Does Modification of the Large Intestinal Microbiome Contribute to the Anti-inflammatory Activity of Fermentable Fiber?

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Abstract

Fiber is an inadequately understood and insufficiently consumed nutrient. This review examines the possible causal relationship between fiber-induced microbiome changes and the anti-inflammatory activity of fiber. To demonstrate the dominant role of fermentable plant fiber in shaping the intestinal microbiome, animal and human fiber-feeding studies are reviewed. Using culture-, PCR- and sequencing-based microbial analyses, a higher prevalence of *Bifidobacterium* and *Lactobacillus* genera was observed from the feeding of different types of fermentable fiber. This finding was reported in studies performed on several host species including human. Health conditions and medications that are linked to intestinal microbial alterations likely also change the large intestinal nutrient environment. The unique gene clusters of *Bifidobacterium* and *Lactobacillus* that enable the catabolism of plant glycans and the ability of *Bifidobacterium* and *Lactobacillus* to reduce the colonization of proteobacteria probably contribute to their prevalence in a fiber-rich intestinal environment. The fiber-induced microbiome changes could contribute to the anti-inflammatory activity of fiber. Although most studies did not measure fecal microbial density nor total daily fecal microbial output (colon microbial load), limited evidence suggests that the increase in intestinal commensal microbial load plays an important role in the anti-inflammatory activity of fiber. Various probiotic supplements including *Bifidobacterium* and *Lactobacillus* showed anti-inflammatory activity only in the presence of fiber that promoted microbial growth as indicated by increasing plasma short-chain fatty acids. Probiotics alone or pure fiber administered under sterile conditions showed no anti-inflammatory activity. The potential mechanisms that could mediate the anti-inflammatory effect of common microbial metabolites are reviewed but more *in vivo* trials are needed. Future studies including simultaneous microbial composition and load measurements are also important.
Key words:
fiber; microbiome; *Bifidobacterium*; inflammation; intestinal commensal microbial load
Introduction

The definition and classification of fibers have been reviewed previously (1). Although these plant-based compounds have diverse structural features, none of them can be digested in the small intestine by mammalian digestive enzymes. In the anaerobic large intestinal lumen, some of them are known to be degraded by microbial enzymes to promote commensal bacterial growth (2,3). This unique property of fiber to undergo fermentative degradation in the large intestine gave rise to nomenclature such as “fermentable fiber” and “prebiotics” (2,4,5). Fermentable fibers are mostly soluble in water and thus the term of soluble fiber is also used. Chemically, fermentable fiber can be glucose-based (polydextrose and resistant starch), fructose-based (fructo-oligosaccharide and inulin), galactose-based (galacto-oligosaccharide and agaro-oligosaccharide) or hexose derivatives such as D-galacturonic acid polymer (pectin) or galactose and mannose-based polymer (guar gum). Some pentose carbohydrates such as arabinose and xylose-based arabinoxylan are also fermentable fiber.

Fiber is essential for optimal health based on its unique ability to increase fecal volume and decrease fecal transit time (6,7). Total fiber is included in the US Dietary Reference Intake tables (8). It is not certain though whether a special requirement for fermentable fiber is needed. One limitation in understanding fiber nutrition is the lack of a comprehensive database for fiber, especially soluble/fermentable fiber, in food items. Using purified fermentable fiber of different structural features, anti-inflammatory activity has been observed in human and animal model studies (9). Inflammation is the cause and consequence of many diseases (10-16) so fiber can also have an impact on health outside the gastrointestinal system. Indeed, anti-inflammatory activity was observed with fibers under different physiological/pathological conditions (9).
However, the mechanism leading to the anti-inflammatory activity of fiber is not clear. Is it possible that this activity of fiber relates to the promotion of certain microbes in the large intestine? If this is the case, we can then make several predictions. First, we expect similarities among various fermentable fibers in their ability to modify the intestinal microbiome. This would explain why fermentable fibers with different structural features can show similar anti-inflammatory activity (9). Secondly, the presence or absence of fermentable fiber should serve as an important modifier of the intestinal microbiome. This is consistent with the anti-inflammatory activity of fermentable fiber having been observed under many different physiological/pathological conditions (9). Thirdly, microbiome changes by themselves, such as an increase in the target bacterial taxonomic units, should also exhibit anti-inflammatory activity independent of fiber supplementation. This would support the hypothesis that a unique microbiome mediates the anti-inflammatory effect of fermentable fiber. Lastly, specific microbial metabolites should also exhibit anti-inflammatory activity. This last suggestion would provide a possible mechanism for the hypothesized causal relationship between a unique microbiome and the anti-inflammatory activity of fermentable fiber. The purpose of this review is to use the relevant literature to address the above four points.

Current status of knowledge

1. Intestinal microbiome and the method of analysis

The presence of an extensive, mostly anaerobic, microbial population in the large intestine of healthy humans and animals has long been recognized. This symbiotic relationship is important for host health as germ-free animals show poor intestinal development (17). The earliest method for the analysis of the intestinal microbiome depended on the ability to culture isolated microbes
The development of sequence-based analyses such as PCR and restriction fragment length polymorphism increased the capability to quantify microbes that are difficult to culture. Further development of 16S ribosomal RNA sequence-based operational taxonomic unit (OTU) analysis allowed a more complete understanding of the host-bacteria symbiotic relationship. The advancement in DNA sequencing technology and data analysis algorithms has led to the application of 16S-independent shotgun metagenomic sequencing for comprehensive OTU analysis.

OTU analysis has both strengths and limitations. Because of its sequence-driven comprehensive coverage at multiple taxonomic levels, it is better at predicting bacterial diversity than earlier techniques. However, because most intestinal bacterial species have not been cultured and sequenced, OTU analysis is still limited in resolving diversity below the genus level. Moreover, OTU analysis by itself gives information on the relative prevalence but not the absolute quantity of different genera. Though the older methods of analyses detect only a limited fraction of the intestinal microbiome, the data can be expressed as per gram physiological sample and thus provide information on the absolute amount of a particular bacterial genus/species.

Shotgun metagenomic sequencing of 1,135 fecal samples from a Dutch cohort revealed the presence of DNA from all four domains: bacteria, archaea, viruses and non-host eukaryotes. Among the sequences amplified from the fecal samples, 97.6% came from bacteria, consistent with the previous conclusion on bacterial dominance in the intestinal microbiome.

Multiple factors influence the composition of an individual’s intestinal microbiome. For example, a maternal contribution to the initial microbiome has been observed. The first stool of newborn mice has been shown to have genetically similar microorganisms to those that were orally inoculated in their pregnant mothers. The exact route of maternal-fetal transmission is
not clear. The birthing process can further modify the intestinal microbiome. Vaginally delivered humans harbored bacteria found in their mother’s vaginal environment whereas skin microbiome contributed more to newborns delivered through cesarean section (26). However, the effect of delivery is not permanent (23). Living environment further modifies the intestinal microbiome. For example, pigs raised in an outdoor environment had a significant higher abundance of Firmicutes, particularly *Lactobacillus*, than those raised indoors (27). As expected, even subtle differences in host genetic background can influence the intestinal microbiome as shown in studies where different inbred strains of mice were raised on the same diet and in the same environment (28,29). Nevertheless, these studies also reported a crucial effect of diet on the intestinal microbiome.

2. Intestinal microbiome changes upon fiber supplementation in animal studies

Results from animal studies on the effect of fermentable fiber feeding are summarized in Table 1. Observations from *in vitro* fiber fermentation were not included because of their limited relevance to the complex fermentation occurring in the human large intestinal lumen. Also excluded were studies using ruminants, aquatic or avian species, studies with confounding factors including studies with disease models, studies without detailed dietary information, and studies with supplements that simultaneously introduced other nutrients.

Among the animal studies summarized in Table 1, cecal and fecal samples were primarily used to determine the intestinal microbiome although some studies also analyzed intestinal contents. Analytical methods ranging from culture to OTU analysis were used. It is important to point out that only sequencing-based analyses have the ability to cover the entire microbiome.
and thus be useful for performing comprehensive diversity analyses. Other earlier methods can only quantify selective taxonomic groups where the analytical tools are available.

Three different types of microbiome-related observations could be found in the studies in Table 1: prevalence, diversity, and density. Prevalence describes the quantitative presence of a particular taxonomic group within a fixed amount of biological sample. Diversity can be used to describe the fiber feeding-induced microbial population pattern changes, if any. Density is defined as the total microbes within a fixed amount of cecal, colon or fecal sample. A decrease in density does not necessarily reflect a reduction in total microbes at an anatomical site. For example, in the only study that measured total bacteria in the biological sample from each animal, an increase in the cecal total microbial load was reported despite a lower cecal microbial density after fiber-feeding (30). Without the information on daily total fecal output in different groups, comparing fecal microbial density may not be useful.

Of the studies summarized in Table 1, only 6 studies used the sequencing-based analysis of prevalence so the results on prevalence are incomplete. Nevertheless, most studies found an increased presence in the phyla Actinobacteria (especially the genus *Bifidobacterium*), and/or Firmicutes such as *Lactobacillus* after fiber feeding. Some studies also observed a decrease in Clostridiaceae or *Clostridium*. Two studies reported a decrease in *E. coli*, a member of Proteobacteria although two others found an increase in Proteobacteria.

The review summarized in Table 1 further uncovered several important pieces of information. The studies included here were done using different basal diets and fermentable fiber supplementations given to male and female mice and rats of different strains as well as pigs of different breeds. The ages of the animals ranged from newly weaned to adult (Table 1, Host).

The consistent outcome of increasing *Bifidobacterium* and *Lactobacillus* suggests that age,
gender and host genetic background do not alter the microbiome response to fermentable fibers. Although one study lasted for over 100 days, a few studies found similar effects after two weeks of fiber feeding (Table 1, Duration).

Because of the differences in substrate and oxygen availability along the gastrointestinal tract, it is expected that microbial composition varies among different parts of this tract (31,32). Cecal samples and feces show different physical characteristics, the former freely dissociate from each other while the latter tend to aggregate (unpublished observation from the author’s lab). However, based on the analyses done on cecal, colonic and fecal samples in Table 1, it seems that the microbiome pattern change in feces represents the microbial response to fiber in the intestine reasonably well. Of the 21 studies in Table 1, an increase in Actinobacteria/Bifidobacterium in response to fermentable fiber was observed in four studies that examined the combined cecal and ileal/colonic contents (33-36); two studies that examined cecal content (30,37); and three studies that examined feces (38-40). Also, of the 21 studies in Table 1, an increase in Lactobacillaceae/Lactobacillus in response to fermentable fiber was observed in two studies that examined the cecal and ileal/colonic contents (34,35); three studies that examined cecal content (41-43); and five studies that examined feces (38,39,44-46). In a preliminary study using OTU-based Procrustes analysis of microbiomes (47), the 6 pairs of cecal-fecal samples from mice that were fed an AIN-93G diet or an AIN-93G diet supplemented with 5% inulin showed a modest cecal-fecal correlation (p=0.0445) (unpublished observation from the author’s lab). The consistency among these results supports the conclusion that fecal samples provide reasonably good representation at the genus level for the response of large intestinal microbiome to fermentable fiber.
Studies in animal models reveal some gaps in our knowledge of dietary regulation of the intestinal microbiome. A few recent OTU-based studies included the diversity analysis of the microbiome. Although supplementation with sugar beet pulp plus inulin was found to increase intestinal microbiome diversity if added to a diet with low fermentable fiber (48), the addition of purified fiber to a plant-based diet did not seem to have the same effect (37,49). In fact, dietary supplementation with purified fiber tends to decrease microbiome diversity (45,49,50). It is not clear whether the changes in diversity as well as prevalence were due to preferential changes in the rate of growth or in the loss of certain bacteria. Understanding the basis of the observed microbiome changes requires information on microbial density and total load. This information was lacking in the diversity studies discussed above.

Microbial density of cecal or fecal samples was measured in some other studies where microbial diversity was not analyzed (Table 1) (30,33,35,38,39,41,42,51,52). When fermentable fiber was added to a diet lacking well-fermented fiber, microbial density generally increased (33,38,51). In contrast, the addition of fermentable fiber to a plant-based or fiber-rich diet did not increase microbial density probably because basal microbial density was already high (30,33,35,38,39,41,42,51,52). One study weighed the total cecum content and thus allowed the calculation of the total cecal microbial load. Although fiber addition to a high fat diet led to a decrease in the microbial density of cecal samples in that study, the total microbial load in the cecum increased (30). In this case it seems that a preferential expansion of *Bifidobacterium*, *Prevotella*, and *Roseburia* led to the changes in the composition of the microbiome. Although fecal samples have been used most frequently for microbiome analysis, no studies have reported the total 24-hr fecal bacterial load. Such measurements could provide information on the daily bacterial turnover in the large intestine.
An important question that still needs to be addressed is the time-dependent effect of fiber. There was only one study where fecal samples were cultured to quantify *Lactobacillus* along a 28-day fiber supplementation time course (44). The results suggest the presence of adaptive changes: an increase in *Lactobacillus* that peaks at 2-3 weeks of fiber supplementation followed by gradual decrease to the control level by 28 days. No information is available on the presence or absence of adaptive changes among other members of the microbiome nor on microbial diversity, density nor load.

3. Intestinal microbiome changes due to increased fiber intake in human studies

Overall, human studies lack dietary control prior to or even during trials. However, if the anti-inflammatory effect of fiber is related to its ability to change the intestinal microbiome, we expect to see similar effects of fiber in the human intestinal microbiome as is observed in animal studies. Table 2 summarizes human studies that have provided fiber intake information. As with the animal studies in Table 1, human studies with potential confounding factors were excluded including human subjects with diseases, studies without dietary information, and studies with fiber supplements that also introduced (53) non-fiber nutrients.

The three measures of microbiome-related observations (prevalence, diversity, and density) follow the same definitions as used in Table 1. Included in Table 2 are results of a range of studies from cross-sectional to the most stringent randomized double-blind placebo-controlled crossover study design. The subjects in Table 2 had a wide range of ages and were given different fermentable fibers for a duration ranging from 14 days to 6 months. With the exception of one study where samples were collected during colonoscopy, all other studies utilized fecal samples (Table 2). Overall, the effects of fermentable fiber on the intestinal microbiome are
remarkably similar between the animal studies summarized in Table 1 and the human studies summarized in Table 2.

Most studies in Table 2 found an increase in the genera of *Bifidobacterium* and *Lactobacillus* upon fiber supplementation while the relative presence of the phyla of Bacteroidetes and Proteobacteria decreased in some studies. This pattern of changes was also observed in the single study analyzing colonoscopy samples (54). In the two studies that included observations on microbiome diversity, diversity was either unchanged or increased by fiber supplementation (53,55). Fiber supplements also either increased or had no effect on microbial density (54,56-65).

No human studies determined the total microbial load and thus it is not possible to conclude whether the microbiome alterations were results of preferential growth among some genera.

Some adult fiber supplement studies assessed the intestinal microbiome at more than one time point. Consistent effects among several time points up to 16 weeks were reported (57,59,62,64). In a multigenerational study using germ-free mice colonized with human intestinal microbiomes via oral gavage of feces, dietary fiber consistently increased the presence of Clostridiales and decreased the presence of Bacteroidales based on an OTU analysis (66)

Two studies examined the dose-dependent effect of fiber. A stepwise increase in the dose of galactooligosaccharide from 0 g to 10 g per day led to a gradual increase in *Bifidobacterium* and a gradual decrease in *Bacteroides* in some individuals (62). Similar to many other biological processes, the effect of fiber on the microbiome was saturatable. Doubling the soluble corn fiber supplement from 10 g/day to 20g/day for a month did not lead to much additional change in the microbiome (55).

In the only study that collected colonic content during colonoscopy (54), proximal and distal colonic samples had similar microbiome changes upon fiber supplementation. This is not
surprising based on the similarity between cecal and fecal microbiomes in response to fiber supplementation in animal studies (Table 1).

4. Changes in the nutrient environment can explain other microbiome changes

A variety of factors such as non-fiber dietary component, development and aging as well as disease and medication have also been reported to change the intestinal microbiome. Could those factors cause changes in the colonic nutrient environment? If so, could the nutrient environmental changes explain the observed microbiome changes? Table 3 is a summary of some additional microbiome observations and the possible role of nutrient environment in each case.

The first factor examined in Table 3 is dietary pattern. The first three mouse-feeding studies (67-69) included macromolecules that cannot be digested and absorbed in small intestine. These macromolecules would have appeared in the large intestine as microbial nutrients and thus affected microbiome composition. The increase in both the prevalence of Bifidobacterium and the microbiome diversity upon fruit or nut ingestion is similar to the outcome of fiber feeding shown in Tables 1 and 2. This is consistent with the fact that fruits and nuts are two known sources of plant fiber. Based on the consistent outcome among fiber, fruit and nut studies, we would have expected to see a decrease in the prevalence of Bifidobacterium and microbiome diversity upon switching to a low fiber diet. This was indeed observed in several high-fat (low-fiber) diet studies (67,70,71).

Relevant observations were also made in several infant development and elderly studies (Table 3, part 2). Although no detailed dietary information was available, the outcome can also be at least partly explained by nutrient availability to the microbes in the large intestine. The
composition of breast milk is expected to vary among women. Also, different preparations of infant formula have different compositions. As a result, fecal Bifidobacterium content was not consistently higher in breast-fed infants in these studies (72-74). In contrast, infant twins (identical or fraternal) living in the same household with similar dietary exposure have similar microbiomes (75). Elders in nursing homes have reduced exposure to environmental microbes because of their restricted mobility. This limitation would also reduce their exposure to a wide variety of food and thus encourage the development of similar and lower diversity intestinal microbiomes within the same facility (76).

Medical conditions or the use of medications to treat these conditions could indirectly change the intestinal microbiome due to alterations in the diet as well as intestinal environment as described in the last part of Table 3. Inflammation can lead to tissue damage and the excessive presence of mucin and endogenous cellular components in the lumen (77). These cellular components are chemically different from plant-based fiber and serve as a carbon source for certain intestinal microorganisms (78-82). In patients using proton pump inhibitors, increased stomach pH can reduce protein digestion in the stomach and small intestine (83,84). The appearance of this undigested dietary protein in the colon then changes the large intestinal nutrient environment (85) and thus can affect the microbiome. Excessive protein intake in normal individuals was also found to affect the intestinal microbiome (86). Increased stomach pH also allows a better survival of oral bacteria passing through on their way to the lower gastrointestinal tract (87).

5. In vitro studies on the potential mechanisms leading to the bacteria population changes following fiber feeding
Do changes in the microbiome always involve the acquisition of new bacterial strains from
the environment? In studying the infection by toxin-producing *Clostridium difficile*, it was
concluded that the pathological strains were initially present in the healthy intestine as minority
members of the community and expanded when the intestinal environment became favorable
(88,89). The finding suggests that microbiome changes in response to fiber could also be the
results of preferential population expansion. This is consistent with the observation that
fermentable fiber supplementation leads to similar intestinal microbial responses in humans and
animals although these host organisms reside in different environments (Tables 1 and 2).

Two possible factors contribute to the preferential expansion and thus higher prevalence of
*Bifidobacteria* and *Lactobacillus* upon fiber feeding. One may be that their genomes evolved to
utilize fermentable fibers (90,91). *Bifidobacterium* possesses unique gene clusters that enable the
catabolism of glycans and glyco-conjugates (92). The ability of *Lactobacillus* to use plant
materials and its niche adaptability have recently been reviewed (93). In contrast, Proteobacteria
such as *E. coli* ferment simple sugars and amino acids preferentially (94). Some members of
*Fusobacterium* are predominantly non-saccharolytic (82). *Desulfovibrio* specializes in the
reduction of sulfur found in protein and animal mucopolysaccharides (95,96). Thus dietary
supplementation with complex fermentable fiber does not give *E. coli*, *Fusobacterium*, nor
*Desulfovibrio* a growth advantage. In fact, a decrease in *E. coli*, *Fusobacterium*, and
*Desulfovibrio* were observed in the fecal samples of some human subjects after increased fiber
intake (Table 2).

The second factor contributing to the preferential expansion of *Bifidobacteria* and
*Lactobacillus* is an interaction among bacterial species. The increased prevalence of
*Bifidobacteria* and *Lactobacillus* upon fiber feeding may further reduce the colonization by
Proteobacteria. There may be direct competition in colonization as shown in a germ-free mouse study using an artificial bacterial community to restrict *Vibrio cholera* colonization (97). In the literature, bacterial metabolites such as short-chain fatty acids (SCFA), have often been considered as growth regulators of the intestinal microbiome (98). Some probiotic culture supernatants were found to have bactericidal activity against intestinal *E. coli* (99) although these supernatants failed to reduce the adhesion of *E. coli* to intestinal epithelial cells and enhanced the biofilm formation of *E. coli*.

6. Evidence that fiber-induced microbiome changes exhibit anti-inflammatory activity

The anti-inflammatory activity of structurally different fermentable fibers has been reviewed (9). If the microbiome change upon fiber feeding contributes to the anti-inflammatory activity, we expect similar microbiome changes to show anti-inflammatory activity in the absence of fermentable fiber. Indeed, in cell studies anti-inflammatory activity of probiotic *Bifidobacterium* and *Lactobacillus* was observed in both macrophage (100-102) and intestinal cells (103,104). However, the relationship between so called “beneficial bacteria” and the anti-inflammatory activity is not unique. Even *Escherichia coli* M17 and *Saccharomyces boulardii* were found to have anti-inflammatory activity in cultured macrophage and dendritic cells, respectively (105,106).

The bacterial families and genera that were enriched upon fermentable fiber supplementation (Tables 1 and 2) overlap with those found in commercial probiotics (107). To delineate the mechanisms behind the anti-inflammatory activity of fermentable fiber, the effects of probiotics are reviewed below. Relevant publications are divided into two sets based on the nature of the control diet. The first set includes those using a fermentable fiber-containing diet such as a
normal human diet or commercial plant-based rodent chow. The second set includes those using purified standard rodent diets (AIN-76 or AIN-93) which contain only poorly fermented cellulose. Some studies even compared the anti-inflammatory effects of prebiotics (fermentable fiber), probiotics (purified bacteria) and synbiotics (pre- plus pro-biotics).

Anti-inflammatory activity was consistently found in probiotic studies done in the presence of fermentable fiber. A chow-fed neonatal mouse study examined the effects of pre- pro- and syn-biotic oral supplementation on pathogen-mediated intestinal inflammation (108). Both prebiotic inulin and *Lactobacillus acidophilus* had anti-inflammatory activity and synbiotic treatment led to a further reduction of inflammation. Probiotic *Bifidobacterium bifidum* PRL2010 (109), *Lactobacillus reuteri* (110), or *Lactobacillus casei* BL23 (111) reduced chemical-induced colitis or lesions in chow-fed mice. Chow-fed rats also showed reduced inflammation following chemical-induced colitis when probiotic *Escherichia coli*, Nissle 1917 was given (112). Nissle 1917 similarly showed anti-inflammatory effects in chow-fed mice subjected to lipopolysaccharide-induced sepsis (112). Another probiotic strain *Lactobacillus fermentum* also reduced lipopolysaccharide-induced inflammatory responses in chow-fed mice (113). In a trial of ulcerative colitis patients, synbiotic therapy (*Bifidobacterium longum* plus inulin) led to reduced inflammation (114). The anti-inflammatory effect of *Lactobacillus* can also be observed in chow-fed IL10-knockout mice that were prone to colitis (100,115) and chow-fed rats with gastric lesions (116,117). A diet containing high levels of poorly fermented cellulose (30%) also showed microbial growth-dependent anti-inflammatory effect in mouse models (118).

In contrast, in studies involving purified diets with only 5% cellulose, anti-inflammatory effects of probiotics were not observed. Synbiotic supplementation of AIN-76 diet with probiotic *Bifidobacterium lactis* and prebiotic resistant starch resulted in protection against chemical-
induced colon carcinogenesis in rats (119). This effect was not observed when the AIN-76 diet was supplemented with \textit{B. lactis} alone (119). Resistant starch alone resulted in limited protection (119). A similar rat model was used to demonstrate the anti-tumorigenic activity of prebiotic inulin and a probiotic mix (\textit{Lactobacillus rhamnosus} and \textit{Bifidobacterium lactis}) in a modified AIN-76 diet (120). While inulin by itself offered some protection, probiotics by themselves had no effect (120). In rats given an AIN76-based high fat/low cellulose diet, inulin and synbiotic supplementations both showed anti-inflammatory activity but probiotic supplementation alone (\textit{Lactobacillus rhamnosus} and \textit{Bifidobacterium lactis} in combination) had no effect (121). In a mouse study using AIN-93 diet, substituting standard casein or whey protein with ADM soy protein isolate resulted in anti-inflammatory activity (122). Because the soy protein isolate contains significant amount of dietary fiber, fiber may have contributed to the anti-inflammatory effect observed in this study. Adding probiotic \textit{Lactobacillus rhamnosus} GG to the soy diet did not lead to further reduction of chemical-induced colon inflammation. \textit{Lactobacillus rhamnosus} GG, by itself, also did not have anti-inflammatory effect in an AIN-93-based diet (122). \textit{In vitro} under sterile conditions, pure fiber showed little protection in the fungal toxin-induced inflammatory responses of cultured intestinal cells (123).

The contrasting outcomes of \textit{in vivo} probiotic supplementation studies in the presence and absence of fermentable fiber as summarized above provide some insights on the anti-inflammatory activity of fermentable fiber. Firstly, the ability of fermentable fiber to promote the growth of bacteria is important as probiotic supplementation of a purified diet with 5% poorly fermented cellulose had no effect. When indicators of bacterial growth such as total intestinal content of SCFA or deconjugation of primary bile salts were measured, these indicators only increased in the presence of fermentable fiber (119,124). Probiotics by themselves had no effect
on SCFA or bile salts (119,124). Secondly, different probiotics all have similar protective
effects. This observation suggests that the anti-inflammatory and anti-tumorigenic effects
observed were not unique to a particular species or even genus of bacteria. In fact, even
commercially cultivated Gram-negative *E. coli* showed protective effects (112).

**7. The importance of total bacterial load in the colon**

Recent sequencing-based intestinal microbiome analyses have made significant discoveries
pertaining to microbial composition and diversity (125-128). These two areas have thus become
a focus of health impact. However, unique composition and diversity may not be the only
important factors in a healthy microbiome. Equally healthy populations were found to have
different microbial composition and diversity (125,126). As reviewed above, anti-inflammatory
effects can be observed by the supplementation of different probiotics as long as a favorable
growth condition, i.e. abundance of fermentable fiber, is available. *In vitro* analysis has directly
linked glycan substrate degradation by *Bacteroides* with polysaccharide capsule biosynthesis
(129). Thus, it is possible that simply having a higher total commensal microbial load in the
colon is important for health. Unfortunately, very little information is available on this perhaps
because of practical difficulties in quantifying total microbial load especially in human studies.

Several pieces of indirect evidence support the importance of total commensal microbial load
in health promotion. Intestinal microbial losses seen after acute secretory diarrhea were similar to
those seen in *Vibrio cholera* infection (130). Antibiotic treatments that lead to the disruption of
the intestinal microbiome (131,132) are a major cause of recurrent *Clostridium difficile* infection
(133). Microbiome transplantation using feces from healthy individuals can cure *Clostridium*
difficile infection with no specific requirement for a particular microbial composition or diversity (134-136).

Some limited evidence also supports that the anti-inflammatory activity of fiber may come from its ability to increase the intestinal commensal microbial load. One rodent study in Table 1 found an increased total microbial load (total bacterial DNA in daily feces) after dietary supplementation with the fermentable fiber, arabinoxylan (30). Three other rodent studies in Table 1 (33,38,51) and two human studies in Table 2 (57,61) found an increased fecal bacterial density (bacteria DNA/g feces) after feeding the fermentable fibers, fructo-oligosaccharide, galacto-oligosaccharide or guar gum. The above four types of fermentable fibers were all found to have the anti-inflammatory activity (42,50,108,120,121,137,138).

To further test the physiological importance of total commensal microbial load in the large intestine, future studies on fiber and microbiome need to include the measurement of 24-hour fecal microbial output and mean fecal microbial DNA density.

8. The possible role of bacterial metabolites in the anti-inflammatory activity of fermentable fiber

If active microbial growth is needed for the anti-inflammatory effect of fermentable fiber as summarized in sections 6 and 7, could certain microbial metabolites contribute to this anti-inflammatory activity? Since the anti-inflammatory effects of fiber were also observed in non-GI tissues (9,139), microbial metabolites that circulate throughout the body could be important. Intestinal microbes have unique as well as shared metabolic pathways with their hosts. A wide range of chemicals have been both predicted computationally and isolated from intestinal microbiomes (140,141). These bacterial metabolites can be detected in the host blood and urine.
The possible anti-inflammatory activity of many of these bacterial metabolites have been studied using cultured cells or animal models (144,145).

Fermentable fiber can directly contribute to the production of these metabolites by serving as substrates or indirectly by altering the microbiome and thus affecting the degradation of non-fiber. In this review, the focus is on bacterial metabolites that are known to be affected by fiber and have established molecular targets for their physiological activity. The list of such metabolites may expand in the future since the physiological significance of bacterial metabolites on the host is still being actively examined.

SCFA are the most well studied bacterial metabolites. They can be made from fermentable fiber by many commensal microbial species and probiotics. In fact, the plasma level of SCFA is a general indicator of overall intestinal microbial fermentation (51,119,146,147). When the levels of plasma SCFA were measured, studies that showed an anti-inflammatory effect of probiotics had higher levels of plasma SCFA independent of the microbial genus and fermentable fiber source (50,119,120). At the molecular level, SCFA activate several G-protein-coupled cell membrane receptors and inhibit several histone deacetylases (148-152). The immune modulatory role of SCFA in the intestine has been directly demonstrated in mouse models and appears to be mediated through the molecular targets mentioned above (153,154). SCFA also reduce the severity of transplantation-induced graft-versus-host disease (154). Additionally, they reduce the level of pro-inflammatory cytokines and the severity of colitis in a Treg-dependent manner (153).

Other organic acids produced during fiber fermentation have also been subjects of interest. For example, fecal and plasma lactate levels rose when rats were given fermentable fiber (155-158). Organic acids can also serve as ligands of some G-protein coupled cell membrane...
receptors (159). However, the increase in organic acids often coincides with the increase in SCFA after fiber feeding. Also, host enzymes using non-fiber nutrients can produce organic acids. Hypothesis-driven studies are needed before the physiological importance of these bacteria-produced organic acids can be concluded.

The metabolites of bile salts may also contribute to the anti-inflammatory activity of fiber. The wide-spectrum of biological activities of bile acids have recently been reviewed (160,161). Primary bile salts are made in the liver and secreted into the small intestine. After serving their function in the absorption of dietary fat, taurine- and glycine-conjugated bile salts mostly return to the liver through transporter-mediated enterohepatic cycling in the terminal ileum (162). In the colon, leftover bile salts can be deconjugated by bacterial bile salt hydrolase found mainly in Gram-positive intestinal bacteria including the probiotics *Lactobacillus* and *Bifidobacterium* (161,163,164). In a mouse study, dietary inulin or inulin plus *Bifidobacterium*, but not *Bifidobacterium* by itself, can promote bile salt deconjugation (124).

The deconjugation reaction, by removing the growth-promoting bile salts and generating the growth-inhibiting free bile acids, can directly limit the growth of *Clostridium difficile* which is a leading cause of antibiotic-associated diarrhea (165,166). Bile salt deconjugation also allows the conversion of hepatic primary bile acids to secondary bile acids by bacterial enzymes (162). Secondary bile acids have higher affinity for bile acid receptors including nuclear farnesoid X receptor (FXRα) and the cell membrane G-protein-coupled receptor TGR5 (160,161). Bile acids additionally have affinity for the nuclear pregnane X receptor (PXR), which also binds to a wide spectrum of other endogenous and exogenous chemicals (167). The PXR gene has FXR binding sites. Feeding mice with bile acid led to an FXR-dependent induction of PXR expression (168). Several lines of evidences support an anti-inflammatory activity of bile acids in the liver and
intestine. Bile acids showed anti-inflammatory activity in cell studies (160,161). Patients with inflammatory bowel diseases showed altered bile acid profiles (160,161). Finally, mice with a FXRα or TGR5 gene knockout suffered from increased inflammation in the liver and intestine (160). However, in vivo rescue experiments using bile acids have not been done.

Colonic bacteria can degrade dietary or endogenous tryptophan to unique indoles including skatole (169). These metabolites can bind to the nuclear aryl hydrocarbon receptor AHR. AHR activation or gene knockout can promote or suppress inflammatory responses and have been linked to beneficial or harmful biological effects, respectively (169,170). Two recent studies examined the effect of dietary fiber on tryptophan catabolism in the intestine. Fiber-rich soybean husk supplementation to dogs led to a change in the intestinal microbiome with an increase in fecal SCFA and a decrease in fecal indole and skatole (157). SCFA and indole are likely produced by different intestinal microbes that use different carbon sources (171). Patients with end-stage renal disease and restricted fruit and vegetable intake exhibited the expansion of indole-forming microbes and reduction of SCFA-producing microbes (171). Because AHR has a wide spectrum of ligands, the contribution of bacteria-produced tryptophan metabolites likely depends on other environmental and dietary conditions. The physiological importance of tryptophan metabolites is thus far from conclusive.

Conclusions

Fiber is a required nutrient with the US Dietary Reference Intake of fiber at ~30 g/day for adults. In developed countries, the ingestion of fiber is generally low relative to the recommendation (172). A US National Health and Nutrition Examination Survey found that only 10.3% of adults have sufficient fiber intake and the average intake is less than 50% of the daily
requirement (173). The anti-inflammatory activity of fiber has been studied extensively (9). In this review, the ability of various fermentable fibers to increase *Bifidobacteria* and *Lactobacillus* and likely the total microbial load in the intestine is hypothesized as the mechanism leading to the anti-inflammatory activity of fermentable fiber. Diets containing only poorly fermentable fiber lead to a reduced fecal microbial content and cannot support the growth of probiotics such as *Bifidobacteria* and *Lactobacillus*. These low fermentable fiber-diets also fail to show an anti-inflammatory effect. The emerging nutritional importance of fermentable fiber supports the need to promote fiber ingestion and a specific recommendation for a daily fermentable fiber requirement.
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Increases Bifidobacteria, but Not Insulin Sensitivity, in Obese Prediabetic Individuals.


Table 1. Summary of changes in the intestinal microbiome after increasing the intake of fermentable fiber in animal studies

<table>
<thead>
<tr>
<th>Host (Age, sex, N/group)</th>
<th>Basal diet</th>
<th>Treatment</th>
<th>Duration* (day)</th>
<th>Effect of fiber on microbiome</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Mouse</strong></td>
<td></td>
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<tr>
<td>BALB/c (3 wk, M, 8-11)</td>
<td>No fiber diet</td>
<td>Supplement 3% FOS/d in tap water</td>
<td>14<strong>C</strong></td>
<td>Bifidobacterium(^A) (gum arabic or XOS had no effects)</td>
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<td>NA</td>
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<tr>
<td></td>
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<td></td>
<td></td>
<td>(33)C</td>
</tr>
<tr>
<td>C57/BL/6J (9 wk, M, 8)</td>
<td>Purified 35% fat, 26% CHO diet</td>
<td>10% arabininoxylan mixed with 90% Basal diet</td>
<td>28<strong>E</strong></td>
<td>Bacteroids/Prevotella(^B) Bifidobacterium(^A) Roseburia(^F)</td>
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<td>NA</td>
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<td>↓↑ (total)</td>
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<td>(30)G</td>
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<tr>
<td>ICR (4-6 wk, F, 10)</td>
<td>AIN-93M 10% rice bran into Basal diet</td>
<td>28<strong>F</strong></td>
<td>Lactobacillus(^F) (from d 11-25)</td>
<td>NA</td>
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<tr>
<td></td>
<td>2% guar gum diet</td>
<td>10% guar gum into Basal diet</td>
<td>14<strong>F</strong></td>
<td>E. coli(^F)</td>
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<td>(51)S</td>
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<tr>
<td>C57/BL/6J (10 wk, M, 10)</td>
<td>Cereal-based 4% fiber diet</td>
<td>Supplement 0.3 g FOS/d in water (~10% of diet)</td>
<td>56<strong>C</strong></td>
<td>Actinobacteria Proteobacteria Verrucomicrobia</td>
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<td>Firmicutes</td>
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<td>(37)S</td>
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<tr>
<td>BALB/c (8 wk, F, 6)</td>
<td>AIN-93G 7.5% resistant maltodextrin into Basal diet</td>
<td>7.5% resistant maltodextrin into Basal diet</td>
<td>14<strong>C</strong></td>
<td>Coriobacteriaceae(^A)</td>
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<td>Clostridiales(^F)</td>
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<tr>
<td>C57/BL/6J (18 wk, obese M,6)</td>
<td>AIN-93G-based 45% fat diet</td>
<td>10% FOS or 10% inulin in Basal diet</td>
<td>28<strong>F</strong></td>
<td>Coriobacteriaceae(^A) Lactobacillus(^F) Verrucomicrobiacea(^F)</td>
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<td></td>
<td>Clostridiales(^F) Ruminococcus(^F)</td>
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<td>(42)S</td>
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<tr>
<td>C57/BL/6N (5 wk, M,8)</td>
<td>32% fat diet, plain water</td>
<td>Basal diet and 3% (w/w) AGOS in drinking water</td>
<td>28<strong>F</strong></td>
<td>Clostridium XVIII(^F) Lactobacillus(^F) Prevotella(^B)</td>
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<td></td>
<td>Clostridium XIV(^F)</td>
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<td>(46)T</td>
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<tr>
<td>C57/BL/6J (4 wk, M,15)</td>
<td>Diet with 45% kcal from fat and supplemented with digestible corn starch</td>
<td>Basal diet with 20% resistant corn starch instead</td>
<td>70(^C)</td>
<td>Lactobacilliaceae(^F) Ruminococcus(^F)</td>
</tr>
<tr>
<td></td>
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<td></td>
<td></td>
<td>Clostridium(^F) Coriobacteriales(^F) Lachnospiraceae(^F) Ruminococcus(^F)</td>
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<td>(43)S</td>
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<tr>
<td></td>
<td>Wistar (adult, M, 4-5)</td>
<td>Rapeseed oil and lard-based high-fat diet</td>
<td>9% pectin or 8% guar gum in Basal diet</td>
<td>21c</td>
</tr>
<tr>
<td></td>
<td>Wistar (4 wk, F, 5)</td>
<td>Purified diet with 5% cellulose</td>
<td>5% FOS replacing cellulose</td>
<td>28c</td>
</tr>
<tr>
<td>Pig</td>
<td>Yorkshire x Hampshire x Landrace (6 wk, MF, 4)</td>
<td>Corn-, Soy-based diet</td>
<td>4% different types of inulin replacing corn starch in Basal diet</td>
<td>35CC</td>
</tr>
<tr>
<td></td>
<td>Duroc x Landrace x Yorkshire (28 d, MF, 5)</td>
<td>Maize-, soy-based diet</td>
<td>10-30% pea fiber replacing 10-30% maize in Basal diet</td>
<td>132C</td>
</tr>
<tr>
<td></td>
<td>DanBred × Duroc (10 d,</td>
<td>Cereal-based diet</td>
<td>2% inulin in Basal diet</td>
<td>40CC</td>
</tr>
<tr>
<td>M, 8) Landrace × Yorkshire (1 d,MF,10)</td>
<td>Commercial milk replacer diet</td>
<td>Milk replacer supplemented with 0.8% GOS</td>
<td>26†</td>
<td>Bifidobacterium‡</td>
</tr>
<tr>
<td>---</td>
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</tr>
<tr>
<td>Seghers Hybrid × Piétrain (28 d,MF,6)</td>
<td>Purified fiber-free diet</td>
<td>5% arabinoxylan replacing corn starch in Basal diet</td>
<td>30‡</td>
<td>Lactobacillus‡</td>
</tr>
</tbody>
</table>

AGOS, agaro-oligosaccharide; d, day; FOS, fructo-oligosaccharide; GOS, galacto-oligosaccharide; XOS, xylo-oligosaccharide; NA, information not available; □, no effect.

*The superscript abbreviation shown after the duration description indicates the sample type used. C: cecal content; CC: cecal and colon content; F: feces; IC: ileum and colon content

†List of bacteria follows the alphabetical order. The superscript abbreviation shown after each indicates the phylum it belongs to. A, Actinobacteria; B, Bacteroidetes; F, Firmicutes; P, Proteobacteria; V, Verrucomicrobiaceae

‡The letter shown after the reference number indicates the method used for microbial analysis. C, CFU determined by plating; G, 16S-rRNA-based denaturing gradient gel electrophoresis; P, quantitative PCR; S, 16S-rRNA-based sequencing and operational taxonomic unit (OUT) analysis; T: terminal restriction fragment length polymorphism.
### Table 2. Summary of changes in the intestinal microbiome after increasing the intake of fermentable fiber in human subjects of various age groups

**OBSERVATIONAL STUDY**

<table>
<thead>
<tr>
<th>Type</th>
<th>Cohort* (N)</th>
<th>Fiber intake measurement</th>
<th>Study population†</th>
<th>Effect of fiber on microbiome</th>
<th>ref‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross-sectional on fibers from different sources</td>
<td>58±13 y old (82)</td>
<td>Self-administered food frequency questionnaire followed by USDA nutrient database</td>
<td>Before non-GI or oncological surgery‡</td>
<td>Clostridia* (fruit, vegetable) Bifidobacterium* (bean)</td>
<td>NA NA</td>
</tr>
</tbody>
</table>

**CLINICAL TRIAL**

<table>
<thead>
<tr>
<th>Type</th>
<th>Cohort* (N)</th>
<th>Treatment</th>
<th>Duration†</th>
<th>Effect of fiber on microbiome</th>
<th>ref‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controlled 64% carbohydrate diet supplement</td>
<td>21-48 y old (8)</td>
<td>15 g/d FOS replacing sucrose in biscuits</td>
<td>45 d, FOS on day 16-30§</td>
<td>Bifidobacterium*</td>
<td>NA</td>
</tr>
<tr>
<td>Controlled 58-64% carbohydrate diet supplement</td>
<td>20-34 y old (11)</td>
<td>4 g/d FOS as supplement in tablet and drink</td>
<td>42 d total, FOS on d 7-32§</td>
<td>Bifidobacterium*</td>
<td>NA</td>
</tr>
<tr>
<td>Supplement</td>
<td>Fiber: 35-72 y old (14), Control: 31-81 y old (15)</td>
<td>Fiber group given a mixture of 2.5 g inulin and 2.5 g FOS supplement three times a day</td>
<td>14 d fiber then 1 d colonoscopy preparation diet^co</td>
<td>Bifidobacterium* Eubacterium* Lactobacillus*</td>
<td>NA</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled</td>
<td>18-45 y old pregnant women: Fiber (17) No (16)</td>
<td>3 g GOS/FOS 9:1 mix or placebo (6 g maltodextrin), 3 times a day in drink</td>
<td>From 24-wk to 37-wk of pregnancy^e</td>
<td>Bifidobacterium*</td>
<td>NA</td>
</tr>
<tr>
<td>Study Type</td>
<td>Age Range</td>
<td>Intervention</td>
<td>Duration</td>
<td>Microbiota</td>
<td>Outcomes</td>
</tr>
<tr>
<td>------------------------------------------------</td>
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<tr>
<td>Randomized double-blind placebo-controlled crossover</td>
<td>64-79 y old (41)</td>
<td>5.5 g/d GOS or placebo (maltodextrin) in water</td>
<td>70 d each with 28 d washout in between $^F$</td>
<td>Bifidobacterium $^A$ Clostridium $^F$ Eubacterium $^F$ Lactobacillus $^F$ Enterococcus $^F$</td>
<td>Bacteroides $^B$ Desulfovibrio $^B$ E. coli $^F$</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled supplement</td>
<td>Healthy formula-fed infant: Fiber (22) No (24)</td>
<td>Infant formula with or without 6 g GOS/FOS 9:1 mix per liter</td>
<td>6 months (From birth to 6 months old) $^F$</td>
<td>Bifidobacterium $^A$</td>
<td>NA NA</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled crossover</td>
<td>20-42 y old (31)</td>
<td>10 g/d very-long-chain inulin or placebo (maltodextrin) in water</td>
<td>14 d low-pre- and probiotic diet and then 21 d each with 21 d washout in between $^F$</td>
<td>Bifidobacterium $^A$ Lactobacillus $^F$</td>
<td>Bacteroides-Prevotella $^B$</td>
</tr>
<tr>
<td>Supplement</td>
<td>21 y old (17)</td>
<td>10 g inulin twice a day</td>
<td>28 d $^F$</td>
<td>Bifidobacterium $^A$</td>
<td>NA NA</td>
</tr>
<tr>
<td>Blind supplement</td>
<td>19-50 y old (18)</td>
<td>0, 2.5, 5, 10 g/d GOS in chocolate chew (sugar and corn syrup in the control chew)</td>
<td>21 d each in rising dose, then 14 d washout $^F$</td>
<td>Bifidobacterium $^A$</td>
<td>Bacteroides $^B$</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled crossover</td>
<td>28±4 y old men (20)</td>
<td>0 or 21 g/d polydextrose or soluble corn fiber in 3 snack bars</td>
<td>21 d each with no washout $^F$</td>
<td>Clostridiaceae $^F$ Dialister $^F$ Faecalibacterium $^F$ Lactobacillus $^F$</td>
<td>Bifidobacterium $^A$ Dorea $^B$ Enterobacteriaceae $^B$ Ruminococcus $^B$</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled crossover</td>
<td>Healthy formula-fed infant: Fiber (53) No (55)</td>
<td>Infant formula with or without 8 g FOS and inulin 1:1 mix per liter</td>
<td>3 months (From birth to three months old) $^F$</td>
<td>Bacteroides $^B$ Enterobacteriaceae $^B$</td>
<td>NA</td>
</tr>
<tr>
<td>Randomized double-blind placebo-controlled crossover</td>
<td>18-65 y old with mean BMI &gt;30 (45)</td>
<td>5.5 g/d GOS or placebo (maltodextrin) in water</td>
<td>84 d each with 28 d washout in between $^F$</td>
<td>Bifidobacterium $^A$</td>
<td>Bacteroides $^B$ Desulfovibrio $^B$</td>
</tr>
<tr>
<td>Study Design</td>
<td>Age (n)</td>
<td>Intervention</td>
<td>Duration</td>
<td>Microbiota</td>
<td>Outcome</td>
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<tr>
<td>Controlled 53% carbohydrate diet randomized double-blind crossover</td>
<td>12-15 y old (24)</td>
<td>0 or 12 g/d soluble corn fiber supplement in 2 meals</td>
<td>21 d</td>
<td>Clostridiales&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>each</td>
<td>Parabacteroides&lt;sup&gt;B&lt;/sup&gt;</td>
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<td>separated</td>
<td>Ruminococcaceae&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>by</td>
<td>Coprococcus&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>7 d</td>
<td>Enterococcus&lt;sup&gt;F&lt;/sup&gt;</td>
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<tr>
<td>Randomized dose-response double-blind crossover</td>
<td>11-14 y old females (28)</td>
<td>0, 10 or 20 g/d soluble corn fiber supplement, ½ in muffin, ½ in drink</td>
<td>28 d</td>
<td>Bifidobacterium&lt;sup&gt;A&lt;/sup&gt;</td>
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<td>(maltodextrin placebo)</td>
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<td>Dialister&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>28 d</td>
<td>Anaerostipes&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>washout</td>
<td>Dorea&lt;sup&gt;F&lt;/sup&gt;</td>
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<td>Ruminococcaceae&lt;sup&gt;F&lt;/sup&gt;</td>
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<tr>
<td>Randomized dose-response double-blind placebo-controlled</td>
<td>19-56 y old (10/group, total 100)</td>
<td>0, 5, 10, 20 g/d HMOs or placebo (glucose) as breakfast drink</td>
<td>14 d</td>
<td>Bifidobacterium&lt;sup&gt;A&lt;/sup&gt;</td>
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<tr>
<td>Supplement</td>
<td>University undergraduate students</td>
<td>48 g/d raw potato starch (50% resistant starch) in 2 meal drink</td>
<td>7 d</td>
<td>Bifidobacterium&lt;sup&gt;A&lt;/sup&gt;</td>
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<td></td>
<td>3 d</td>
<td>Acclimation&lt;sup&gt;F&lt;/sup&gt;</td>
<td></td>
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<tr>
<td>Randomized dose-response double-blind</td>
<td>18-50 yr old (8/group, total 24)</td>
<td>8, 14, 21 g/d soluble corn fiber in 2 beverages</td>
<td>14 d</td>
<td>Bifidobacterium&lt;sup&gt;A&lt;/sup&gt;</td>
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<tr>
<td>Randomized double-blind placebo-controlled</td>
<td>45-70 yr old, BMI 28-40 (44)</td>
<td>15 g/d GOS or placebo (maltodextrin) in 3 meal drink</td>
<td>84 d</td>
<td>Bacteroides&lt;sup&gt;B&lt;/sup&gt;</td>
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<td></td>
<td></td>
<td></td>
<td>Bifidobacterium&lt;sup&gt;A&lt;/sup&gt;</td>
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</tbody>
</table>

FOS, fructo-oligosaccharide; GOS, galacto-oligosaccharide; HMO, human milk oligosaccharides, 2'-O-fucosyllactose, lacto-N-neotetraose, or mix or the two; NA, information not available; □, no effect.

*Cohorts included both genders unless indicated otherwise.

†The superscript abbreviation shown after the study duration description indicates the sample type used. CO, colon content collected during colonoscopy; F, feces

‡List of bacteria follows the alphabetical order. The superscript abbreviation shown after each indicates the phylum it belongs to. A, Actinobacteria; B, Bacteroidetes; F, Firmicutes; FU, Fusobacteria; P, Proteobacteria
The letters shown after the reference number indicate the method used for microbial analysis. C, CFU determined by plating; CH, Human Intestinal Tract Chip; F, 16S rRNA-based FISH (fluorescence in-situ hybridization) analysis; G, 16S-rRNA-based denaturing gradient gel electrophoresis; P, quantitative PCR; S, 16S-rRNA-based sequencing and operational taxonomic unit (OUT) analysis.
## Table 3. Summary of observations on the intestinal microbiome changes that can at least be partially explained by the intestinal nutrient environment

<table>
<thead>
<tr>
<th>Host*</th>
<th>Method†</th>
<th>Observations on the intestinal microbiome (ref)</th>
<th>Intestinal nutrient environment as a factor (ref)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Dietary pattern</strong></td>
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<tr>
<td>M</td>
<td>S</td>
<td>Feeding salmon cartilage proteoglycan led to alteration in the intestinal microbiome (68)</td>
<td>Proteoglycan can be used by intestinal commensal as a substrate (185) and thus its ingestion can affect the microbiome.</td>
</tr>
<tr>
<td>M</td>
<td>S</td>
<td>Fruit or nut supplementation led to microbiome changes such as increases in <em>Bifidobacterium</em> and diversity (67,69)</td>
<td>Fruits and nuts are good dietary sources of fermentable fibers and other prebiotic compounds (67,184)</td>
</tr>
<tr>
<td>H,M,P</td>
<td>S</td>
<td>High fat diet led to changes such as the depletion of <em>Bacteroides</em> and <em>Bifidobacterium</em> and a decrease in diversity (67,70,71)</td>
<td>High fat diet led to lower intake of fermentable fiber and thus a lower fiber presence in the intestine (185). It can also increase the unabsorbed fat in the colon (186)</td>
</tr>
<tr>
<td><strong>Development and aging</strong></td>
<td></td>
<td></td>
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<tr>
<td>H</td>
<td>A, P</td>
<td>Fraternal twins shared developmental changes (75)</td>
<td>Twins likely given the same breast milk, formula and solid food</td>
</tr>
<tr>
<td>H</td>
<td>P, S</td>
<td>Breast-fed and formula-fed infants did not have consistent differences in intestinal microbiome from study to study (72-74)</td>
<td>The composition of breast milk and infant formula can be different from study to study so the impact on the intestinal microbiome varied.</td>
</tr>
<tr>
<td>H</td>
<td>S</td>
<td>Infant gut microbiome developed features of the adult microbiome upon switching to the table food (187)</td>
<td>Infant microbiome had functional genes for the metabolism of polysaccharide in table food prior to the diet switching (187). Table food introduction likely leads to the preferential expansion of those species that have already colonized in the infant gut.</td>
</tr>
<tr>
<td>H</td>
<td>S</td>
<td>Different birth delivery modes led to transient but not long-term difference in microbiome (23,26,188)</td>
<td>The effect of delivery mode was overridden by later life dietary factors which then contribute to the inter-individual variations (23).</td>
</tr>
<tr>
<td>H</td>
<td>S</td>
<td>Elderly in long-term care facility has less microbiome diversity and the composition correlates with residence location (76).</td>
<td>Residents in each long-term care facility have limited but quite uniformed food choices and the food choices could be different between facilities (189)</td>
</tr>
<tr>
<td><strong>Disease and medication</strong></td>
<td></td>
<td></td>
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<tr>
<td>H</td>
<td>C, G, P, S, T</td>
<td>Patients with Inflammatory Bowel Diseases (IBD) have altered intestinal microbiome such as a decrease in <em>Bacteroidetes</em> and <em>Firmicutes</em> and higher γ-Proteobacteria (190-194).</td>
<td>IBD could lead to different dietary pattern (195) and lower fruit and fiber intake (196,197). Although dietary protein is usually well digested and absorbed in the small intestine, host mucin and cellular protein at the site of tissue inflammation/damage could serve as unique substrates for microbes (78,81).</td>
</tr>
<tr>
<td>H</td>
<td>M, S</td>
<td>Patients using proton pump inhibitors (PPI) showed decreased diversity and higher presence of oral bacteria (23,198)</td>
<td>PPI users have different dietary pattern (199). Higher gastric luminal pH in PPI users could spare orally-ingested microbes and thus a better chance for orally-ingested microbes to reach colon (85,87)</td>
</tr>
</tbody>
</table>
*Study subjects included both genders. H, human; M, mouse; P, primates

†The methods used for microbial analysis included: A, microarray; C, bacterial culturing; G, 16S-rRNA-based denaturing gradient gel electrophoresis; M: megagenomic sequencing analysis; P, qPCR; S, 16S rRNA sequencing and OTU analysis; T, terminal restriction fragment length polymorphism