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Heather Rasmussen
University of Nebraska - Lincoln, heather.rasmussen@unl.edu

Bruce R. Hamaker
Purdue University, hamakerb@purdue.edu

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Prebiotics and Inflammatory Bowel Disease

Heather E. Rasmussen, PhD, RDN,[1] and
Bruce R. Hamaker, PhD[2]

1 Department of Clinical Nutrition, Rush University Medical Center,
1700 W Van Buren Street, Suite 425, Chicago, IL 60612

2 Department of Food Science, Purdue University,
745 Agriculture Mall Drive, West Lafayette, IN 47907

Corresponding author — H. Rasmussen

Abstract
Inflammatory bowel disease risk factors include poor diet, and corresponding low intake of dietary fiber, specifically prebiotics, which is fermented by the gut microbiota. Dietary fibers, many of which are potential prebiotics, have hundreds to thousands of unique chemical structures that may promote bacteria or bacterial groups to provide beneficial health effects. In vitro and in vivo animal models provide some support for the use of prebiotics for inflammatory bowel disease through inflammation reduction. Studies using prebiotics in patients with inflammatory bowel disease are limited and focus on only a select few prebiotic substances.

Keywords: Inflammatory bowel disease, Ulcerative colitis, Crohn disease, Prebiotics, Fiber

Introduction

Prebiotics are fermentable carbohydrates that vary greatly in chemical structure, giving rise to digestion by specific gut microbiota and eliciting discrete beneficial functions. Although hundreds to thousands of fermentable dietary fibers, which are potential prebiotic substances, exist in nature, use of prebiotics in research is often limited to a few distinct structural types. Research centered on prebiotic interventions to beneficially modify the gut milieu is

increasing and includes modifying microbiota, improving intestinal barrier function, and producing beneficial metabolites for both local and systemic health benefit. Despite increasing use, limited data exist for prebiotic benefit for certain conditions, including inflammatory bowel disease (IBD). This article reviews prebiotic types and the various ways in which they modify the gastrointestinal tract related to IBD. The use of select prebiotics in IBD is described in detail, highlighting their potential effectiveness, as well as the lack of evidence, for their clinical use. Recommendations for future research are made.

Prebiotics: Definition and Structure

The term prebiotics has, over time, undergone some changes in its definition, although it still adheres to the concept of carbohydrates that make their way to the large intestine where they are fermented and promote beneficial bacteria.[1] At the time of the original definition in the 1990s, a focus was put on oligosaccharides, and larger soluble fibers, because it was found that certain of such carbohydrates promoted 2 genera of beneficial bacteria, namely *Bifidobacterium* and *Lactobacillus*.[2] The term prebiotics became synonymous with oligosaccharides, such as fructooligosaccharides (FOS) and galactooligosaccharides (GOS), as they were accepted in the scientific, although not necessarily the regulatory, community to promote a healthy colon through the favoring of these bacteria. It was true, too, that other dietary carbohydrates promote 1 or both of *Bifidobacterium* spp and *Lactobacillus* spp, and in the scientific literature examples can be found that also are claimed as prebiotic, such as resistant starch and b-glucans. However, as more was learned regarding other relevant beneficial colonic bacteria and the importance of maintaining a favorable gut ecosystem for health, it has become apparent that the concept of prebiotics has a broader, and perhaps more complicated, role in gut health.

Prebiotics are found within the larger class of carbohydrates known as dietary fiber. These carbohydrates include all plant carbohydrates taken in the diet, plus lignin, and although fibers can be broken down into various subfractions, in the current discussion fiber may best be divided into fermentable and nonfermentable fibers. Because prebiotics are all fermentable, a case could be made for a beneficial effect of all fermentable fibers and that they promote beneficial bacteria. Hence, the concept of prebiotics could potentially take in many types of fermentable fibers comprising both oligosaccharides and polysaccharides. In contrast, nonfermentable fibers are recognized for their water-holding property and laxation capacity, although it is not known whether nonfermentable fibers could also induce an environment in the colon in which beneficial bacteria might flourish.

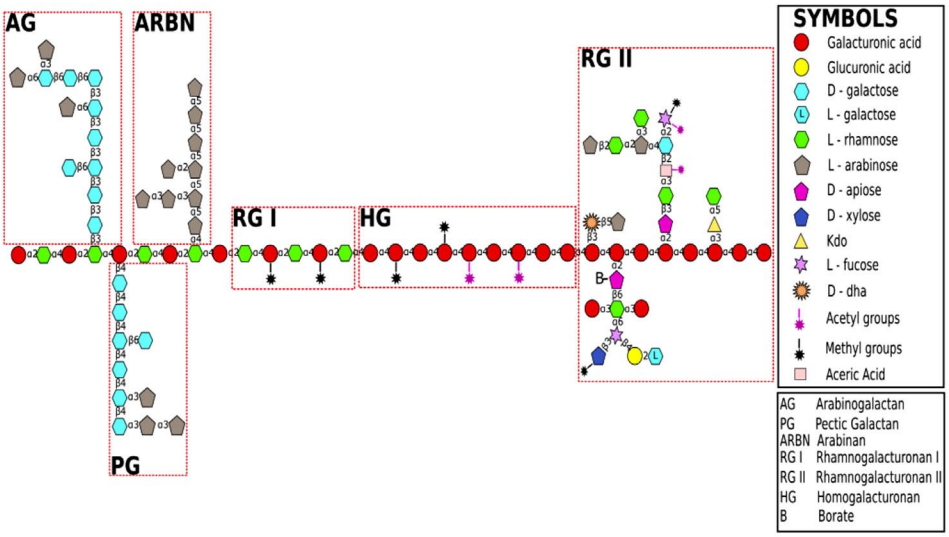

Fig. 1. Cell wall pectin chemical structure. AG, arabinogalactan; ARBN, arabinan; B, borate; HG, homogalacturonan; PG, pectic galactan; RG I, rhamnogalacturonan I; RG II, rhamnogalacturonan II. (Data from Hamaker BR, Tuncil YE. A perspective on the complexity of dietary fiber structures and their potential effect on the gut microbiota. *J Mol Biol* 2014;426(23):3842; with permission.)

Perhaps what is not well recognized by scientists and clinicians specializing in gastrointestinal health and the gut microbiome is the broad and complex range of dietary fiber chemical and physical structures that exist (see the review by Hamaker and Tuncil,[3] 2014). All dietary fibers, and therefore prebiotics, are composed of 1 or more sugar units (e.g., glucose, fructose, galactose, arabinose) or sugar acids (e.g., galacturonic and glucuronic acid) that are linked via glycosidic bonds. Although dietary fibers are chemically and physically classified in various ways, for the purpose of the current discussion related to IBD, it is perhaps useful to think of them as (1) plant cell wall polysaccharides of the cereals (mostly composed of cellulose, arabinoxylans, b-glucans, but also small amounts of pectin and even inulin in wheat), legumes (cellulose, pectin, galactans), tubers (cellulose, pectin), and fruits and vegetables (mostly composed of cellulose, pectins, xyloglucans); (2) plant storage oligosaccharides and polysaccharides, such as starch (those entering the large intestines being resistant starch) and inulin; (3) plant exudates (e.g., gum arabic); and (4) animal-based carbohydrates (e.g., galactooligosaccharides, chitin/chitosan). As discussed here, most prebiotics used in human studies for patients with IBD are in the oligosaccharide and inulin classes: classes 2 and 4, respectively. Plant polysaccharides can have complicated chemical structures (Fig. 1 for the example of pectin),[3] which gut bacteria can use through specialized abilities to access and metabolize certain structural components.

Down to the strain level, colonic bacteria have encoded in their genomes the ability to degrade certain carbohydrates they encounter and to absorb and metabolize the simple sugars released. The authors have proposed that there is high specificity of bacteria for carbohydrate chemical and physical structures and that beneficial bacteria can potentially be favored through fiber selection.[3]

Prebiotic Function

Prebiotic, or fermentable dietary fiber, function in the colon depends on several factors, including obvious ones like fiber type and structure, as well as an individual's gut microbiota community members and structure. Also relevant to prebiotic function are such things as cross-feeding, bacteriocins, and phage communities that influence how fibers are used. However, it is likely that prebiotic dietary fibers can shift the gut microbiome and have a beneficial effect on health, because the bacteria evolved under dietary stresses and were selected for, in significant part, based on their ability to access carbohydrates and use them efficiently for their maintenance and growth.

Fermentable dietary fibers function in the colon by providing essential food to the microbiota. Because individual bacteria, and groups or consortia of bacteria, have different abilities to use carbohydrates and must compete with other bacteria for them, there is a growing recognition that mixtures of fibers are more likely to promote growth of a wider range of bacteria than single fibers. Along with this, there is a generally accepted concept that more diverse bacterial communities are better for health than less diverse ones.[4] Much still needs to be learned regarding fibers and their action in the colon, and what mixtures are best suited for the microbiome and health, although some things are known. In addition to the function of FOS, GOS, and inulin in promoting *Bifidobacterium* and *Lactobacillus*, certain other beneficial genera and groups of bacteria have been studied in relation to fiber types for their promotion. The *Clostridium* clusters IV and IVa bacteria have drawn interest because they are associated with the mucosal layer of the gut epithelium, and contain several of the butyrogenic bacteria in the colon (i.e., *Faecalibacterium prausnitzii*, *Eubacterium rectales*, *Roseburia infantalis*); there is also some evidence that insoluble (and fermentable) fibers favor these groups.[3,5,6]

Inflammatory Bowel Disease

IBD is increasing, both in the United States and in less-developed countries.[7,8] The disease is characterized by immune activation in the gastrointestinal tract, causing inflammation and damage to the mucosa or submucosa.

Ulcerative colitis (UC) differs from Crohn disease (CD) in presentation, with disease activity focused on the colon and rectum in UC and intermittent disease activity throughout the gastrointestinal tract in CD. IBD is characterized by both activated innate and adaptive immune responses, with response varying by IBD type.[9] Although a T-helper 1–type response is thought to be predominant in CD and a T-helper 2–type response in UC, the stimulation and deregulation of these pathways in each type of IBD is more complex and not so clearly delineated.[10]

The cause of IBD is multifaceted, and a combination of genetic predisposition and environmental stimuli promote IBD. Genetic susceptibility to IBD is greater in CD; genes involved in signaling between the immune system and microbiota have been associated with IBD susceptibility (e.g., nucleotide-binding oligomerization domain– containing protein 2 [NOD2], interleukin [IL]-23R, IL-10). An immune response in genetically predisposed individuals can be triggered by environmental stimuli through the modern lifestyle; sometimes these are otherwise innocuous. For example, drugs (e.g., antibiotics, nonsteroidal anti-inflammatory drugs), as well as infectious agents, stress, and diet, may all contribute to IBD.[11] Also, environmental stimuli can have opposing effects on IBD disease type; cigarette smoking increases CD risk but may be protective in UC. Some of these environmental stimuli may modify gut microbiota, creating an environment that is more susceptible to IBD development.

What Is the Involvement of Microbiota in Inflammatory Bowel Disease?

The gastrointestinal microbiota is composed of bacteria, viruses, and fungi, but the manipulation of just the bacterial component of the microbiota is the focus of the IBD literature to date. All components of the microbiota intimately interact with the host immune system, including communication between bacterial species and dendritic cells (DCs) to drive differentiation of T cells toward either an effector or regulatory T-cell response. In the context of IBD, it is not clear whether the microbiota drive changes in the host immune system or the host changes the microbiota through aberrant immune activation; likely it is a combination of the two interactions that contributes to IBD susceptibility.

The involvement of the gut microbiota in IBD was recently reviewed.[12,13] Evidence of the influence of the microbiota/immune system interaction on IBD is convincing; however, alterations in specific microbiota that increase IBD disease risk or disease course are not completely clear. Overall, patients with IBD have less microbial diversity and increased mucosal bacteria than healthy individuals.[12,14] Individual bacterial species also may differ between those with IBD and healthy individuals, with more adherent-invasive

Escherichia coli and Enterobacteriaceae, among others,[12] in those with IBD. In addition, several taxa may be decreased, including *Bifidobacterium* and *F prausnitizii*.[12,15–17] CD recurrence has been associated with low levels of *F prausnitizii*.[18]

Although differences in microbiota composition between healthy individuals and those with IBD provide insight into microbiota's potential role in IBD, this does not indicate how, or whether, these differences contribute an altered intestinal milieu. Differing metabolites were found in fecal samples between patients with CD and healthy concordant twins.[19] Compared with healthy subjects, fecal butyrate concentrations were lower in those with IBD compared with healthy controls.[20] Maintenance or improvement in butyrate concentrations is especially important because butyrate is a primary energy source for the colonic mucosa, contributes to gut epithelial barrier integrity, and shows anti-inflammatory activity.[21] More literature on the contribution of microbial metabolites to IBD disease course is warranted.

Dietary Strategies to Minimize Progression and Symptoms of Inflammatory Bowel Disease: Is There a Niche for Prebiotics?

Management of IBD through medication (e.g., aminosalicylates, antibiotics, anti–tumor necrosis factor alpha therapy, and corticosteroids) is often needed to control disease activity; however, medication management is not always effective. This lack of efficacy may lead to uncontrolled inflammation and complications such as rectal bleeding, bowel obstruction, and intestinal resection, the occurrence of which depends on IBD type. These complications, along with intermittent diarrhea, may lead to malnutrition and weight loss. Whereas/although nutritional inadequacy, may be addressed by elemental diets or parenteral nutrition; recommendations for IBD when in remission or in less active disease suggest dietary fiber manipulation as a component of treatment.

Low-fiber diets are recommended for acute exacerbation or strictures. This minimization of fiber intake may be detrimental to encouraging a beneficial microbial environment. However, during remission, a high-fiber diet is warranted to maintain normal bowel habit, minimize gastrointestinal symptoms, and promote a healthy intestinal milieu. These recommendations focus largely on the inclusion of dietary fiber in the context of a diet high in fruits, vegetables, and whole grains. However, dietary fiber intake in the United States is inadequate (17 g/d),[22] as it is in other countries around the world. Thus, supplementation with select fibers that target specific bacteria and other components of gut health is warranted. As highlighted earlier, a structure-function relationship exists with prebiotics, suggesting that a specific prebiotic could be identified to target enhancement of a desired

specific bacterial strain based on examining these structure-function relationships. However, on the whole, this has not been thoughtfully considered when selecting prebiotics, nor has it been fully researched. In addition, because uncertainty surrounds the specific bacterial taxa and metabolites that differ between both healthy individuals and those with IBD, as well as between those with UC and CD, it is currently difficult to accurately identify specific dietary modifiers for IBD because the targets of modification are not clearly known. Despite this, investigators have attempted to provide prebiotic interventions in both animal models and in humans.

Use Of Prebiotics in *in vitro* and Animal Models as a Foundation for the Use in Humans with Inflammatory Bowel Disease

A few studies have examined the effect of potential prebiotic fibers using in vitro fermentation of microbiota from patients with IBD. Rose and colleagues[23] (2010) showed the effect of a fabricated butyrate-producing fiber on the microbiota communities of patients with IBD with inactive CD and active UC. The test fiber was an alginate-based starch-entrapped microsphere, and application in vitro fermentation system resulted in slower fermentation than FOS, but with similar butyrate levels; a maintenance of low pH better than FOS; and a reduction in patients with inactive CD of potentially harmful gut bacteria (species of *Bacteroides*, *Enterococcus*, *Fusobacterium*, and *Veillonella*) compared with FOS.

In recent studies in our laboratory at Purdue University on in vitro fecal fermentation assessment of dietary fibers on patients with CD and UC, many patients had microbiota with low capacity to generate short-chain fatty acids (SCFAs), which correlated with the loss of the Bacteroidetes phylum. Patients with CD and UC microbiota had lower diversity than healthy controls. It seemed that the severity of dysbiosis dictates the SCFA production with fiber supplementation. When fed in vitro a mixture of fibers containing equal amounts of FOS, b-glucan, pectin, and arabinoxylan (soluble), there was a promotion of SCFAs and gas production in the CD group that was better than when any single fiber was given. In the fiber mixture group, the *Bacteroides* genus was increased, although there was no significant pattern of microbiota change related to the fiber mixture among the individuals with CD and UC. *Bacteroides* was increased by all the fibers. Thus, in vitro human fecal fermentation analysis seems to have potential in screening dietary fibers for prebiotic effect, but studies comparing in vitro with human intervention results must still be done.

In animals, there are several studies using mostly the dextran sodium sulfate model to induce UC in mice, which show a beneficial effect of prebiotics on gut bacteria. For instance, prebiotic fructans increased amounts

of *Bifidobacterium* and *Lactobacillus* in colitis-induced mice.[24,25] Larrosa and colleagues[26] (2009) studied the potential prebiotic effect of the noncarbohydrate phenolic compound, resveratrol, in rats with DSS-induced colitis and found increased levels of *Bifidobacterium* and *Lactobacillus*, and lower amounts of *E coli* and Enterobacteriaceae. In addition, in a mouse model of colitis, FOS increased luminal *Bifidobacterium* and reduced disease activity.[27]

Overall, there is a good indication of prebiotic effect resulting in improvements in microbiota community structure in IBD-type conditions. A more systematic approach toward understanding how prebiotics could optimally be used through the aforementioned, as well as additional, approaches is desired (e.g., with maximum effect on creating favorable microbiota shifts, with concomitant low levels of bloating and discomfort).

Use of Prebiotics in Humans with Inflammatory Bowel Disease: Are They Effective?

In human studies reporting treatment outcomes in patients with IBD, degree of disease activity is assessed through biomarkers (e.g., C-reactive protein, fecal calprotectin, IL-10), established indices (Crohn disease activity index [CDAI] or Harvey-Bradshaw index [HBI]), or self-report of specific outcomes such as gastrointestinal symptoms or quality-of-life improvement. In addition, and germane to this topic, microbiota composition and metabolite production (e.g., SCFAs) can be measured to identify the prebiotic capacity of the supplement, as well as to provide a potential mechanism for disease improvement.

As discussed here, prebiotics are often specific carbohydrate structures that may be categorized as a type of dietary fiber. Although several researchers have shown that dietary fiber from whole foods and specific high-fiber dietary patterns can influence IBD outcomes,[28,29] no studies have been done that examine the impact of specific prebiotic-containing whole foods on IBD. Thus, evaluation of the literature to determine the impact of prebiotics on IBD is limited to prebiotic supplementation (Table 1).

Mixed results exist for supplementation of fructan-based prebiotics. A 1-group, open-label study supplemented 15 g of FOS for 3 weeks in 10 patients with CD.[30] Supplementation reduced the HBI score, increased fecal *Bifidobacterium* concentrations, and increased the percentage of IL-10–positive DCs. However, fluorescence in situ hybridization was used to assess changes in microbiota, a method that may not be directly comparable with more common sequencing methods used currently. In addition, the placebo response could have contributed to benefits attributed to the FOS supplement.[31] In a follow-up study by the same group, patients with CD were enrolled in a placebo-controlled randomized controlled trial (RCT) to test the

Table 1. Human intervention studies administering prebiotics in individuals with inflammatory bowel disease

	Study Design/ Intervention Duration	*Sample*	*Prebiotic*	*Clinical Outcomes*	*Molecular/ Microbial Outcomes*
Fructans					
Lindsay et al,[30] 2006	One group, open label 3 wk	Moderately active CD (HBI >5) *n* = 10	15 g FOS (70% oligofructose, 30% inulin)	Decrease in HBI (9.8 [3.1] to 6.9 [3.4], *P* = .01) Decrease in CADI (250.9 [77.8] to 220.6 [127.8], *P* = .39) Increase in patient and physician global assessment scores, *P* < .01 Increased borborygmi, *P* = .049, and flatulence severity, *P* = .009	Increase in fecal *Bifidobacterium*, *P* = .005; no change in mucosal *Bifidobacterium*, *P* = .76 Increase in mucosal *Bifidobacterium* in those who entered disease remission (*n* = 4), *P* = .03 No change in CRP, *P* = .12 Increase in IL-10–positive CD11c + DC (30.1% [38%] to 53.3% [33%], *P* = .06) Increase in DC TLR4 expression (36.8% [32%] to 75.4% [7.9%], P<.001)
Benjamin et al,[32] 2011	Double-blind RCT 4 wk	Active CD (CDAI ≥ 220 plus increased inflammation) *n* = 103	15 g FOS (70% D*P* <10, 30% DP >10) 15 g maltodextrin control	No difference in clinically significant decrease in CDAI (22% FOS and 39% placebo, *P* = .067) No difference in those achieving clinical remission (11% FOS and 20% placebo, *P* = .19) More flatulence (*P* = .004), borborygmi (*P* = .029), and abdominal pain (*P* = .048), than placebo at treatment end	No difference in *Bifidobacterium* (*P* = .20) or *F. prausnitzii* (*P* = .95) between groups after treatment No difference in CRP (*P* = .32) or fecal calprotectin (*P* = .09) between groups after treatment Increase in IL-10–positive CD11c + DC intensity ratio (1.3 [0.6] to 2.0 [1.6], *P* = .04)

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Table 1 *(continued).* Human intervention studies administering prebiotics in individuals with inflammatory bowel disease

	Study Design/ Intervention Duration	*Sample*	*Prebiotic*	*Clinical Outcomes*	*Molecular/ Microbial Outcomes*
De Preter et al,[33] 2013	Double-blind RCT 4 wk	Inactive or moderately active CD (HBI 0–12) *n* = 67	10 g 1:1 OF-IN 10 g maltodextrin control	Decrease in HBI from 4 to 3 (*P* = .048) in prebiotic group, no change in placebo; decrease from 7 to 5 in moderately active patients with CD (*P* = .02) 32% dropout rate in prebiotic group vs 12% in placebo because of side effects, *P* = .07	Increase in *Bifidobacterium longum* (*P* = .03) and decrease in *Ruminococcus gnavus* (*P* = .03) Disease activity correlated with *B. longum* (*r* = 0.894, *P* = .02) in patients with active CD Increase in relative concentration of acetaldehyde (*P* = .001) and butyrate (*P* = .001) in OF-IN group
Casellas et al,[34] 2007	Double-blind RCT 2 wk	Mild to moderate UC (index of Rachmilewitz 6–19) *n* = 19	12 g oligofructose-enriched inulin 12 g maltodextrin	Decrease in clinical disease activity in both groups (*P* < .05), no difference between groups Decrease in dyspepsia scores with oligo-fructose-enriched inulin (*P* < .05)	Decrease in fecal calprotectin with oligofructose-enriched inulin (*P* < .05) No change in inflammatory mediator release (P >.05)
Germinated Barley					
Kanauchi et al,[35] 2003	One group, open label 24 wk	Mild to moderate UC *n* = 21	20–30 g germinated barley (48% protein, 35% fiber, 9% lipid)	Reduction in total clinical activity index score and in 2 of the 6 components (blood in stool, nocturnal diarrhea)[a]	No difference in biochemical parameters[b] Decrease in erythema, granularity, and erosion[a]
Plantago ovata					
Fernandez-Banares et al,[38] 1999	Open-label RCT 1 y	UC in remission *n* = 105	20 g *P. ovata* seeds 1.5 g mesalamine 20 g *P. ovata* seeds plus mesalamine	Treatment effect not associated with probability of relapse, *P* = .67	Increase in fecal butyrate in those taking *P. ovata* seeds, *P* = .018[c]
Fujimori et al,[39] 2009	3-group, randomized trial 4 wk	UC in remission *n* = 120	2 x 10^9 CFU *B. longum* 4.0 g psyllium 2 x 10^9 CFU *B. longum* plus 4.0 g psyllium	Improvement in bowel function subcomponent of IBDQ, *P* = .04	No change in C-reactive protein, P > .05

Abbreviations: CRP, C-reactive protein; IBDQ, IBD quality-of-life questionnaire; OF-IN, oligofructose/inulin; RCT, randomized controlled trial; TLR, Toll-like receptor.

a. *P* value not reported.

b. Biochemical parameters measured were not reported.

c. *n* = 7, specific treatment group not reported.

effectiveness of 15 g of FOS on CD disease activity.[32] No differences in clinical response existed between groups. In addition, no change in fecal *Bifidobacterium* or *F. prausnitzii* was seen with FOS intake, but the proportion of IL-6–positive DCs decreased and the proportion of IL-10 DCs increased with treatment. De Preter and colleagues[33] conducted a double-blind, parallel-group RCT using 10 g of fructan (1:1 inulin to oligofructose) versus a maltodextrin control. In the prebiotic group, butyrate was significantly increased from baseline, and HBI decreased in the entire sample as well as in patients with moderately active disease. In addition, Casellas and colleagues[34] conducted a study with a mixture of inulin and oligofructose (BENEO Synergy 1) and reported decreases in fecal calprotectin in patients with mild to moderately active UC. Importantly, side effects were common in 3 of these studies, contributing to increased dropout in 2. Although most saw a beneficial change in clinical disease activity indices, improvement in molecular outcomes were not consistent between studies.

Although fructan-containing compounds are the most well-known prebiotics, other fibers may have prebiotic capacity and thus may benefit patients with IBD. One such example is germinated barley. Composed of not only fiber (cellulose, hemicellulose, and lignin), malted barley in the form used in IBD studies (termed germinated barley foodstuff, GBF) contains protein and lipid as major and minor components, respectively, of the dietary compound. Several studies by the same researchers reported a benefit of this compound for patients with UC.[35–37] In one study (see Table 1), these researchers provided patients with UC with 20 to 30 g of GBF for 24 weeks.[35] Total clinical activity index score, as well as 2 subcomponents, were reduced with GBF intake; however, the magnitude of change was not clearly reported. Images of the colon and rectum indicated improvement in erythema, granularity, and erosion. Importantly, the study was open label with no control group and thus could not account for the natural change in disease activity over the study duration. In addition, this study did not assess microbiota or metabolites. Also, GBF was stated to be well tolerated, but no supporting data were presented.

In addition, *Plantago ovata* (psyllium) has been used in patients with UC to identify the impact on remission maintenance.[38,39] Supplementation of 20 g of *P. ovata* seeds a day resulted in no difference in remission maintenance compared with mesalamine. Fecal butyrate levels increased with *P. ovata* intake; however, data were presented on only 7 subjects, and it was not stated from which group these subjects originated (see Table 1).[38] In addition, Fujimori and colleagues[39] did not have a control group and thus any change seen with prebiotic treatment (change in bowel function–related quality of life) is difficult to interpret in the context of prebiotic effectiveness.

In addition to studies providing prebiotics, several investigators have supplemented with synbiotics, a combination of prebiotics and probiotics,

with benefit for inflammation[39,40] and improvement in endoscopic score.[41] These studies are not reviewed here because the probiotic component is likely to influence gut microbiota and other measured outcomes, thus obscuring the effect of the prebiotic alone.

Limitations of current studies specifically reporting prebiotic intake in patients with IBD include inconsistency in outcomes, methods used to assess these outcomes, and variations in disease activity. Thus far, identification of a prebiotic that consistently addresses assumedly detrimental changes in microbiota in patients with IBD (e.g., lower *F. prausnitzii*) has not been done in humans. Also, dietary intake was not assessed, thus it is not known whether variation in diet could have affected outcomes. In addition to the lack of available evidence, assumptions about prebiotic consumption to benefit patients with IBD are many. First, IBD risk likely originates early in life; supplementing with prebiotics may modify IBD disease activity, but it is far more effective to create an environment amenable to ideal microbiota development early in life, whether through prebiotic supplementation or modification of other environmental stimuli. Although not emphasized earlier, CD and UC are heterogeneous diseases; it is possible that 1 prebiotic type will not be effective for both CD and UC. In addition to tailoring the prebiotic to the disease type and stage, it is possible that a mixture of prebiotic fibers will be most useful to enhance the functional capacity of a variety of bacteria that may have health benefits for patients with IBD.

Summary

Prebiotics are fermentable carbohydrates with the ability to modify gut microbiota and subsequent metabolites to improve gut health. Results from in vitro and animal studies provide some support for the use of prebiotics to modify a variety of factors, including intestinal-derived inflammation, a key contributor to IBD pathogenesis. Although these studies support prebiotic use in patients with IBD, few prospective, controlled human trials exist. In the studies that have been completed, the prebiotic used varies, making it impossible to provide consensus on its effectiveness. In addition, limited studies exist including functional analyses. It is important to further identify alternative prebiotics with low-bloating characteristics with minimal gas production to provide a tolerable fiber for beneficial modulation of the microbiota, metabolite production, and inflammation reduction. In addition, more needs to be known about mechanisms behind IBD and the specific bacteria involved before targeted prebiotics can be effective.

Disclosures: B.R. Hamaker is a part owner of Nutrabiotix Inc., a company that develops fibers with prebiotic capacity. Dr B.R. Hamaker's involvement in this company has no influence on his statements regarding prebiotic effectiveness for inflammatory bowel disease.

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