pathogenesis of autoimmune diseases (AIDs) is not only attributed to genetic susceptibilities but also environmental factors, among which, a disturbed gut microbiota has attracted increasing attention. Compositional and functional changes of gut microbiota have been reported in various autoimmune diseases, and increasing evidence suggests that disturbed gut microbiota contributes to their immunopathogenesis.

Rheumatoid arthritis (RA). Rheumatoid arthritis (RA) is a systemic autoimmune inflammatory condition that manifests in joint damage. It was recently demonstrated that different environmental factors are involved in the development of both intestinal/

oral dysbiosis and arthritis onset and outcome, among which the most relevant are diet, smoking, and infections [5, 6]. The observation that germ-free mice are protected from development of experimental arthritis [7] suggests a possible role for the microbiome in the pathogenesis of this disease. The composition of the gut microbiota in RA patients free of therapy is severely altered compared to healthy controls. Chen et al. reported that compared with healthy controls, patients with RA show decreased gut microbial diversity, which correlates with autoantibody levels and disease duration [8]. In addition, at the compositional level, patients with RA show an increased abundance of *Prevotella* species, including *Prevotella copri* [8, 9], and recent preclinical phase studies on RA patients in European countries were shown to harbor a high abundance of this species in the intestine, suggesting that dysbiosis precedes the development of arthritis [10]. In contrast, *Faecalibacterium*, which is generally recognized as a beneficial microbe, is decreased in RA patients. Furthermore, the relative abundance of *Collinsella* was found to be increased in RA patients [11]. Interestingly, inoculation of *Collinsella* into collagen-induced arthritis (CIA)-susceptible mice induces severe arthritis. In vitro experiments showed that *Collinsella Aerofaciens* increases gut permeability and induces IL-17A expression, a key cytokine involved in the pathogenesis of RA, suggesting that *Collinsella* is a candidate arthritogenic bacterium in the human intestine [11]. In summary, *Prevotella copri* [12] and *Collinsella* are the dominant gut microbiota in patients with early RA and may be involved in its pathogenesis.

Recent links have been made between dietary intake of short-chain fatty acids (SCFAs) and autoimmune arthritis in mice, wherein SCFAs play an important role in the suppression of inflammation in RA [13, 14]. Mice deficient for SCFA receptors showed exacerbated inflammation in models of RA [14]. Butyrate, one of the most abundant SCFAs, acts as an endogenous histone deacetylase (HDAC) inhibitor and has been shown to decrease inflammation in animal models of RA and other inflammatory diseases [15]. A recent study has revealed a role for intestinal barrier function, and specifically for zonulin, a peptide that controls epithelial tight junction permeability, in regulating the onset of joint disease in mice with collagen-induced arthritis (CIA) and potentially also in patients with RA [16]. Increased levels of

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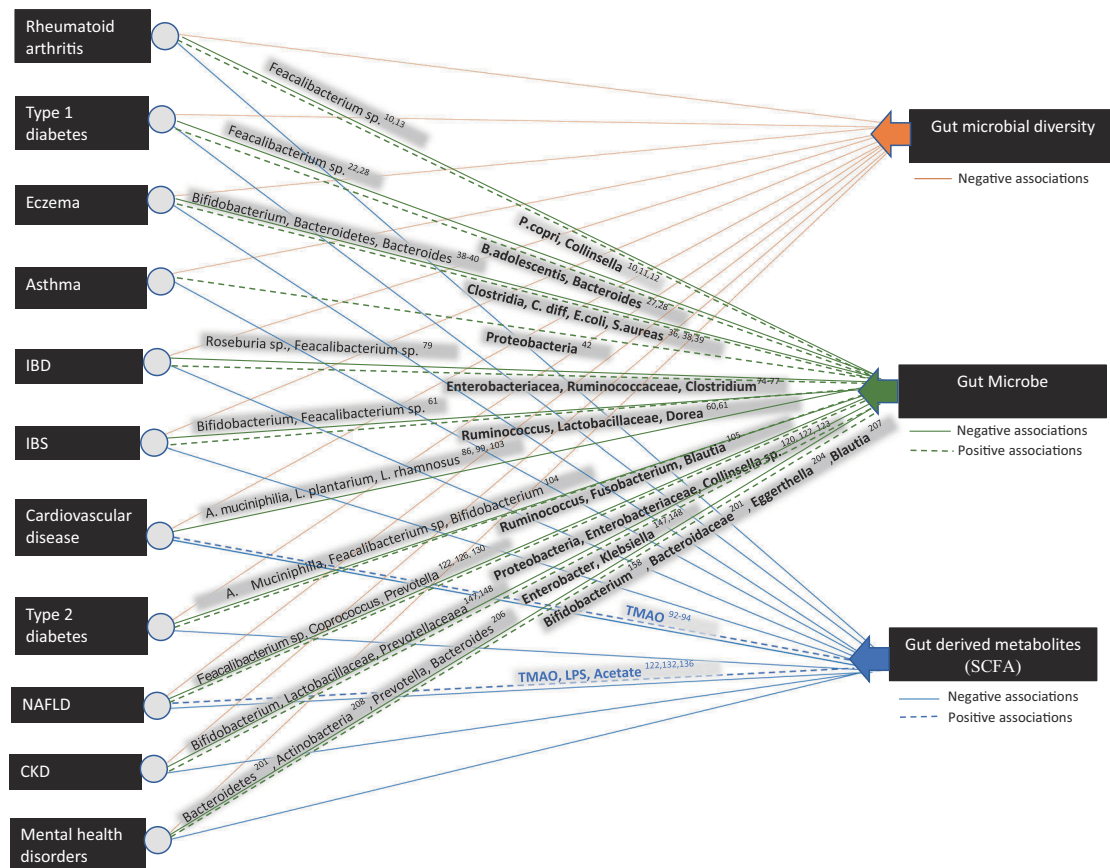


Fig. 1 Schematic representation of the association of the composition of the gut microbiome and gut-derived metabolites with chronic diseases. The solid lines represent negative associations and the dashed lines represent positive associations of the disease phenotype with gut microbes and metabolites.

Table 1. Summary of key findings outlining the role of the gut microbiome in chronic disease.

Key messages

Gut microbiome composition is significantly different in healthy individuals compared to affected individuals with a broad range of chronic diseases. Lower microbiome diversity appears to be a common theme across many of the diseases

Auto-immune diseases, in common with cardiometabolic diseases and irritable bowel syndrome, show low abundances of SCFA producing bacteria such as *Bifidobacterium sp.*, *Faecalibacterium sp.*, *Roseburia sp.*, or *Coprococcus eutactus*

High abundances of pathogenic bacteria (such as *E. coli*, *S. aureus*, and *C. difficile*) are common in some of these diseases

SCFAs but also other microbial metabolites are involved in the health effects of gut microbiome composition and microbial metabolites can be better predictors of health outcomes than microbiome diversity

Gut microbiome composition is modifiable by various therapeutic strategies. Dietary interventions can result in robust changes in both gut microbiome composition and function and in the corresponding health effects

zonulin have been associated with leaky intestinal barrier, dysbiosis, and inflammation. Restoration of the intestinal barrier in the period before clinical arthritis, either by dietary supplementation with the SCFA butyrate or pharmacological agents such as a zonulin antagonist may help delay disease onset and reduce the severity of RA.

Type 1 diabetes (T1D). In humans, intestinal microbiota alterations, including loss of bacterial diversity, preceded the onset of metabolic symptoms associated with T1D [17]. Previous studies have linked several facets of gut health with the onset of T1D in humans and animal models [18–20]. In animal models, antibiotic-induced dysbiosis, altered microbial lipid metabolism, and suppressed enteric Th17 and T-reg cell populations have led to increased incidence of T1DM-like disease in mice [21]. Various human-based studies have also reported altered intestinal

microbiota in connection to T1D from several ethnic groups [1720, 22–24]. The common findings from these studies include increased numbers of Bacteroides species, and deficiency of bacteria that produce SCFAs [25, 26] in cases of T1D. Specifically, the butyrate producer *Faecalibacterium prausnitzii* has been found to be decreased in abundance in children with diabetes-related autoantibodies [26].

In addition, increased intestinal permeability [22] and decreased microbial diversity [17] before T1D diagnosis have been reported. A multicenter case-control study of 783 children, showed that the microbiomes of healthy children contained more genes that were related to the fermentation and the biosynthesis of SCFAs, but these were not consistently associated with the abundance of particular taxa across geographically diverse clinical centers, suggesting that microbial function rather than composition was associated more with T1D [27].

The protective effects of SCFAs in T1D have been elucidated in animal studies that have looked at nonobese diabetic (NOD) mouse models [28]. For example, NOD mice fed specialized diets resulting in high bacterial release of acetate and butyrate were almost completely protected from T1D [28] mainly via the immune-modulating effects of SCFAs. In animal models of autoimmune diabetes, increased gut permeability precedes the development of diabetes, and environmental factors that modulate the permeability thereby modulate the incidence of the disease. Gut permeability appears to be an important factor in the relationship between the intestinal microbiota and the development of T1D. Both gut permeability and inflammation have been linked to the development of T1D in humans [26, 29].

Atopic eczema. Atopic eczema, a chronic inflammatory skin disorder, is most prevalent in early childhood. The pathogenesis of eczema has been attributed to skin-barrier dysfunctions, immune dysregulation as well as environmental–host–microbial interactions [30]. Environmental factors and modern lifestyle trends have been shown to indirectly contribute to pathogenesis of the disease through modulation of the gut microbiome [31].

Previous studies have found that the gut microbiome in early life is associated with age of onset, severity, and remission of atopic eczema [32, 33]. However, the association between gut microbiome diversity and atopic eczema development remains contradictory with few studies reporting an inverse relationship between gut diversity and the severity of atopic eczema [34, 35]. The development of atopic eczema may instead be driven by the interactions between specific gut microbiome signatures, the immune system, and the host. Specifically, in patients with atopic eczema, the proportion of Clostridia, *Clostridium difficile*, *Escherichia coli*, and *Staphylococcus aureus* in the gut microbiome is higher than in healthy controls, whereas that of *Bifidobacteria*, *Bacteroidetes*, and *Bacteroides* is decreased [34, 36–38]. The abundance of Clostridia and *Escherichia coli* in the intestine may be associated with atopic eczema via eosinophilic inflammation [36]. Butyrate-producing bacteria, such as *Coprococcus eutactus*, are increased in infants with milder atopic eczema or healthy infants than in those with severe atopic eczema [34]. Furthermore, fecal samples from patients with atopic eczema showed decreased levels of butyrate and propionate, which have anti-inflammatory effects. This is likely a consequence of a dysbiosis in the SCFA producer *F. prausnitzii* that reduces the number of high butyrate and propionate strains [38].

It is evident that the compositional and proportional differences in the gut microbiome are associated with the development of AID via an immunomodulatory effect of the gut microbiome. The gut microbiome may contribute to the development, persistence, and severity of AID via immunologic, metabolic, and neuroendocrine pathways. It is however still unclear whether compositional changes in the gut microbiome precede the development of atopic eczema, and thereby shift the immune system and disrupt the gut epithelial barrier, making it amenable to the development of atopic eczema.

Atopic asthma. The rapid increase in asthma prevalence in industrialized nations over the past several decades cannot be explained by genetic risk factors alone and is thought to be related to altered environmental exposures associated with Western lifestyles. Early life is the most important period during which microbiota dysbiosis in the gut may lead to the development of many respiratory diseases, as the gut microbiota has a significant influence on immune-cell maturation and resistance to pathogens [39]. A number of validated epidemiological observations have implicated early-life environmental exposures in increased risk for childhood asthma. Many of these exposures are known to shape the nascent gut microbiome, including cesarean birth [40], antibiotic use [41], formula feeding,

and other environmental factors including airborne toxins [42]. Further evidence for an intricate relationship between environmental exposure, the gut microbiome, and allergic airway disease comes from an expanding body of work, particularly those utilizing experimental animal models. For example, treating neonatal mice with antibiotics was shown to diminish gut microbial diversity, alter metabolite profiles, exacerbate immune cell response, and increase susceptibility to allergic lung inflammation [43, 44]. Furthermore, supplementation with SCFAs ameliorated airway inflammation in these mice, with the mechanism attributed to decreased activity of immune-modulating markers such as T cells, IL-4-producing CD4+ T cells, and reduced levels of circulating IgE [44].

Observational studies in humans have identified *Proteobacteria* to be the most dominant phylum overrepresented in patients with asthma compared with nonasthmatic volunteers across several studies [39]. The *Proteobacteria* phylum is represented by potentially pathogenic bacteria, including those that belong to the genera *Haemophilus*, *Moraxella*, and *Neisseria* [39].

Asthma pathogenesis and severity are linked with pro-inflammatory mechanisms. The effects of the gut microbiota on asthma are at least partially mediated by bacterial metabolites, which may influence immune responses in distal parts of the body. The most known metabolites with demonstrated protective properties in human airway inflammation are SCFAs. Children with high amounts of butyrate and propionate in feces at 1 year of age have significantly less atopic sensitization and are less likely to have asthma between 3 and 6 years [45]. In addition, soluble fiber may ameliorate the effects by exerting anti-inflammatory action via SCFAs binding to associated G-protein-coupled receptors (GPCRs) [46, 47].

Of recent interest are studies showing that gut bacteria in humans are able to produce other metabolites with pro- and anti-inflammatory potential, such as biogenic amines (including histamine) [48] and oxylipins such as 12,13-diHOME [49]. The number of histamine-secreting bacteria is significantly higher in fecal samples of asthma patients compared with nonasthmatic volunteers [50]. Furthermore, the number of histamine-secreting bacteria correlates with disease severity.

Although the mechanisms mediating communication between the gut and lungs are still unclear, it has been suggested that epithelial cells, other structural cells, and immune cells absorb signals from the gut endothelium to form a local cytokine microenvironment, which leads to changes in immune responses at distal sites [51]. Specifically, SCFAs derived from gut bacteria have inhibitory effects on proinflammatory responses in the lungs.

Gut microbiome–gut inflammation/bowel disorders

Irritable bowel syndrome (IBS). IBS is generally characterized by abdominal pain, discomfort, and altered bowel habits. Although the etiology is multifactorial, recent understanding of the pathophysiology of IBS has revealed that variations in the normal gut microbiota may have a role to play in the low-grade intestinal inflammation associated with the syndrome [52]. Microbial dysbiosis in the gut is thought to be involved in IBS pathogenesis [53] and a recent study revealed a clear separation between the gut microbiota of patients with IBS and that of the controls. IBS was characterized by an increase in *Firmicutes* and, more specifically, in the numbers of *Ruminococcus*, *Clostridium*, and *Dorea*, in addition to a marked reduction of beneficial microbes such as *Bifidobacterium* and *Faecalibacterium spp.* [54]. Furthermore, systematic reviews have demonstrated the potentially harmful microbiota in patients with IBS, including phylum *Proteobacteria*, family *Enterobacteriaceae* (phylum *Proteobacteria*), family *Lactobacillaceae*, and genus *Bacteroides* (phylum *Bacteroidetes*). The *Enterobacteriaceae* family contains several pathogenic bacteria; for instance, *Escherichia*, *Shigella*, *Campylobacter*, and *Salmonella* [55]. These could either suggest previous intestinal

infection in such patients or a change in the intestinal environment. By-products from these potentially harmful bacteria have been associated with some of the classical symptoms of IBS, including abdominal pain, bloating, and diarrhea [55].

The most consistent finding of a potentially “protective” bacterial group in IBS patients was found in the group of uncultured *Clostridiales*. Although the association is not causal and the mechanism of a protective effect in IBS symptoms is unclear. The genus *Faecalibacterium*, especially *Faecalibacterium prausnitzii*, which belongs to the similar order as the uncultured *Clostridia*, has been associated with maintaining gut mucosal health. This bacterium was considered as the main butyrate-producing and anti-inflammatory organism [56] and reduced IBS symptoms via mediation of IL-17 expression in a rat model [57, 58], as well as maintained gut-barrier integrity [59]. Furthermore, the genus *Bifidobacterium* was decreased significantly in IBS patients regardless of IBS subtype. Therefore, it was another promising potential genus in ameliorating IBS symptoms. A systematic review of probiotics in IBS has highlighted that *Bifidobacterium*-containing interventions reduce IBS symptoms, which are not seen in products that contain *Lactobacillus* alone [60].

Management of IBS symptoms can be achieved by the restriction of fermentable oligosaccharides, disaccharides, monosaccharides, and polyols (FODMAP). Clinical studies have now shown the clinical efficacy of the low FODMAP diet in reducing IBS symptoms [61]. One consequence of this dietary intervention is its impact on gut microbiome composition as FODMAPs can modulate microbial composition and microbial metabolite production [62] and not all IBS subjects respond and there may be challenges with implementing a low FODMAP diet. Given the role of the microbiome in metabolizing poorly absorbed carbohydrates that depend on a person’s microbiome composition, that there has been increasing attention on the potential role of the gut microbiome in predicting low FODMAP diet efficacy [62] and recent data suggest that there are potential baseline differences in microbiome activity and composition, which can distinguish between low FODMAP diet responders and nonresponders [63].

Inflammatory bowel disease (IBD). Long-lasting inflammation and ulceration of the colon are predominantly the main characteristics of IBD, which are features of Crohn’s disease (CD) and ulcerative colitis (UC). IBD, encompassing both ulcerative colitis and Crohn’s disease, is characterized by chronic and relapsing inflammation of the GI tract. The onset of both conditions is, in general, not thought to be due to a single causal organism but by a general microbial dysbiosis in the gut [64]. A role for gut microbes in the manifestation of IBD has been indicated by a number of studies and the gut microbiota are thought to be essential components in the development of mucosal lesions [65]. The alterations in the composition and functionality of the gut microbiota in IBD compared with non-IBD controls have been shown previously. In general, microbial dysbiosis in IBD is characterized by a decrease in diversity and stability of the microbiota [66–69]. Specifically, a decrease in Firmicutes and an increase in Proteobacteria taxa is the most consistent outcome from IBD microbiome studies. Furthermore, a common signature of microbial dysbiosis among IBD patients, especially in (active) CD, is the decreased abundance of Firmicutes bacteria belonging to the families *Ruminococcaceae* and *Lachnospiraceae* as opposed to healthy control samples [70–73]. Both families are important functional members of the human gut microbiota since most butyrate-producing bacteria from the human gut belong to them. Therefore, depletion of these bacterial families in IBD can be linked to the observed disturbance on a functional level, including a lower butyrate-producing capacity of the IBD microbiota [74]. In addition, a metagenomic and proteomics study in ileal CD microbiota demonstrated an underrepresentation of genes for SCFA production and a decrease in metagenomic reads and proteins of important butyrate

producers *Faecalibacterium prausnitzii* and *Roseburia sp.* [75].

Butyrate has therapeutic potential in IBD because it serves as the main energy source for colonocytes, enhances epithelial barrier integrity, and inhibits inflammation. Recent observational and interventional studies have explored an alternative approach of probiotics, which involves the consumption of butyrate-producing bacteria to increase in situ butyrate production [76–78]. This may suggest that targeting microbial dysbiosis by supplementing butyrate-producing bacteria could restore gut homeostasis and health in IBD.

Gut microbiome composition and cardiometabolic diseases

Cardiovascular disease. The alterations in gut microbiota composition and the metabolic potential of gut microbiota have been identified as a contributing factor in Cardiovascular Disease (CVD) development [79]. Recently, mechanistic links between the gut microbiota and the severity of myocardial infarction have been reported in rats [80, 81]. Hypertension is the most prevalent modifiable risk factor for CVD. However, results from human studies remain scarce and conflicting. In the TwinsUK cohort [82], self-reported hypertension was not related to 68 various microbiota markers. Furthermore, in the CARDIA study of 529 individuals an increase in alpha diversity resulted in a modest decrease in objectively measured systolic blood pressure (BP) [83]. More recently, the association between the gut microbiome and hypertension was studied on the well-phenotyped population of 6953 individuals as part of the FINRISK study [84] using standardized BP measurements. Although the associations between overall gut taxonomic composition and BP were weak, individuals with hypertension demonstrated changes in several microbiota genera, with most of these genera belonging to the Firmicutes phylum. Interestingly, most of the negative associations with BP belonged to the *Lactobacillus* species, specifically the greater abundance of *Lactobacillus paracasei*, a known probiotic that was associated with lower mean arterial pressure and lower dietary sodium intake which has also been reported previously by Wilck et al. [85].

Metabolism of certain dietary components such as choline and carnitine, which comprise a large component of a Western diet, has been shown to increase risk of cardiovascular disease mainly via the metabolism of these compounds to produce trimethylamine oxide (TMAO) [86, 87]. Gut-derived metabolites such as SCFAs have been recently shown to modulate blood pressure [88]. The suggested mechanism of SCFAs to modulate blood pressure is via the host G-protein coupled receptor (GPR) pathways that impact renin secretion and blood pressure regulation [88]. A series of studies using GPR41 knockout mice further supports involvement of these receptors in blood pressure control. This suggests that the gut microbiota are potentially intertwined functionally to control blood pressure, and their dysfunctions could be associated with hypertension. A recent study found that a Mediterranean diet which typically encompasses a high fiber diet followed by fasting was shown to reduce systolic blood pressure, need for anti-hypertensive medications, body-mass index at three months post intervention compared to following a Mediterranean diet alone [89]. These data highlight fasting followed by a shift to a health-promoting diet as a promising non-pharmacological intervention for patients with hypertension and other cardiometabolic diseases.

In rodent model studies, the administration of probiotics such as *Lactobacillus plantarum* and *Lactobacillus rhamnosus* was associated with improved ventricular function and attenuated heart failure after myocardial infarction [80, 90]. Furthermore, a meta-analysis demonstrated a significant decrease in blood pressure in patients treated with probiotics [91]. Lastly, supplementation of atherosclerosis-prone mice with *A. muciniphila*, a mucus colonizer protected against atherosclerosis development induced by feeding a Western diet [92]. These observations may

suggest that probiotics use, in combination with standard medication, could offer additional benefits in the prevention and management of cardiovascular events.

Type 2 diabetes. Adults with T2DM have an altered gut microbiota composition compared to healthy controls. However, it is unclear whether these changes represent a cause or an effect and required further investigation. Among the commonly reported findings, the genera of *Bifidobacterium*, *Bacteroides*, *Faecalibacterium*, *Akkermansia*, and *Roseburia* were negatively associated with T2D, while the genera of *Ruminococcus*, *Fusobacterium*, and *Blautia* were positively associated with T2D [93, 94]. A large metagenome-wide association study found a moderate degree of gut dysbiosis in patients with T2DM [95]. Of the identifiable bacterial species, the control samples were enriched in various butyrate-producing bacteria and increased abundance of *Lactobacillus* spp., while patients with T2DM were characterized by an increase in certain opportunistic pathogens, such as a number of *Clostridium* spp. [95]. Overall, T2DM was associated with a reduced abundance of butyrate-producing bacteria and SCFAs, in particular butyrate which has been linked with insulin sensitivity [9, 96, 97]. The link between SCFAs and insulin sensitivity lies in the ability of SCFAs to trigger the secretion of GLP-1 by intestinal L-cells via specific G protein receptors (GPR41, GPR43) which has a substantial impact on pancreatic function and insulin release, as well as central effects regulating appetite [98, 99].

In addition to SCFAs, many other metabolites have been implicated in the role of gut microbiome composition and risk to T2DM. We have in fact reported reproducible associations between serum metabolites of microbial origin and gut microbiome alpha diversity in 1018 individuals from the Twins UK cohort [100]. The circulating levels of these metabolites were combined into a microbiome-metabolite score using a linear combination. Importantly the association of the microbiome metabolite score with cardiometabolic traits was stronger than the association between gut microbiome diversity and the same clinical traits. Specifically, the microbiome metabolite score was associated with prevalence and incidence of T2DM in the discovery cohort and this result was replicated in a multi-ethnic independent US cohort ($n = 1522$) showing the relevance of microbiome-derived metabolites in predicting risk and supporting their role as the mechanistic link between microbiome composition and health [100].

Non-alcoholic fatty liver disease (NAFLD). Non-alcoholic fatty liver disease (NAFLD) and the more advanced stage non-alcoholic steatohepatitis (NASH) are common comorbidities of obesity and T2DM with an increasing burden for society [101]. There is an increasing body of evidence linking the gut-liver axis to the development of NAFLD. Gut dysbiosis is directly related with increased intestinal permeability as a consequence of epithelial barrier deterioration, tight junctions' alteration and bacterial translocation causing endotoxemia, which might reach and damage the liver through the portal vein [102–104]. Several studies have revealed alterations in the gut microbiome in people with NAFLD compared with healthy controls. We and others have reported a decrease in both alpha and beta diversities in NAFLD and its more advanced stages compared to healthy controls [105, 106]. Case control studies have reported consistent altered microbial signatures at phylum level such as increased *Proteobacteria* [107–110], at family level such as increased *Enterobacteriaceae* and genera such as an increase in the abundance of *Collinsella* sp, *Escherichia*, *Dorea* and a decrease in the abundance of *Coprococcus*, *Eubacterium*, *Faecalibacterium* and *Prevotella* [107, 111]. Similar microbial signatures were found in NASH as outlined in this recent review [112]. Although these initial results suggest a measurable contrast in microbial signatures between

individuals with hepatic steatosis and controls, there are, however, large discrepancies found across studies with varying results in the literature. However, a common microbial signature that has been associated with other metabolic diseases is the reduction of levels of the butyrate producer *F. prausnitzii* in the more advanced forms of NAFLD [106, 113].

Several hypotheses have provided mechanistic insights into the pathways of how the gut microbiota might contribute to NAFLD development and its disease progression. Specific microbial species such as *Collinsella* sp. have been shown to metabolize bile acids to oxo-bile acid intermediates which may increase intestinal permeability and contribute to the development of NAFLD [114, 115]. Increased intestinal permeability may lead to lipopolysaccharide (LPS) release to the host, which can trigger tissue and systemic inflammation. Furthermore, the action of microbially-produced metabolites (including TMAO, choline or ethanol) and bile acid signaling can also affect host immunity [108, 116, 117]. Interestingly, unlike other diseases, SCFAs appear to prevent but also promote the development of NAFLD and NASH depending on the signaling pathway or mechanism they activate. Amongst the SCFAs, acetate was found to be enriched in fecal samples from adults with more advanced stages of NAFLD (i.e. fibrosis) [110], whereas butyrate and propionate were enriched in fecal samples from adults with mild or moderate NAFLD. This may suggest that levels and subtypes of SCFAs correlate with the severity of fatty liver disease. Since each SCFA exerts specific and somehow different metabolic effects, assessing their balance both at the fecal and systemic level in patients and after a dietary intervention using different substrates may help provide more information on their overall role in NAFLD development, exacerbation or improvement.

On the basis of the above, advances in discovering gut microbiota or microbiota-related metabolite signatures could be used as noninvasive diagnostic tools in NAFLD and its etiology.

Chronic kidney disease (CKD)

There has been a growing interest in studying the composition of the gut microbiota in patients with CKD as well as the mechanisms by which gut dysbiosis contributes to CKD progression. The influence of the gut microbiota on the gut–kidney axis acts in a reciprocal way with either CKD significantly modifying the composition and functions of the gut microbiota. Alternatively, the gut microbiota is able to manipulate the processes leading to CKD onset and progression through inflammatory, endocrine, and neurologic pathways. Therefore, understanding the complex interaction between these two organs may provide novel interventions to prevent the progression of CKD by targeting the gut microbiota.

The existence of intestinal microbiota alterations such as decrease of microbial richness, diversity, and uniformity has been related to CKD [118]. Patients with CKD show a lower colonization of *Bifidobacterium* sp, *Lactobacillaceae*, *Bacteroidaceae*, *Akkermansia*, and *Prevotellaceae* genera, and higher intestinal levels of *Enterobacteriaceae*, particularly *Enterobacter*, *Klebsiella*, and *Escherichia*, and also increased levels of Enterococci and *Clostridium perfringens* [119, 120]. The decrease in the abundance of *Akkermansia muciniphilla*, an important probiotic, in patients with CKD negatively correlated with plasma IL-10 levels, suggesting that an altered microbiota in CKD may promote chronic systemic inflammation [121]. This chronic systemic inflammation state represents a major risk factor for CKD progression.

CDK patients are characterized by decreased consumption of dietary fibers that are required for SCFA production. Lack of dietary fibers leads to increased amino nitrogen, which can be transformed into uremic toxins by the gut microbiota [122]. Patients with CKD are characterized by an imbalance between fermentative and proteolytic microbiota in favor of the latter. The imbalance in favor of proteolytic species is related to

detrimental effects and also has a fundamental role in the progression of CKD [123]. Moreover, the main SCFAs especially butyrate, were found to be reduced in the feces and serum of patients during CKD development [123]. Further research is however needed to determine whether increasing levels of circulating SCFAs would provide any direct clinical benefit in patients with CKD.

Several experimental and clinical studies have shown the beneficial effects of prebiotic, probiotic, and synbiotic supplementation on gut microbiota–renal axis [124]. These have emerged as a potential therapeutic intervention to restore the imbalance of the gut microbiota, reduce inflammation or oxidative stress markers and modulate gut-derived uremic toxins, such as P-cresyl sulfate (PCS), indoxyl sulfate (IS), and trimethylamine N-oxide (TMAO), which have been implicated in the progression of CKD [125–127].

Mental health disorders

Gut microbes have been shown to also influence neurological functions and these links have been termed the “gut–brain axis” [128]. The gut microbiota communicates with the brain through three major pathways—the neural pathway (vagus nerve, enteric nervous system), the immune pathway (cytokines), and the endocrine pathway (HPA axis, gut hormones). Impaired functioning of this connection can lead to manifestation of mental disorders. Common gut microbial species belonging to the phylum Firmicutes and Actinobacteria, and the genera *Bacteroides* and *Bifidobacterium*, may be contributing to mental health disorders [129]. Different mental disorders are characterized by the differential gut microbial community that is generally predominated by a bacterial genus or a family as summarized in Table 2. Notably, in some of the disorders, there is an overabundance of specific microbial species. For example, abundance of *Lactobacillus sp.* and *Bifidobacterium sp.* in disorders like schizophrenia (SCZ) [130] and attention-deficit hyperactivity disorder (ADHD) [131], respectively. The probable reason for this can be attributed to the complexity of the gut microbiota.

Gut microbiota modulates the gut–brain axis via numerous direct and indirect ways. This includes maintaining gut permeability by modulating the integrity of tight junctions in the gut epithelium, producing a wide variety of metabolites including neurotransmitters, SCFAs, and amino acids. These gut-derived metabolites can affect the central nervous system by acting locally on the enteric nervous system or enter circulation and affect the brain. Furthermore, alteration in the levels of gut microbial metabolites, such as SCFAs, ammonia, tryptophan, and histamine have shown to be associated, directly or by breaking down into neuroactive catabolites with various neurological conditions like Parkinson’s disease (PD) [132], anorexia nervosa (AN) [133], Alzheimer’s disease (AD) [134], autism spectrum disorder (ASD) [135], and chronic stress and depression [136]. However, whether this disruption of homeostasis in the mental health disorders is the cause or effect of the alterations in gut microbiota and its functions is not emphatically clear and requires more studies.

Further, considering the evidence, several studies have been undertaken to specifically target the gut microbiota through different therapeutic interventions including administration of pre- and probiotics (psychobiotics) to treat mental health disorders and/or their symptoms [137, 138]. Human-intervention studies with psychotics such as the probiotic combinations of lactobacilli and Bifidobacteria showed significant reduction in psychological distress [139], improved cognition and communication among patients with AD [140] and ASD [141], and improving symptoms among PD patients [142]. Based on the promising effects of psychobiotics on modulating the gut–brain axis, more clinical trials are currently being conducted to identify the bacterial strains as potential candidates for treatment of mental disorders.

The gut microbiome as a therapeutic target in chronic diseases

Given the tight interplay between enteric microbial symbionts and host immunity (Fig. 1), efforts have focused on implementing various strategies targeting the gut microbiota to manage or prevent chronic diseases. Clinical approaches to modify gut microbiota generally focus on depleting overabundant members or the overall microbial load using antibiotics or antifungal agents, modulation through diet, or supplementation with live microbes (single or mixed species). There are a variety of proposed therapeutic approaches, such as dietary modifications, prebiotics, probiotics, and TMAO-synthesis inhibitors, to target the gut microbiome. More recently, fecal microbial transplantation (FMT) has been used in a range of infectious, neurological, and GI conditions, with promising outcomes (Table 3).

More recently, the composition of the gut microbiome has been implicated in predicting the severity of COVID-19 possibly via its immune-modulatory properties. More specifically, gut commensals with known immunomodulatory potential, such as *Faecalibacterium prausnitzii*, *Eubacterium rectale*, and *Bifidobacterium adolescentis*, were found to be significantly under-represented in patients with COVID-19 compared with healthy controls and were also associated with disease severity after taking account of antibiotic use and patient age [143]. Furthermore, the microbial imbalance found in the COVID patients was also associated with raised levels of inflammatory cytokines and blood markers of tissue damage, such as C-reactive protein and certain enzymes. Based on these findings, increasing the levels of beneficial gut species depleted in COVID-19 could serve as a novel avenue to mitigate severe disease, highlighting the importance of the gut microbiota in the pathophysiology of COVID-19.

Despite encouraging evidence from animal models in which inflammatory conditions were successfully treated via gut microbiota manipulation, data from human trials is less conclusive. Findings from recent work showed that the ability of an introduced microbe to successfully colonize the gut depends on the structure of the resident gut microbiota [144], a factor that has so far been overlooked in microbial intervention-based clinical trials and that might explain discrepancies in animal models and

Table 2. Studies (or reviews) on non-dietary interventions targeting the gut microbiome.

Therapy	Indication	Type of study/Reference
FMT	T2D/metabolic syndrome	Interventional studies [163, 151]
FMT	or C difficile infection –	Systematic review of RCTs [164]
FMT	for ulcerative colitis –	Systematic review of RCTs [165]
FMT	T1D –	RCT in [166]
TMAO synthesis inhibitors	Lowering cholesterol and bile acid metabolism	Preclinical [167]
TMAO synthesis inhibitors	Chronic kidney disease	Preclinical [168]
TMAO synthesis inhibitors	Heart disease	Preclinical [169]

Table 3. Summary table of key findings.

Disease group	Specific disease	Gut microbes	Main findings
Autoimmune diseases	Rheumatoid arthritis	<i>Prevotella copri</i> ,	Increased in abundance [12, 13]
		<i>Collinsella</i> sp.,	Increased in abundance [13]
		<i>Faecalibacterium</i> sp.	Decreased in abundance, links to SCFA production [25]
	Type-1 diabetes	<i>Dialister invisus</i> ., <i>Gemella sanguinis</i> ., <i>Bifidobacterium longum</i>	Increased in abundance (children), gut permeability [25]
		<i>F. prausnitzii</i>	Decreased in abundance (children), butyrate (SCFA) production [28]
	Atopic eczema	<i>Clostridium difficile</i>	Increased in abundance [37]
		<i>Escherichia coli</i>	Increased in abundance, eosinophilic inflammation [37]
		<i>Staphylococcus aureus</i>	Increased in abundance [37]
		<i>Bifidobacteria</i> spp.	Decreased in abundance [37]
		<i>Bacteroidetes</i> spp.	Decreased in abundance [38, 39]
<i>Coprococcus eutactus</i>		Decreased (in children), linked to butyrate production [39]	
Atopic asthma	<i>F. prausnitzii</i>	Increased in abundance, SCFA production [41]	
	Various— <i>Clostridium</i> , <i>Pediococcus</i> , <i>Escherichia</i> , <i>Klebsiella</i> , <i>Morganella</i> , and <i>Proteus</i> spp.	Increased in abundance, increased bioamine (histamine) production [55]	
	<i>Enterococcus faecalis</i> , <i>Streptococcus</i> spp., <i>Bifidobacterium bifidum</i> ., <i>Lactobacillus</i> spp.	Increased in abundance, increased bioamine (histamine) levels, increased epoxide hydrolase production of oxylipins (12,13-diHOME) [55, 56]	
Gut inflammation disorders	Irritable bowel syndrome	<i>Ruminococcus</i> spp., <i>Clostridium</i> spp., <i>Dorea</i> spp.	Increased in abundance [62]
		<i>Bifidobacterium</i> spp.	Decreased significantly in abundance (all IBS subtypes) [62, 68]
		<i>Faecalibacterium</i> spp.	Decreased in abundance, anti-inflammatory, butyrate production [62, 64, 65]
	Inflammatory bowel disease	<i>Enterobacteriaceae</i> spp.	Increased, links to previous intestinal infection and pathogen byproducts [63]
		<i>Lactobacillaceae</i> spp., <i>Bacteroides</i> spp.	Increased in abundance [63]
		<i>Ruminococcaceae</i> spp., <i>Lachnospiraceae</i> spp.	Decreased in microbiome, butyrate production [78–81]
Cardiometabolic diseases	Cardiovascular disease (including hypertension)	<i>Faecalibacterium prausnitzii</i> , <i>Roseburia</i> sp.	Decreased in microbiome, butyrate production [83]
		<i>Lactobacillus plantarum</i> , <i>Lactobacillus rhamnosus</i>	Improved ventricular function and attenuated heart failure after myocardial infarction [90, 107]. Improved blood pressure [110]
	Type-2 diabetes	<i>Akkermansia muciniphila</i>	Protected against atherosclerosis in mice [111]
		<i>Bifidobacterium</i> , <i>Bacteroides</i> , <i>Faecalibacterium</i> <i>Akkermansia</i> and <i>Roseburia</i> spp.	Negative association [112, 113]
		<i>Ruminococcus</i> , <i>Fusobacterium</i> , and <i>Blautia</i>	Positive association [112, 113]
		<i>Lactobacillus</i> spp.	Enriched in control microbiome, butyrate production [112, 114, 115], insulin sensitivity through GLP-1 [116–120]
		<i>Clostridium</i> spp.	Increased, opportunistic pathogen
NAFLD	<i>Collinsell</i> spp.	Increased in abundance [128]. Increased intestinal permeability and lipopolysaccharide release through metabolism of bile-acids to oxo-bile [144, 145]	
	<i>Escherichia</i> spp., <i>Dorea</i> spp.	Increased in abundance [131, 135, 136]	
	<i>Coprococcus</i> spp., <i>Eubacterium</i> spp., <i>Faecalibacterium</i> spp., <i>Prevotella</i> spp.	Decreased in abundance [131, 135, 137]	
Chronic kidney disease		<i>Bifidobacterium</i> , <i>Lactobacillaceae</i> , <i>Prevotellaceae</i>	Decreased in abundance, SCFA producers associated with anti-inflammatory cytokines [148, 149]

Table 3 continued

Disease group	Specific disease	Gut microbes	Main findings
		<i>Enterobacter</i>	Increased in abundance [149]
		<i>Klebsiella</i>	Increased in abundance, pathogen associated with inflammatory disease states including Crohn's [148, 149]
		<i>Clostridium perfringens</i>	Increased in abundance, pathogen associated with intestinal diseases [148]
Mental health disorders	SCZ, ADHD	<i>Lactobacillus</i> spp, <i>Bifidobacterium</i>	Increased in abundance in specific disorders such as SCZ and ADHD [157, 158]
	General anxiety disorder (GAD)	<i>Bacteroidetes</i> , <i>Ruminococcus gnavus</i> , and <i>Fusobacterium</i> <i>Bacteroidaceae</i> , <i>Enterobacteriaceae</i> , and <i>Burkholderiaceae</i>	Decreased in abundance in general anxiety disorder (GAD) [170]. Increased in abundance in GAD [171, 172]
	Post- traumatic stress disorder (PTSD)	Actinobacteria, Lentisphaerae, and Verrucomicrobia	Decreased in abundance in post-traumatic stress disorder (PTSD) [173]
	Depression	<i>Eggerthella</i> ., <i>Holdemania</i> , <i>Turicibacter</i> , <i>Paraprevotella</i> <i>Prevotella</i> , <i>Dialister</i>	Increased in abundance amongst individuals with depression [174, 175]. Decreased in abundance amongst individuals with depression [176]
	Dementia	<i>Escherichia</i> , <i>Blautia</i> , <i>Bifidobacterium</i> , <i>Streptococcus</i> , <i>Lactobacillus</i> , <i>Dorea</i> spp <i>Actinobacteria</i> , <i>Bacteroides</i>	Increased in abundance amongst individuals with dementia [177]. Decreased in abundance amongst individuals with dementia [177]

human trials. Nonetheless, intervention with a multispecies consortium of bacteria has shown to be effective in the maintenance of remission in patients with UC but not in those with CD [145]. Meta-analysis of intervention trials in which various combinations of bacterial strains were administered to adults with T2DM showed moderate improvements in hyperglycemia [146]. Moreover, probiotic supplementation during the first 27 days of life reduced the risk of islet autoimmunity in a large multicenter prospective cohort study of children at high genetic risk for T1DM, compared with no supplementation or supplementation later in infancy [147].

Intervention studies involving live microbial supplementation have also shown encouraging results, although more attention to microbial strain selection based on functional attributes, defined timing or duration of supplementation, and/or tailoring of the supplemented organisms to the endogenous gut microbiome of the recipient may significantly improve the efficacy in future studies. Ongoing studies are focused on understanding the basis of microbe-microbe interactions in order to identify discrete gut microbiomes that more readily respond to specific microbial interventions.

There is also a great need for tailored interventions that consider the microbial individuality of the recipient in order to prevent or manage chronic diseases. Such approaches are likely to result in a transition away from historically used probiotic strains, which are frequently poorly adapted to the enteric microenvironment, toward personalized multispecies microbial consortia sourced from healthy human enteric ecosystems. To further enhance the efficacy of microbial supplementation, nutritional support in the form of targeted dietary modifications, tailored to the specific substrate requirements [148], should also be considered as discussed in the section below. Such an integrated approach to microbiome-based therapeutics, built on independent observations in the field of gut microbiome research, may offer more effective, predictable, and sustainable microbial restitution in cases of chronic disease in which microbiome perturbation and functional gene loss are prominent features.

FMT has proven effective in >90% of patients with recurrent antibiotic-resistant *C. difficile* infection [149]. The success rate of FMT administration for other chronic intestinal inflammatory conditions such as IBD, however, is more modest, with clinical

remission being less predictable [150]. More recently, FMT has been applied to chronic inflammatory conditions affecting organs distal to the GI tract. FMT from lean donors improved insulin sensitivity in men with obesity and metabolic syndrome, and this improvement was linked to changes in plasma metabolites, in particular increased gamma-aminobutyric acid (GABA), tryptophan, and phenylalanine [151].

Effects of a healthy diet are mediated via the gut microbiome

The most obvious way of targeting the gut microbiome is through dietary modifications. Already, several controlled clinical dietary intervention studies targeting the human gut microbiota have been reported [2, 152]. For example, diets rich in fiber were shown to significantly improve glucose control and promote a healthier metabolic profile in T2DM patients as well as reduce the risk of coronary heart disease [153]. Other studies showed marked interindividual variation in postprandial glycemic responses after consumption of identical meals [154, 155]. The consideration of microbial composition alongside known disease-risk factors (i.e., body mass index, fasting glucose) enabled accurate glucose-response prediction, thus allowing the design of more effective, personalized diets for improved glycemic control [155] in these studies.

Some of these same studies have recently investigated the links between gut microbiome structure, habitual diet, and blood cardiometabolic markers [156] in a cohort of 1100 healthy individuals from the United States and the United Kingdom. This study reported that microbial diversity and composition were highly correlated with both fasting and postprandial biomarkers. The strongest associations were with high-density lipoprotein cholesterol (HDL), which positively correlated with microbial species richness. Cardiometabolic markers, which have in the recent past been shown to be strongly predictive of incident diabetes and heart disease, such as glycoprotein acetyl (GlycA) were also associated (positively or negatively) with microbiome richness. One of the most striking findings of the study was that gut microbiome composition is a better predictor of postprandial triglyceride and insulin concentrations than of glucose levels. The authors also reported that the diversity of healthy plant-based foods in habitual diet shapes gut microbiome composition. Approximately 10% of the variance in gut microbial composition could be explained by variation in healthy eating patterns [156].

Bacterial species were found to segregate into groups associated with more and less healthy plant- and animal-based foods. In addition, the authors reported a microbial signature of cardiometabolic health levels consistent across diet, obesity indicators, and cardiometabolic risks. The authors reported a consistent set of microbial species that strongly linked to all of the following: healthy eating patterns, indicators of obesity and cardiometabolic health, and fasting and postprandial circulating metabolites connected with cardiometabolic risk [156]. Other much smaller studies have also reported that dietary habits are strongly correlated with gut microbiome composition, disease status, and SCFA production [129].

Although a key weakness of the above study is its cross-sectional observational nature, consistent changes in gut microbiome composition and health outcomes have been recently reported by an international consortium investigating the effect of 12 months of Mediterranean diet on 612 elderly individuals from five countries [157]. Shankar Ghosh et al. [157] reported significant differences in the association patterns of bacterial taxa that increased (DietPositive) or decreased (DietNegative) in response to the Mediterranean diet intervention. The DietPositive bacteria had consistent negative associations (significantly lower than the DietNegative bacteria) with the pro-inflammatory circulating markers hsCRP and IL-17 levels as well as with functional measures associated with increased frailty. In contrast, DietPositive bacterial taxa showed positive correlations with measures of improved cognitive function, hand-grip strength, and two of the anti-inflammatory cytokines. DietPositive species included butyrogenic taxa such as *F. prausnitzii*, *Eubacterium* and *Roseburia*, whereas DietNegative bacteria included *Ruminococcus torques*, *Collinsella aerofaciens*, *Coprococcus comes*, *Dorea formicigenerans*, and *Clostridium ramosum*. Interestingly, there is no overlap between the "DietPositive" bacteria whose abundance increased after 12 months of a Med Diet reported by Shankar Ghosh et al. [157] and the taxa associated with "healthy diet indices" reported by Asnicar et al. On the other hand, the "DietPositive" and "DietNegative" taxa have substantial overlap with results from our own recent interventional study. We compared the changes in gut microbiome composition after 6 weeks of 500 mg of omega-3 fatty acids or 20 g of soluble fiber (inulin) in 70 middle-age and elderly individuals who had low fiber intake at baseline [158]. We found that, consistent with what is known of prebiotics such as inulin, that *Bifidobacterium sp* was remarkably increased and this correlated with butyrate production. On the other hand, omega-3 supplementation resulted in a significant decrease in *Collinsella sp*, both of which are in line with the findings from the multicenter Mediterranean diet intervention [157]. Importantly, many of the changes in bacterial abundances and SCFA concentrations were accompanied by decreases in inflammatory or atherogenic molecular mediators such as VLDL or IL4. Unlike the effects seen through a complex dietary intervention, such as the Mediterranean diet, we showed that it is possible to see significant effects both on microbiome composition and cardiometabolic health mediators.

Other recent studies have highlighted the role of the type of dietary fat on gut microbiome composition. In a randomized trial, 38 overweight and obese subjects were assigned to consume an excess of 1000 kcal/day of diets rich in saturated fat, unsaturated fat, or simple sugars for 3 weeks [159]. The relative abundances of individual taxa were altered in a diet-specific manner, wherein the overfeeding of saturated fat increased *Proteobacteria*, while unsaturated fat increased butyrate producers.

It is indeed possible to target the increase of specific taxa and the production of specific metabolites and the extent to which different carbohydrate sources (digestible by gut bacteria but not by humans) alter gut microbiome composition and function was recently tested by Deehan et al. [148] in a randomized controlled trial using a four-arm design. They gave increasing doses of three forms of resistant starch from maize, potato, or tapioca and a human-digestible corn starch (placebo) to 10 healthy volunteers

per arm. They compared the effect of these carbohydrate substrates on gut microbiome composition in humans and found that chemically modified resistant starches with small structural differences induced highly specific effects on the gut microbiome that direct changes in the output of either propionate or butyrate. Dominant effects were remarkably consistent within treatment groups and dose-dependent with a plateau at a dose of 35 g/day. For example, maize-derived resistant starch resulted in increases in *B. adolescentis*, *E. rectale*, *Oscillibacter*, and *Ruminococcus*-related taxa and this correlated with increases in butyrate production. Tapioca-resistant starch on the other hand, which induced shifts in propionate proportions, as positively correlated with increases in *P. distasonis* an important succinate-producing bacterium. Succinate is then converted to propionate by other commensal bacteria in the gut. This very elegant design also clearly demonstrated the dose dependency between carbohydrate sources and the production of specific SCFAs. Similar strong and specific effects on gut microbiome composition have been shown by many interventional studies, both in healthy [160, 161] and diseased populations [162].

WHERE IS THIS FIELD MOVING TOWARD?

Over the past decade, considerable evidence from both animal and human studies has accumulated showing a clear link between the gut microbiome in chronic diseases, including inflammatory autoimmune disorders, gut inflammation-related disorders, and cardiometabolic diseases (Fig. 1). It is increasingly clear that bacterial metabolites are at least in part, the key agents involved in the role of the gut microbiome on human health and among such metabolites, SCFAs appear to be the most important ones. Butyrate-producing bacteria are associated with lower risk of inflammatory autoimmune and cardiometabolic diseases, and also irritable bowel syndrome (Table 1). A number of therapeutic strategies to target the gut microbiome are possible, but nutritional changes appear to be the most obvious, noninvasive, and immediate way of altering the gut microbiome composition and function. Recent randomized controlled trials have shown that both composition and function respond in consistent ways to specific dietary interventions. Dietary fiber and unsaturated fat, separately or in a healthy diet such as the Mediterranean diet, result in higher relative abundances of butyrate-producing bacteria and these bacteria and the SCFAs produced in turn result in improved health outcomes. Different types of dietary fiber result in different bacterial changes and different SCFAs. The possibility of designing dietary interventions targeted specifically at increasing certain bacterial metabolites to improve cardiometabolic and inflammatory health outcomes appears well within reach within the next half decade.

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COMPETING INTERESTS

The authors declare no competing interests.

ADDITIONAL INFORMATION

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