

Review

The Role of Different Dietary Fibers in Modulating Human Gut Microbiota

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Abstract

Dietary fiber (DF) has a profound influence on human health mainly by modulating the gut microbiota. This review provides an overview of DF derived from cereals, legumes, fruits, vegetables, fungi, and seaweeds, specifically addressing the relationship between microbial utilization and source-specific structural characteristics (such as linking patterns, conformation, solubility, and fermentability). Due to these structural properties, different DFs display selective microbial responses that favor fermentation and the production of short-chain fatty acids (SCFAs). These microbial responses and fermentation-derived metabolites associated with DF intake may contribute to reduced risk of obesity, diabetes, inflammatory bowel disease, and other chronic disorders. This review does not address the trial heterogeneity, dose response, safety, and conflicting evidence, and much of the available evidence is largely observational and heterogeneous. Future studies should focus on dose–response trials of defined DF structures with standardized microbiome and metabolomic endpoints, including validation in human interventions. This review summarizes the DF source and structure, selective changes in the microbiota across various study types, including in vitro, animal models, and human studies, and how these relate to overall health.

Keywords: dietary fibers; gut microbiota; fiber structure; SCFAs; health

1. Introduction

Dietary fiber (DF) includes non-digestible carbohydrates and lignin that resist hydrolysis and absorption in the human small intestine. Codex Alimentarius defines DF as edible carbohydrate polymers with ≥ 10 monomeric units. It also notes that national authorities can decide whether to include non-digestible carbohydrates with a degree of polymerization (DP) between 3 and 9. The European Food Safety Authority (EFSA) panel on Dietetic Products, Nutrition and Allergies (NDA Panel) adopts a broader approach and includes resistant oligosaccharides with $DP \geq 3$, citing evidence of ‘fiber-like’ physiological effects, including promotion of a healthy gut microflora and SCFA production in the colon [1]. This review adopts the EFSA definition and includes resistant oligosaccharides ($DP \geq 3$), thereby considering inulin-type fructans, FOS, GOS, Xylo-oligosaccharides (XOS), pectin-derived oligosaccharides, and AXOS as dietary fiber. The health benefits of DF come from several mechanisms, including better bowel regulation, modulation of glycemic response, interactions with bile acids, and fermentation by the colonic microbiota. Gut microbes metabolize fermentable fibers into SCFAs, primarily acetate, propionate, and butyrate. These metabolites are important in maintaining host metabolic balance, regulating immune



Academic Editor: Ivan Cruz-Chamorro

Received: 30 January 2026

Revised: 20 February 2026

Accepted: 3 March 2026

Published: 11 March 2026

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function, strengthening the intestinal barrier, and reducing chronic inflammation [2,3]. The human genome encodes very few carbohydrate-active enzymes; it relies mainly on microbial ones. For instance, *Bacteroides* species possess hundreds of CAZymes, which allow them to degrade many different types of DFs [4]. Specific fibers selectively enrich beneficial bacterial taxa, such as *Bifidobacterium* and *Lactobacillus* [5], underscoring the importance of fiber structure in shaping gut ecology. Gut microbiota profiles differ between populations because of variations in diet, lifestyle, and environment. The diet common in western regions, high in fat and low in fiber, is linked with lower microbial diversity and a high risk of metabolic disease. Conversely, fiber-rich diets support microbial balance and resilience [6]. However, interindividual variation in microbial responses to DF highlights the need for personalized nutrition strategies. This review follows a three-part framework: (i) to summarize the structural and chemical diversity of DFs across major food groups, (ii) to map key DF features such as solubility, DP, linkage pattern, and molecular weight (MW) to selective microbial utilization and SCFA responses, (iii) to highlight evidence linking DF–microbiota interactions to clinical endpoints.

2. Types of DF in the Human Diet

Over the years, inconsistencies have persisted in characterizing dietary fiber (DF) among different disciplines. Food scientists typically characterize DF using physicochemical parameters such as solubility, MW, degree of polymerization, monomeric composition, structural conformation, and linkage patterns [7]. These traits are closely linked to their key functional properties, such as gelling property, fermentability, viscosity, bioavailability, and microbial specificity. Together, these properties influence the production of SCFAs and host physiological responses. Meanwhile, using terms like whole grains, vegetables, and product extracts and linking them to health-related functions and interactions with the gut microbiota without describing their structural features leads to ambiguous results or generalized conclusions. The discrepancy may further confuse the understanding of the DF type-specific functions in gut microbes. Examples of characterizing different DF types are listed in Table 1. As shown in Table 1, in most DF studies, DF is commonly classified based on its solubility, viscosity, and fermentability [8], with solubility and fermentability being the most widely accepted terms for studying their health benefits. Therefore, DF falls into two main categories: insoluble or less fermentable fibers (cellulose, hemicellulose, lignin) that do not dissolve in water and are less readily fermented by gut microbiota. However, some IDF are partially/poorly fermentable. Its primary functions are to add bulk to stool and aid digestion. Soluble dietary fibers (SDF) like pectin, gums, and mucilage are readily dissolved in water; some are viscous/gel-forming, whereas others are non-viscous yet readily fermentable. These fibers are then broken down by gut microbes, producing SCFAs, which support gut health [9,10].

Since gut microflora is closely related to the types of polysaccharides, a systematic investigation into food sources, their associated types of polysaccharides, and their functions on the gut microbiome is essential. Cereal grains, legumes, fruits and vegetables, mushrooms, and seaweeds are well known as good sources of DFs; however, their corresponding effect on gut microbiomes is not well elaborated, although some research has been carried out sporadically. This review will consolidate current findings on DFs from a diverse food source and their associated impacts on gut microbiota. The food subcategories for this review were selected from the Food Frequency Questionnaire of a research project to represent some commonly consumed foods within each category.

Table 1. Comprehensive classification of dietary fiber.

Classification Basis	Category	Examples	Refs.
Origin	Plant	Cellulose, Hemicellulose, Lignin, Pectin, Inulin, β -glucan, Resistant starch, Gums, Mucilage, Algal polysaccharides	[11,12]
	Microbial	Chitin, Yeast β -glucan, Xanthan gum	
Composition	Carbohydrates	Cellulose, Hemicellulose, β -glucan, Inulin, Fructo-oligosaccharide, Galacto-oligosaccharide, Xylo-oligosaccharide, Resistant starch	[12,13]
	Non-Carbohydrates	Lignin, Chitin	
Carbohydrate Structure	Non-Starch Polysaccharides	Cellulose, Hemicellulose, Pectin, Gums, Mucilage, β -glucan, Chitin	[2]
	Resistant Starch	Resistant Starch types 1–5	
	Non-Digestible Oligosaccharides	Fructo-oligosaccharide, Galacto-oligosaccharide, Xylo-oligosaccharide, Inulin, Resistant maltodextrin, Raffinose	
Solubility	Soluble Fiber	Oligosaccharides, Pectin, β -glucan, Gums, Mucilage, Inulin	[14,15]
	Insoluble Fiber	Cellulose, some Hemicellulose, Lignin, Resistant starch	
Fermentability	High	Inulin, Fructo-oligosaccharide, Pectin, Galacto-oligosaccharide, β -glucan, Mucilage, Arabinoxylan	[16,17]
	Low	Lignin, Cellulose, Resistant starch 5	
Viscosity	Viscous	Pectin, β -glucan, Guar gum, Psyllium	[16,18]
	Non-viscous	Cellulose, Hemicellulose, Inulin	
Molecular weight	Low MW	Fructo-oligosaccharide, Galacto-oligosaccharide, Xylo-oligosaccharides, Inulin	[19]
	High MW	Pectin, Cellulose, β -glucan, Resistant starch 1–5, Lignin	

2.1. Cereal Grains

Cereal grains are widely consumed staples and represent a major source of dietary fiber in many diets. Their fiber content and composition differ based on species, cultivar, and processing method. Generally, fiber in cereals is concentrated in the outer layers of the kernel. Cereal fiber plays a major role in dietary fiber and gut microbiota interaction. Cereal grains are well reported with various types of DF, as shown in Table 2.

Table 2. Dietary fiber characteristics across diverse food sources: composition, structure, conformation, and concentration.

Food Categories		TDF (%)	Main DFs	Chemical Composition	Linkage Pattern	Conformation	Concentration	References
Cereal Grains	Wheat	11.60–12.70	Arabinoxylan	Ara and Xyl	β -(1→4) glycosidic linkages	Flexible Random coil	70%	[20–22]
	Oat	10–38	β -glucan	D-glucose units	β -(1→3) and β -(1→4)	Random coil	3–7%	[7,21,23,24]
	Rye	14.70–20.90	Arabinoxylan	Ara and Xyl	β -(1→4) glycosidic linkages	Helical	3.10–12.10%	[21,25,26]
	Barley	10.00–27.90	β -glucan	D-glucose units	β -(1→3) and β -(1→4)	Triple helix/Random coil	2–10%	[7,25,27]

Table 2. Cont.

Food Categories	TDF (%)	Main DFs	Chemical Composition	Linkage Pattern	Conformation	Concentration	References
Legumes/Pulses	Soybean	9.19–9.45	Pectic polysaccharides	HG and RG-I	β -(1→4) galactans; α -(1→3)/ α -(1→5) arabinan, α -(1→4) galacturonan backbone	Random coil	7.12 ± 0.24% [28–30]
	Mung bean	25.30	Resistant starch	Glucose units (Amylose and amylopectin)	Mostly α -(1→4)-linked D-glucopyranosyl bonds chains with α -(1→6)-linked D-glucopyranosyl branch	Double helix	7% [31–33]
	Red Kidney bean	15–35	Pectic polysaccharides	Ara, Uronic acids, mainly GalA, Gal, Xyl, Man, Glc	HG: Linear α -(1→4)-D-GalA; RG-I: Repeating α -(1→2)-L-Rha and α -(1→4)-D-GalA backbone, branched with Ara and Gal	Mixed	— [34–37]
Vegetables	Celery	1.00–1.80	Pectic polysaccharides	GalA, Rha, Ara, Gal	α -(1→4)-D-galacturonan Rhamnose inserted via α -(1→2) linkages Side chains: Ara and Gal attached at Rha O-4 positions	—	— [38,39]
	Sugar beet pulp	67.60–70.00	Pectin	GalA residues with side chains	α -(1→4)-glycosidic linkages and α (1→2)	Semi-flexible random coil	23% [40–43]
	Okra	8.16	Mucilage	Man, Rha, GlcA, Glc, Ara, GalA, Gal, and xyl	α -(1→2)-linked rhamnosyl and α -(1→4)-linked galacturonosyl residues, with dimeric β -(1→4)-linked galactan side chains	Air-core sphere	11.44% [44–47]
	Onion	14–31	Pectic polysaccharides	GalA, Gal, and small amounts of xyl, Glc, Ara, Rha	(1→2)-linked α -L-Rha-(1→4)- α -D-GalA (RG-I) Side chains: Mainly (1→4)- β -D-Gal, also (1→3)- β -D-Gal and (1→5)- α -L-Ara	—	0.5% [12,48,49]
	Apple	2–3	Pectin	GalA	α -(1→4)-d-GalA backbone/neutral sugar side chains, some ester groups	Helix	16% [50,51]
Others	Orange	1.60	Pectin	GalA	α -(1→4) glycosidic linkages	Helix	0.50–3.5% [12,52,53]
	Button mushroom	31 ± 1.40	β -glucan	D-Glc	β -(1→3) and β -(1→6)	Triple-helix	8.6–12.30% [54–56]
	Seaweed	33–50	Carrageenan	Sulfated galactans (Gal + 3,6-anhydro-Gal)	Alternating α (1→3) b-D-galactopyranose, β -(1→4)-linked 3,6-anhydro-D-galactopyranose residue	Double helix/random coil	18.73% (C. jubata) [7,57–60]
			Alginate	Mannuronic and guluronic acid	(1→4)-linked α -l-guluronic acid and (1→4)-linked β -d-mannuronic acid	—	36.88% (S. muticum)

Abbreviations: Ara, arabinose; Gal, galactose; Glc, glucose; Man, mannose; Rha, rhamnose; Xyl, xylose; GalA, galacturonic acid; GlcA, glucuronic acid; HG, homogalacturonan; RG-I, rhamnogalacturonan I.

2.1.1. Wheat

In wholewheat grain, total dietary fiber (TDF) is around 11.60–12.70% on a dry matter basis (DM basis) [20]. The distribution of DF varies among wheat fractions: the bran significantly contributes to DF content, ranging from 36.50 to 52.40% [61]. Whereas the principal fiber components in the starchy endosperm cell walls are arabinoxylan (AX) and β -D-glucan. In wheat, AX makes up around 70% of the TDF. Structurally, AX is built from

a straight β -(1 $\rightarrow$ 4)-linked chain of D-xylopyranosyl residues, which form the backbone of the molecules [21]. AX molecules are either water-extractable or water-unextractable. The water-extractable AX (WE-AX) has a lower molecular complexity, fewer cross-links, and better solubility. Due to the extensive cross-linking through ferulic acid bridges in water-unextractable AX, it shows reduced solubility. Typically, the MW of water extractable AX ranges from 10 to 10,000 kDa, whereas water unextractable fractions are often higher than 10,000 kDa. When AX goes through enzymatic hydrolysis by xylanases and arabinofuranosidases, it produces arabinoxylan oligosaccharides (AXOS) and XOS [62]. AX adopts a random coil conformation in aqueous solution, which contributes to its functional and rheological properties in food systems [7,22]. In wheat, the β -glucan content falls from 0.50 to 1.50%, which is much less than the levels found in barley and oats. Most of the β -glucan is located in the aleurone and subaleurone layers of the kernel [63]. Besides β -glucan, wheat also contains cellulose, a small amount of glucomannans, and hemicellulose [7,21]. Most studies report that wheat bran and AXOS increase gut microbiota diversity/abundance at intake as low as 6–8 g/day, and the effects are detectable from 24 h to 52 weeks [64]. AXOS enriches Bacteroidales and Clostridia, while *Bifidobacterium* grows more with shorter AXOS, and *Lactobacillaceae* grow more with longer AXOS [65]. A 12-week AXOS trial showed a softened stool consistency and an increase in *Bifidobacterium* levels. However, gut transit and energy metabolism were unchanged, but alpha diversity decreased despite the bifidogenic response [66].

2.1.2. Oat

Oats (*Avena sativa*) are known for their high amount of SDF and insoluble dietary fiber (IDF). In dehulled oats, TDF content typically falls between 10 and 38% on a DM basis, depending on the cultivar and the grain processing methods. Oat bran usually contains 12–24% dietary fiber, with the exact amount influenced by cultivar, growing location, weather conditions, and fertilization practices. The primary components of oat fiber are β -glucan and AX. β -glucans are predominantly located in the endosperm, whereas cellulose, AX, and lignin are mainly concentrated in the bran. Among these, β -glucan content ranges explicitly from 2.30% to 8.50%, depending on the variety and processing conditions. [7,21,27,67]. Oat β -glucans are linear homopolysaccharides composed of D-glucopyranosyl residues linked by a combination of approximately 30% β -(1 $\rightarrow$ 3) and 70% β -(1 $\rightarrow$ 4) glycosidic bonds. These linkages create cellotriosyl and cellotetraosyl units separated by β -(1 $\rightarrow$ 3) bonds, which provide flexibility and high water-binding capacity, as a result contributing to their solubility and viscosity [21,24]. In aqueous solution, β -glucans exhibit a disordered random coil conformation [7]. The degree of polymerization, ratio of β -(1 $\rightarrow$ 3) and β -(1 $\rightarrow$ 4) linkage types, 3D conformation, and solubility all influence the physicochemical properties and biological activity of β -glucan [68]. Oat β -glucans help significantly reduce total and low-density lipoprotein cholesterol [23]. In people with high cholesterol, an eight-week drink containing 5 or 10 g of β -glucans from oats effectively lowered total cholesterol, postprandial glucose, and insulin levels [69]. β -glucan MW influences SCFA output during in vitro fermentation. Oat beta-glucan hydrolysates with lower MW produce higher total SCFAs (acetate, propionate, and butyrate) while the overall SCFA pattern remained similar to intact β -glucan [70]. The U.S. FDA has authorized a health claim stating that β -glucan, the primary SDF in oats, contributes to a reduced risk of coronary heart disease (CHD) when at least 3 g or more per day is consumed from qualified oat sources as part of a diet low in saturated fat and cholesterol [71].

2.1.3. Rye

Rye (*Secale cereale* L.) is notably rich in dietary fiber, with TDF ranging from 14.70 to 20.90% on a DM basis and made up mainly of AX, fructans, cellulose, and β -glucans [21]. The majority of rye DF is in the insoluble fraction, with IDF constituting approximately 10.80–16.00%, and SDF ranging from 3.40 to 6.60%. The inner endosperm contains about 12% DF, whereas the outer endosperm and bran layers contain between 22% and 38% on a DM basis. β -glucans are present in rye cell walls at concentrations of 1.30–2.20%, contributing to the grain's solubility characteristics. In addition, rye bran and the outer endosperm layer contain approximately 2.90% cellulose and 1.10% lignin. AX is the dominant fiber component in rye, accounting for 3.10–12.10% of TDF, commonly 7–12% in whole grain and reaching up to 37% in bran fractions [25,72]. Rye AX can adopt a helical conformation [26]. Rye is also comparatively high in fructans, which are chains of β -D-fructofuranosyl units with or without a terminal glucose residue. They act as an essential source of SDF in rye and support beneficial effects on digestive health [21]. Rye AX resists upper gut digestion and shows high solubility and viscosity in the small intestine. In the colon, WE-AX ferments readily and helps to enhance butyrate formation [73]. Comparing whole-rye and refined rye, one study found that whole-rye intake improves the Bacillota/Bacteroidota (formerly Firmicutes/Bacteroidetes) ratio and fecal microbiota diversity [74].

2.1.4. Barley

Barley (*Hordeum vulgare* L.) is uniquely rich in β -glucans, AX, RS, and cellulose [75]. Barley DF ranges from 10.00 to 27.90% [25]. In untreated barley, the IDF is typically higher at around 12.40% compared with SDF, which falls between 4.73% and 5.70% on a DM basis [76]. In barley, β -glucans content falls within 3–11% [7]. A key difference from oats and rye with barley is that the highest amount of β -glucan in barley sits in the endosperm. This anatomical trait confers a relative stability to β -glucan content during common processing steps [77]. Structurally, β -glucans exhibit source-dependent structural diversity, often form right-handed triple helices stabilized by interchain hydrogen bonds, but shift to a disordered random coil conformation in aqueous solution [7,27]. In humans, providing 3 g/day high-molecular-weight β -glucan helps to increase Bacteroidota and decrease Bacillota. At the genus level, *Bacteroides* increased, and *Dorea* decreased, and these taxonomic shifts correlated with cardiovascular disease markers, whereas low-MW β -glucan showed minimal effects [78]. Both the FDA and the European Food Safety Authority (EFSA) have recognized barley β -glucan for its clinically validated roles in cholesterol-lowering and glycemic response-controlling properties of barley and oat β -glucan [79–81].

2.1.5. Buckwheat

Both common and Tartary buckwheat (*Fagopyrum esculentum*) are fiber-rich pseudocereals with high levels of resistant starch, typically about 27.00–33.50%. The DF content in buckwheat groats is 7.00–11.90%, lower than in cereals like wheat, barley, and oats, with around 70% being water-soluble [21]. Studies examining six buckwheat genotypes report TDF between 20 and 26%, but the amount falls substantially after dehulling. Dehulled buckwheat seeds contain about 2.90% IDF and 2.40% SDF, and this profile is similar in both standard and Tartary buckwheat. The water-soluble fiber fraction predominantly comprises pectin, arabinogalactans, and xyloglucans. Buckwheat DF is composed of 1.80% pectin, 39% hemicellulose, 20% lignin, and 39% cellulose [82]. Hemicellulosic polysaccharides in the buckwheat DF are mostly xyloglucans [25]. Their non-starch polysaccharides mainly include pectic polysaccharides, notably arabinans with a high degree of branching, and smaller quantities of linear galactan and homogalacturonan (HG) [83]. Research on buckwheat DF's effects on gut microbiota is limited. Animal and in vitro studies report that

SDF from tartary buckwheat bran helps produce higher fecal SCFAs and often increases alpha diversity. However, taxonomic shifts vary across studies [84].

2.2. Legumes

Legumes have been increasingly utilized in extrusion cooking because they are rich in fiber and protein, low in calories, and naturally gluten-free. With DF content ranging from 13.10 to 35.30%, legumes are a rich source of DF compared with other plant-based foods such as tubers and cereals [85].

2.2.1. Soybean

DFs in soybean (*Glycine max*) come mainly from the hull and cotyledons and are predominantly composed of pectic polysaccharides. Soybean seeds exhibited high TDF content, with yellow varieties containing approximately 13.70–16.50% and green varieties containing 9.19–9.45%. Green soybeans tend to have more arabinose (19–20%) and xylose (19–21%) contents relative to yellow soybeans, which contain 11–14% arabinose and 12–14% xylose. Mannose is detected in minor proportions, ranging from 2 to 4% in yellow and 1–2% in green soybean varieties [29]. The pectic components are structurally characterized by HG and rhamnogalacturonan-I (RG-I) domains, featuring linear backbones of GalA and rhamnose connected via α -(1→4) and α -(1→2) glycosidic linkages, respectively. These backbones are further substituted with branched side chains composed mainly of β -(1→4)-linked galactans and α -(1→3) and α -(1→5)-linked arabinans [28,86]. Soybean soluble polysaccharide (SSPS) exhibits an overall conformation consistent with a highly branched, flexible random coil in aqueous solution, with individual polymer branches or domains possessing localized rigidity at the nanoscale [30]. Soybean okara, the pulp byproduct from soymilk/tofu, has very high TDF (54–55%). Enzyme-assisted processing increases okara SDF and produces higher SCFAs during fecal fermentation. Okara enhances bifidobacteria and lactobacilli, while suppressing Clostridia and Bacteroides [87]. In a high-fat diet rat model, smaller-particle okara insoluble dietary fiber (OIDF-10 μ m) partially restored dysbiosis, including a reduced Bacillota/Bacteroidota ratio and a larger rebound of Bacteroidetes compared with larger particle sizes [88].

2.2.2. Mung Bean

Mung beans (*Vigna radiata* L.) are an excellent source of DF, primarily consisting of non-starch polysaccharides. The TDF content of mung beans was approximately 25.30%, which is comparatively higher than that of cereals such as rice and wheat [33,89]. Mung beans are a good source of RS. RS accounts for about 11% of the total starch content in mung beans [90]. The resistant starch content varies depending on the processing method. For instance, raw mung beans contain approximately 7.1% RS, germinated mung beans have up to 17.50% RS, boiled mung beans have around 12.58% RS, and pressure-cooked mung beans have approximately 8.36% RS [31]. Mung bean starch is composed of glucose units mainly arranged as α -(1→4)-linked D-glucopyranosyl chains with α -(1→6) branch points. The chains form semi-crystalline granules with A-type crystallinity and exhibit double-helical conformations, primarily arising from amylopectin side chains [32]. Mung bean coat is rich in DF; it contains ~76.20% IDF and ~2.40% SDF (DM basis). In prediabetic mice, 3% (*w/w*) mung bean coat for 12 weeks increased fecal SCFAs and enriched *Roseburia* and *Bifidobacterium* [91]. Currently, there is limited evidence linking the structural features of mung bean dietary fiber to specific microbiota responses.

2.2.3. Red Kidney Bean

Red kidney bean (*Phaseolus vulgaris*) pectic polysaccharides are structurally complex carbohydrate polymers, which are concentrated in the seed coat and cotyledon cell walls.

These pectins are significant not only for their roles in holding up plant tissue but also for their functional properties in food systems and potential health benefits. Red kidney bean TDF ranges between 15% and 35% [35,37]. Those pectins are rich in arabinose (38.60%) and GalA (23.40%), along with appreciable amounts of galactose (12.70%), xylose (11.20%), mannose (6.40%), and glucose (6.10%) [35], indicating a highly branched and heterogeneous macromolecular architecture. Structurally, these pectins consist of HG and RG-I domains. The HG domain comprises linear chains of α -(1 $\rightarrow$ 4)-linked D-galacturonic acid (GalA) residues, a relatively “smooth” regions of the pectin, while the RG-I domain features a disaccharide backbone of alternating α -(1 $\rightarrow$ 2)-linked L-rhamnose and α -(1 $\rightarrow$ 4)-linked GalA, extensively substituted with arabinose and galactose side chains at the C-4 position of rhamnose, giving rise to the highly branched “hairy” regions. These structural motifs form a three-dimensional network of pectin, contributing to its physicochemical properties, including gelling capacity, hydration, and water retention [34]. Although the chain conformations of legume-derived pectins are still being mapped, recent work suggests some ordered structures, including triple-helix formations as indicated by Congo red binding shifts, and semi-crystalline arrangements by scanning electron microscopy (SEM) and X-ray diffraction (XRD) analyses [36]. Kidney beans show prebiotic potential. It increases *Bifidobacterium*, suppresses *Fusobacterium*, and raises SCFAs. In rats, whole beans and bean hulls lowered serum cholesterol and altered gut microbiota and caecal fermentation [92,93].

2.3. Vegetables

Vegetables are important for our fiber intake, which provides a wide range of fiber polymers. Their fiber content varies by species and the parts of the plants. Thermal processing, fermentation, and mechanical disruption can significantly alter DF structure and fermentability, which may shift microbiota responses; this should be considered when extrapolating from raw composition tables (Table 2). This includes SDF, like pectin, and IDF, such as cellulose and hemicellulose. These compositional differences influence fermentability and, consequently, potential impacts on gut microbial ecology and SCFA production.

2.3.1. Celery

Celery (*Apium graveolens*) stalks contain about 1.00–1.80% TDF on a fresh-weight basis (FW basis) [39]. Pectic polysaccharides are the most abundant fiber in celery, and when extracted from celery stalks, yield approximately 5.80% of the DM basis [38]. Evidence on celery DF's effects on gut microbiota is limited. Fermented celery juice helps to reduce weight gain, dyslipidemia, and hyperglycemia in high-fat diet mice more than plain juice. It also shifted the gut microbiota by raising *Lactobacillus*, *Ruminococcaceae*, *Faecalibaculum*, and *Blautia*, while lowering *Alloprevotella* and *Helicobacter* [94].

2.3.2. Sugar Beet

Sugar beet (*Beta vulgaris*) DF contains a high amount of pectin, which is approximately 23% [40,95]. Most of the pectin is HG, a linear α -(1 $\rightarrow$ 4)-linked GalA backbone, which constitutes roughly 60% of the total pectin content in sugar beet. The GalA units are variably methyl-esterified at the C-6 position and O-acetylated at O-2 and O-3, with the degree of methyl esterification determining the solubility, gelling behavior, and functional interactions of the pectin. Additionally, sugar beet pectin contains oligosaccharide regions with up to 20 alternating rhamnose and GalA units, indicative of RG-I structures. Analysis with dilute acid hydrolysis also finds the β -GlcA-(1 $\rightarrow$ 3) side chains linked to GalA residues, contributing to the structural heterogeneity and biofunctional properties of the pectin [43]. Due to its high RG-I content and short HG regions, sugar beet pectin shows increased molecular flexibility. That allows for intramolecular twisting and folding that result in a

compact, semi-flexible random coil conformation [42]. In human fecal fermentation, sugar beet-derived oligosaccharide (SBO) and sugar beet pulp consistently enrich *Bifidobacterium* and *Bacteroides*. SBO is usable by a broader range of *Bifidobacterium* strains [96].

2.3.3. Okra

Okra (*Abelmoschus esculentus*) is a fiber-dense vegetable. DF is reported as the most abundant macronutrient in fresh okra pods (8.16% FW). Okra mucilage can be recovered at appreciable yields (11.44% reported using a water-based extraction), which supports its use as a functional hydrocolloid ingredient. Because of its viscosity and polysaccharide composition, okra mucilage is widely discussed for technological roles such as thickening, stabilizing, and for health-relevant functions. A large fraction of okra carbohydrates occurs as mucilage, which is responsible for the characteristic viscosity and “slimy” texture in aqueous systems [45,47]. Chemically, okra mucilage is rich in acidic/pectic polysaccharides. Pectin is highlighted as the main polysaccharides commonly contain mannose, rhamnose, glucuronic acid, glucose, arabinose, galactose, and xylose [45]. Structurally, okra polysaccharides have been described as pectic polymers with a repeating unit of α -(1→2)-linked rhamnosyl and α -(1→4)-linked galacturonosyl residues, with dimeric β -(1→4)-linked galactan side chains (substituted at O-4 of part of the rhamnosyl residues) [44]. An air-core sphere conformation with branching chains has been reported for an okra pectic polysaccharide (reported MW $\approx 2.19 \times 10^5$ Da; Rg ≈ 27.0 nm in 0.9% NaCl) [46]. An okra-derived pectic polysaccharide showed limited degradation during simulated upper-GI digestion but was substantially utilized during in vitro fecal fermentation. This causes shifts in gut microbiota composition and enhanced SCFA production. After 48 h of fermentation, the okra polysaccharide group showed higher SCFAs, including increased acetate and propionate [97].

2.3.4. Onion

Onion (*Allium cepa*) is an important DF source in which cellulose and pectic polysaccharides are major DF components. The whole onion TDF range from 14.90 to 31.00% depending on the variety [49]. Pectin in the onion bulb has been reported as $\sim 0.5\%$ FW, and its pectic polysaccharides are characterized by a high content of galactose residues [48]. Lu et al. [98] reported that fermentation outcomes depend on cell-wall structure. Intact onion cell walls, fermentation occurs more slowly at first compared to the equivalent model polysaccharide mixtures. However, it can support significant SCFA production at later time points as the carbohydrates become accessible.

2.3.5. Potatoes

Potatoes (*Solanum tuberosum*) DF include cellulose, hemicellulose, pectin, lignin, and resistant starch. In potatoes, cellulose and hemicellulose contribute significantly to the TDF content [99,100], with RS levels influenced by processing conditions rather than cultivar. Cooked potatoes and cooled after cooking have higher levels of RS because of retrogradation [101]. Chilled potatoes exhibit the highest RS content (4.30%), followed by chilled and reheated potatoes (3.50%), and freshly cooked hot potatoes (3.10%). On average, a medium-sized potato contains 2 g of DF, representing $\sim 7\%$ of the recommended daily intake [102]. In a 4-week randomized, double blind, placebo-controlled, three-arm trial (75 randomized; 72 included in the analysis), resistant potato starch (3.5 or 7 g/day) was compared with a digestible corn starch placebo. The 3.5 g/day group showed a significant increase in *Bifidobacterium* and *Akkermansia* versus placebo, while the 7 g/day group showed a similar change that did not reach statistical significance [103].

2.3.6. Brussels Sprouts

Brussels sprouts (*Brassica oleracea* var. *gemmifera*) are widely known for their health-promoting properties [104]. According to the USDA [105], Brussels sprouts contain 4.80% DF. A ½ cup serving of Brussels sprouts provides approximately 3.80% of total fiber, comprising around 2% SDF and 1.80% IDF [106]. In human microbiota-associated rats, a diet containing Brussels sprouts altered predominant fecal populations and increased acetate in cecal SCFAs [107].

2.4. Fruits

Fruits provide diverse DF, with pectin as a dominant soluble fraction in many species and significant contributions from insoluble cell-wall polysaccharides. The source-dependent structure of these fibers shapes their physicochemical behavior and impacts on gut microbiota and SCFA generation.

2.4.1. Apple

Apple (*Malus domestica*) is a notable dietary source of fiber, providing approximately 2–3% of TDF of FW, comprising 1.57% of SDF and 0.67% of IDF [108]. Apple is a rich source of DF, composed primarily of pectin. Pectin forms a significant portion of the SDF in apples and helps with gelling, stabilizing, and health-promoting properties. In aqueous solution, apple pectin takes a stable right-handed helical conformation because of the torsional geometry of the α -(1→4)-linked GalA residues within the HG backbone [50]. Pectin can be regarded as one of the most complex natural macromolecules, as up to 17 monosaccharides are connected by more than 20 linkages. Since many of its structural elements within pectins were determined over time, it is widely believed that all kinds of pectins share these same basic structural repeating elements, and they vary simply in quantity, along with a defined basic pattern of chemical constitution [43]. Different apple varieties affect gut microbiota differently. Among the three apple varieties, Renetta Canada, Golden Delicious, and Pink Lady, all can alter gut microbiota and SCFAs, but Renetta Canada shows significant changes compared with the others [109].

2.4.2. Citrus Fruits

Citrus fruits are rich sources of DF, including pectin, cellulose, hemicellulose, and lignin [110,111]. The main fiber in citrus fruits is pectin, which is mainly found in the rinds and peels [112]. On a DM basis, citrus peels contain approximately 12.00–23.03% pectin, 24.52–37.08% cellulose, 7.57–11.04% hemicellulose, and 7.00–7.56% lignin [113]. Citrus pectins/pomace tend to favor *Bacteroides* and *Prevotella*, and this depends on the degree of methyl-esterification, MW, and RG-I structures [114].

2.4.3. Blueberries

On a DM basis, blueberry pomace contains approximately 60.80% TDF, of which 46.20% is IDF and 14.60% is SDF. This fiber comprises major polysaccharides, including pectin, xyloglucan, arabinoxylan, and mannan. Blueberry pomace is rich in IDF, predominantly composed of methyl-esterified and acetylated RG-I pectin. The pectin structure has 4,5-unsaturated groups at the non-reducing ends that help to its functional properties. This blueberry pectin exhibits a flexible random coil structure [115]. Anthocyanins in blueberries serve as substrates for bifidobacteria, supporting their growth. The synergistic interaction between blueberry pectin and anthocyanins enhances prebiotic activity, potentially exerting a dual prebiotic effect [116,117].

2.5. Others

Edible fungi (mushrooms) and seaweeds provide structurally diverse polysaccharides not found in land plants. Important fibers include β -glucans and chitinous polysaccharides in mushrooms, and sulfated and non-sulfated polysaccharides in seaweeds. These polymers have prebiotic-like effects and broader health-related benefits.

2.5.1. Edible Fungi

Mushrooms are a diverse group of macrofungi. More than 12,000 species have been classified, and about 2000 are edible [118]. The TDF in wild-growing edible mushrooms ranges from 24 to 37%, including 2–4% SDF and 12–21% IDF on a DM basis [54]. The spore-bearing fruiting bodies of fungi are valued globally for their diverse nutritional and medicinal properties and contain beneficial DFs [119]. β -glucans are found in cereals, yeasts, mushrooms, some bacteria, and seaweeds. Compared to other sources of β -glucans, such as oat and barley, β -glucans in mushrooms exhibit unique branching patterns where D-glucose monomers are linked by β -(1 $\rightarrow$ 3) and β -(1 $\rightarrow$ 6) glycosidic bonds [55,69]. Mushroom-derived β -glucans have shown immune-modulating and metabolic effects in preclinical models and some human trials; however, dose, purity, and context vary widely, so extrapolation to habitual mushroom intake needs caution. Because of these benefits, β -glucans are often included in functional foods, nutraceuticals, and therapeutic formulations [120,121]. In contrast, β -glucans from cereals primarily manage cholesterol and blood sugar levels [69]. Factors such as structure, solubility, branching degree, and MW significantly influence their biological activities. Their branching and linkages enable them to form complex three-dimensional structures, like triple-helical conformations, which are essential to their function [55,120]. Besides β -glucan, mushrooms also contain chitin, a structural component of mushroom cell walls. Chitin makes up around 6–9% of DM in button mushroom (*Agaricus bisporus*) and up to 8% in the pileus of shiitake (*Lentinula edodes*). This contributes to their rigidity and role as IDF [122]. The effects of mushroom polysaccharides on the gut microbiome are influenced by MW, monosaccharide composition, and glycosidic linkage type. They can increase SCFAs, strengthen the intestinal barrier, and modulate lipid metabolism [123].

2.5.2. Seaweed

Seaweed stands out due to its higher soluble-to-insoluble fiber ratio compared to land vegetables, a characteristic that enhances its prebiotic potential [124]. Seaweed, such as red algae (*Chondrus*, *Porphyra*/Nori), brown algae (*Fucus*, *Laminaria*/*Saccharina*), and green algae, are all rich sources of DF, with distinct variations in SDF and IDF content across phyla. Red algae typically contain 15–22% of their DM as SDF, rendering them rich in fermentable polysaccharides with established prebiotic potential. Brown algae, in contrast, are higher in IDF, with a content ranging from 27 to 40% of DM basis, contributing to bulk formation and stool regulation. Green seaweed *Caulerpa chemnitzia* exhibits the highest reported DF content, surpassing that of *Acanthophora spicifera*, *Ulva intestinalis*, *Ulva rigida*, and *Sargassum wightii*. Seaweeds generally contain 33–50% DF, with green species often having higher DF than red and brown varieties [59,124]. On average, seaweed provides 24.50% SDF and 21.80% IDF. Their chemical structure varies depending on the type of seaweed. Red algae are rich in agar, carrageenan, and agaropectin. Green algae contain xyloglucan, cellulose, hemicellulose, and xylopyranose. Brown algae are distinguished by their fucoidan, alginates, and laminarin (a β -glucan with the main chain of β -(1 $\rightarrow$ 3) glycosidic bonds and β -(1 $\rightarrow$ 6) side chains [79]). The β -glucan was reported to have anti-inflammatory, cholesterol-lowering, and immunomodulatory effects [57,60]. Carrageenan structure consists of linear chains of D-galactose units and 3,6-anhydro-galactose arranged

in an alternating pattern and linked by α -(1 $\rightarrow$ 3) and β -(1 $\rightarrow$ 4) glycosidic bonds. In aqueous solution, κ - and ι -carrageenans adopt random coil conformations at elevated temperatures. When cooled, these shapes change into double-helical structures. In contrast, λ -carrageenan maintains a flexible, ribbon-like conformation [7,57]. Alginate is a linear anionic polysaccharide composed of (1 $\rightarrow$ 4)-linked β -D-mannuronic acid (M) and α -L-guluronic acid (G) residues arranged in homopolymeric (M-blocks or G-blocks) and heteropolymeric (MG-blocks) sequences [58]. Simpler non-sulphated algal polysaccharides like alginate and laminarin are generally well fermented. Their MW ranges are ~30–300 kDa for alginate and ~4–5 kDa for laminarin. By contrast, sulphated polysaccharides show structure-dependent limits. Native carrageenan, fucoidan, and ulvan are poorly fermented [125].

3. Mechanisms of DF Interaction with Gut Microbiota

Bacteria are present throughout the body, and most reside in the colon, where approximately 10^{13} – 10^{14} bacteria reside [126], where they play a critical role in fermenting DFs that escape digestion in the upper gastrointestinal tract. DF's fermentability and microbial specificity are influenced by the degree of polymerization, particle size, solubility, and viscosity. The gut microbiome more rapidly ferments fibers with low degrees of polymerization. Smaller particles make it easier for microbial enzyme interactions, while highly soluble viscous fibers are more resistant to fermentation due to increased water retention and bulk-forming capacity [2].

3.1. Role of Enzymes

The human genome encodes only about 17 enzymes for carbohydrate digestion, which limits their ability to break down most carbohydrates independently. In contrast, a single gut bacterium, *Bacteroides thetaiotaomicron*, possesses over 260 carbohydrate-digesting enzymes [127,128]. The gut and oral microbiomes have their own set of carbohydrate-active enzymes (CAZymes), but the gut microbiome stands out with a more advanced capacity for breaking down complex carbohydrates [129]. As shown in Figure 1, DFs are converted into molecules absorbable by the intestinal lining through the activity of three broad enzyme families: glycoside hydrolases (GHs), carbohydrate esterases (CEs), glycosyltransferases (GTs), and polysaccharide lyases (PLs). Those CAZymes help degrade DF into absorbable human components, such as butyrate [127]. Specific clusters of CAZyme genes are designed to degrade particular structures in DFs, enabling various types of microbes to thrive depending on the fiber structure [130].

The dominant bacterial groups in the human colon include Bacillota (~65%), Bacteroidota (~25%), Actinomycetota (~5%), and Pseudomonadota (Proteobacteria) (~8%), at the phylum level. An imbalance in this can cause diseases such as liver disease, inflammatory disease, obesity, type 2 diabetes, ulcerative colitis, and other metabolic disorders [2,131–133]. In healthy adults, the relative abundance of Bacteroidota ranges from ~15–90%, while that of Bacillota varies from ~70–5%. These shifts impact the microbiota's ability to break down complex carbohydrates due to differences in CAZyme content. As a result, CAZymes may serve as biomarkers for gut microbiota functional diversity [4]. Members of the phylum Bacteroidota encode an extensive suite of CAZymes, particularly glycoside hydrolases (GHs) and polysaccharide lyases (PLs), which enable the efficient degradation of diverse plant polysaccharides. In contrast, Bacillota produce a more specialized but potent set of GHs, especially those targeting starches and fibers, along with carbohydrate-binding modules (CBMs) that facilitate SCFA production. Actinomycetota, particularly *Bifidobacterium* species, are rich in GH families that specialize in oligosaccharide metabolism, often acting on fiber breakdown intermediates. Although less dominant in

fiber decomposition, Pseudomonadota contribute to the degradation network through the production of CEs and GTs [129,134,135].

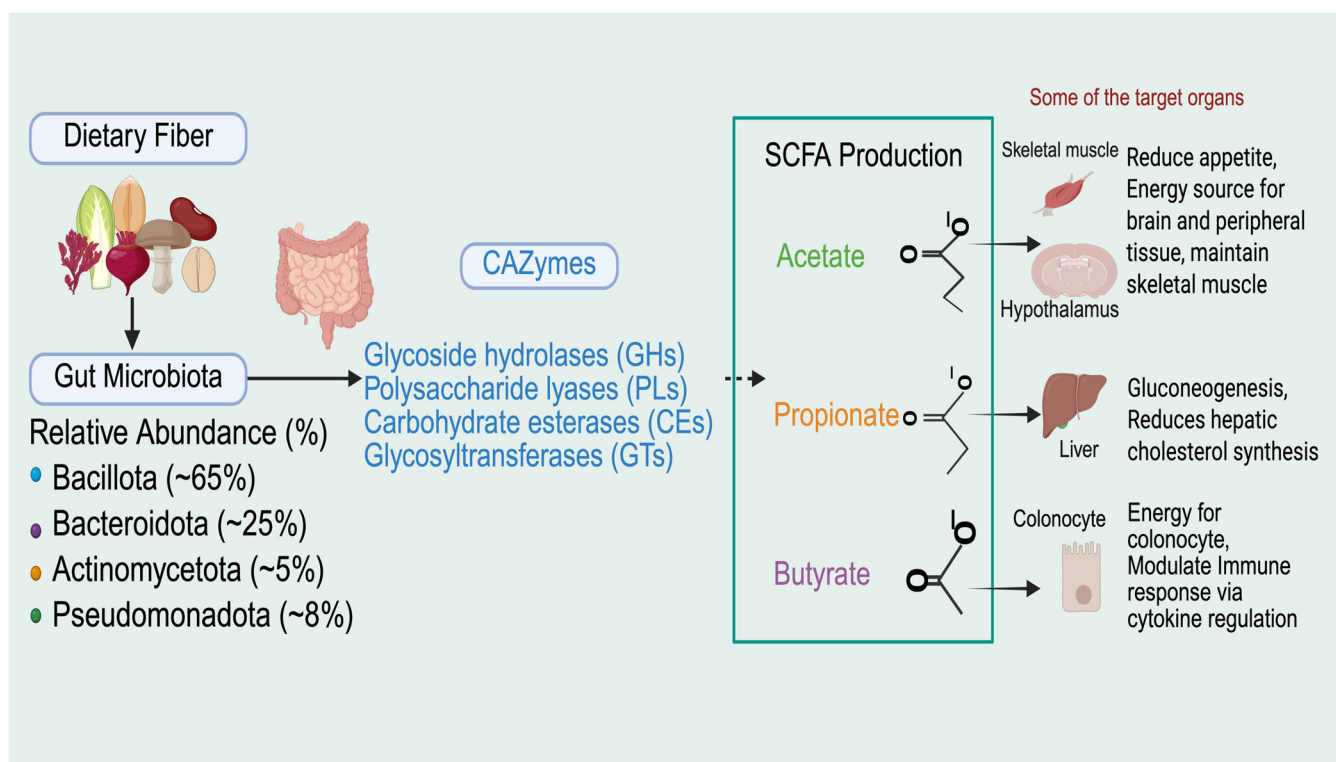


Figure 1. Microbial CAZyme activity and SCFA production.

3.2. Short-Chain Fatty Acids Production

The chemical structure of DF influences the rate of fermentability by gut microbiota [132]. When soluble dietary fibers (SDFs) reach the intestine, gut bacteria partially or fully break them down through anaerobic fermentation, generating metabolites such as short-chain fatty acids (SCFAs). SCFAs are small organic acids with fewer than six carbon atoms, and the most common ones are acetate (C2), propionate (C3), and butyrate (C4) [136,137]. Poorly fermented DF produces few acids, mainly acetic acid, by gut microbiota. Highly fermentable fibers produce large amounts of SCFAs in different ratios. Butyrate is the primary energy source for colonocytes. It supports epithelial cell proliferation and integrity, and modulates immune responses via cytokine regulation. Acetate is systemically absorbed and utilized in peripheral tissues, including the heart, brain, kidneys, and skeletal muscles. It provides a significant source of energy in the brain and peripheral tissue and also helps to reduce appetite. Propionate is primarily taken up by the liver, where it contributes to gluconeogenesis, reduces hepatic cholesterol synthesis, and may synergistically enhance the anti-carcinogenic effects of butyrate [138–140]. Several factors, including specific DF, such as inulin-type fructans and RS, influence butyrate production. Those fibers increase the potential for butyrate production by enhancing butyrate-producing bacteria [141]. Members of the phylum Bacillota, including *Faecalibacterium prausnitzii*, *Clostridium* spp., and *Eubacterium* spp., contribute significantly to colonic butyrate production [142]. Synergistic interactions between *F. prausnitzii* when cultured with *Bacteroides thetaiotaomicron* show increased butyrate production [143]. However, *Bacteroides* mainly help produce acetate and propionate [144]. Potato resistant starch significantly increases total SCFAs, especially butyrate. In contrast, resistant starch from maize and inulin tend to change the composition of fecal microbiota but do not substantially enhance butyrate production in feces [145]. Additionally, AX oligosaccharides exhibit bifidogenic properties

and promote the growth of butyrate-producing bacteria, further supporting gut health [146]. SCFAs are passively absorbed across the colonic epithelium, which contributes to both local and systemic physiological effects [147]. This shows that different types or combinations of fibers can influence how fermentation happens in the gut and shape both the kind and amount of SCFAs produced [148]. Generally, high-fiber diets are associated with an increased abundance of SCFA-producing bacteria. For example, the Mediterranean diet improves the abundance of *Faecalibacterium prausnitzii* and *Roseburia* spp. High-fiber diets also promote the growth of *Lactobacillus*, *Bifidobacterium*, *Prevotella*, and *Faecalibacterium* spp. Plant-based diets also increase the prevalence of *Prevotella*, *Bifidobacterium*, *Lactobacillus*, *Bacteroides*, and *Akkermansia*. On the other hand, low-fiber diets are associated with reduced fiber-degrading capacity and lower SCFA production. High-protein diets increase the levels of *Bacteroides*, *Bacillus*, *Clostridium*, *Propionibacterium*, and *Fusobacterium*. Ketogenic and Western diets generally increase the abundance of *Bacteroides*, *Bilophila*, *Alistipes*, *Blautia*, and *Ruminococcus*, but reduce the beneficial *Bifidobacterium* and *Bacillota*, as shown in Figure 2 [149].

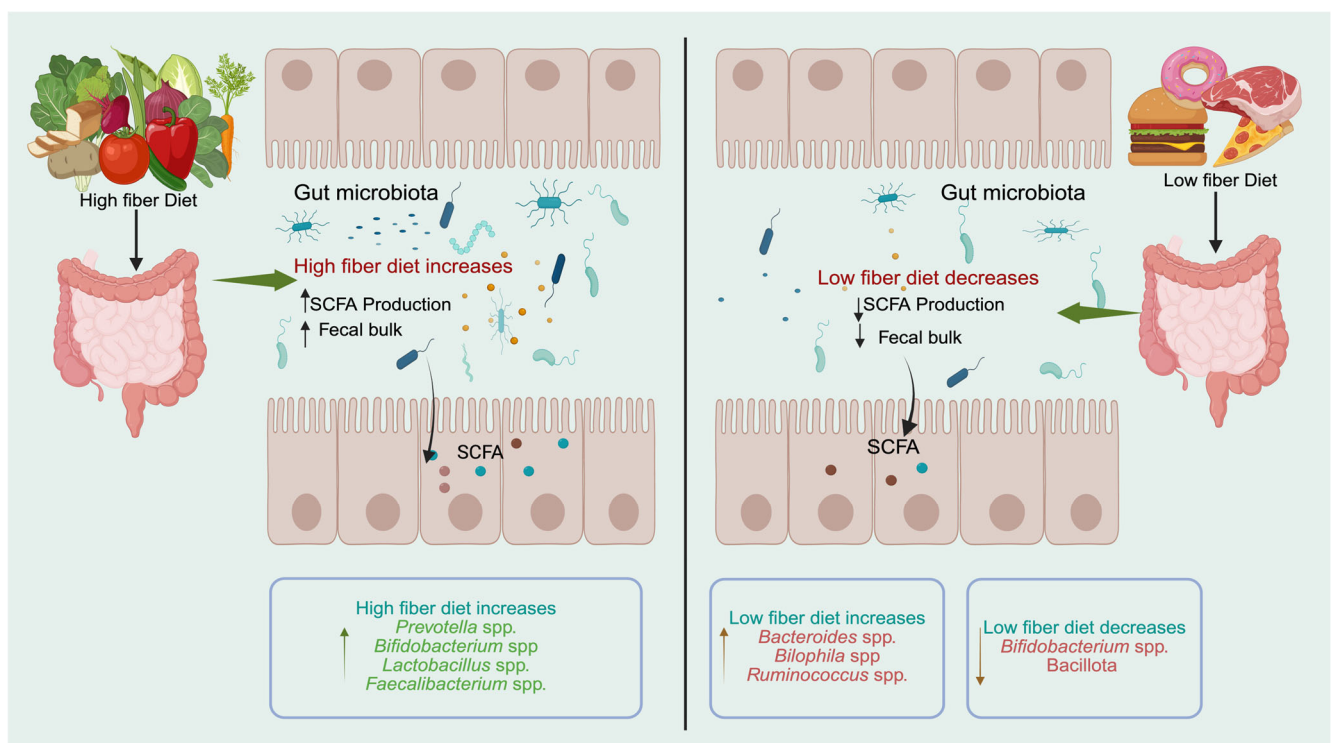


Figure 2. High vs. low dietary fiber: microbiota shift.

3.3. Fiber-Bacteria Specificity

The types of DF affect the fermentation in the gut. Factors that influence the rate and extent of fermentation include side chains, linkage types, degree of methylation, physical form, and fiber crystallinity. For example, the fermentation rate of ferulic acid-cross-linked AXs slows down because of the side chain and terminal linkage, and the fermentation of pectin is more dependent on the degree of methylation than the polymerization [132]. Different fiber structures induce unique microbiota changes. For example, apple pectin has been shown to promote *Eubacterium eligens* more effectively than inulin [150]. Some prebiotic soluble oligosaccharides, such as Fructo-oligosaccharide (FOS), GOS, xylitol-oligosaccharides, and isomalto-oligosaccharides, undergo rapid fermentation. In contrast, larger soluble polysaccharides, like inulin, arabinoxylan, β -glucan, and RS types 2 and 3, are only partially fermented, leaving less than 10% in the feces. Less soluble substances, including insoluble

arabinoxylan, starch granules, bran fiber, and bacterial cellulose, contain tightly packed crystalline structures and are fermented slowly. As summarized in Figure 3, different types of DFs have distinct effects on the gut microbiome [132]. AX can be fermented by *Roseburia*, *Bacteroides*, *Prevotella*, and *Porphyromonas* [147]; AX oligosaccharides increase *Bifidobacterium* species (e.g., *B. adolescentis* and *B. longum*), *Faecalibacterium prausnitzii*, *Ruminococcus*, *Dorea*, *Eubacterium rectale*, *Eubacterium hallii*, *Roseburia*, *Coprococcus*, and *Anaerostipes* species [146].

Roseburia primarily uses arabinogalactans and glucomannans. In contrast, *Clostridia* spp. including *C. thermocellum*, are more potent in breaking down xyloglucan [151]. FOS increases the *Bifidobacterium* and *Lactobacillus* species, while galacto-oligosaccharide (GOS) increases *Lactobacillaceae* and *Lachnospiraceae* and decreases *Ruminococcaceae* [152]. *Bifidobacterium* and *Lactobacillus* increase when introduced to inulin and GOS [153]. *Bacteroides thetaiotaomicron*, *Bacillus*, *Agrobacterium*, *Pseudomonas*, *Prevotella*, and *Ralstonia* ferment pectin [68,154]; another study found that pectin increases *Bifidobacterium*, *Lactobacillus*, and *Faecalibaculum* spp. [152]. Mechanistically, *Bacteroides thetaiotaomicron* can act as a primary pectin degrader by breaking pectin into oligosaccharides for uptake and further metabolism by other bacteria [155]. Resistant potato starch causes about a 6.5-fold increase in the relative abundance of *Bifidobacterium faecale/adolescentis/stercoris* sequences, while resistant maize starch leads to a 2.5-fold increase in *Ruminococcus bromii* [145]. *Eubacterium rectale*, *Bacteroides thetaiotaomicron*, and *Bifidobacterium adolescentis* showed limited utilization of resistant starch alone, but in co-culture their utilization increased when *R. bromii* was present, supporting its role as a keystone resistant-starch degrader [156]. RS4 consumption increases *Actinomycetota* and *Bacteroidota* while decreasing *Bacillota*. Also, oat β -glucan helps to increase *Bacteroidota* and *Bifidobacteria* while decreasing *Bacillota* [147], in addition to *Bifidobacterium*. Guan et al. [152] reported an increase in *Lactobacillus*. Inulin-type fructans hydrolyzed by *Bifidobacterium* in the colon increase the abundance of *Bifidobacterium* from 6.69 to 15.07% [2,157], while inulin increases the abundance of *Anaerostipes hadrus* [145], *Prevotellaceae*, *Bifidobacterium*, and *Lactobacillus* [152]. Polydextrose increases *Bifidobacterium*, and psyllium husk boosts *Anaerostipes*. When wheat bran is combined with psyllium husk, it further enhances *Anaerostipes*. Oligosaccharides support beneficial bacteria like *Bifidobacterium*, aiding in stool consistency and overall gut function [158]. Two weeks of partially hydrolyzed guar gum consumption increased the abundance of *Bifidobacterium*, *Ruminococcus*, and *Megasphaera*, while those who took the placebo did not show this increase [159]. Beyond fiber structure, responses also depend on baseline microbiota and baseline dietary patterns, because it varies across individuals. For instance, only the *Prevotella*-rich baseline microbiota cluster demonstrated a distinct overall shift in community composition in response to the resistant starch intervention in a 6-week trial comparing resistant-starch-rich unripe banana flour with inulin, while the *Bacteroides*-rich cluster showed minimal overall change [160].

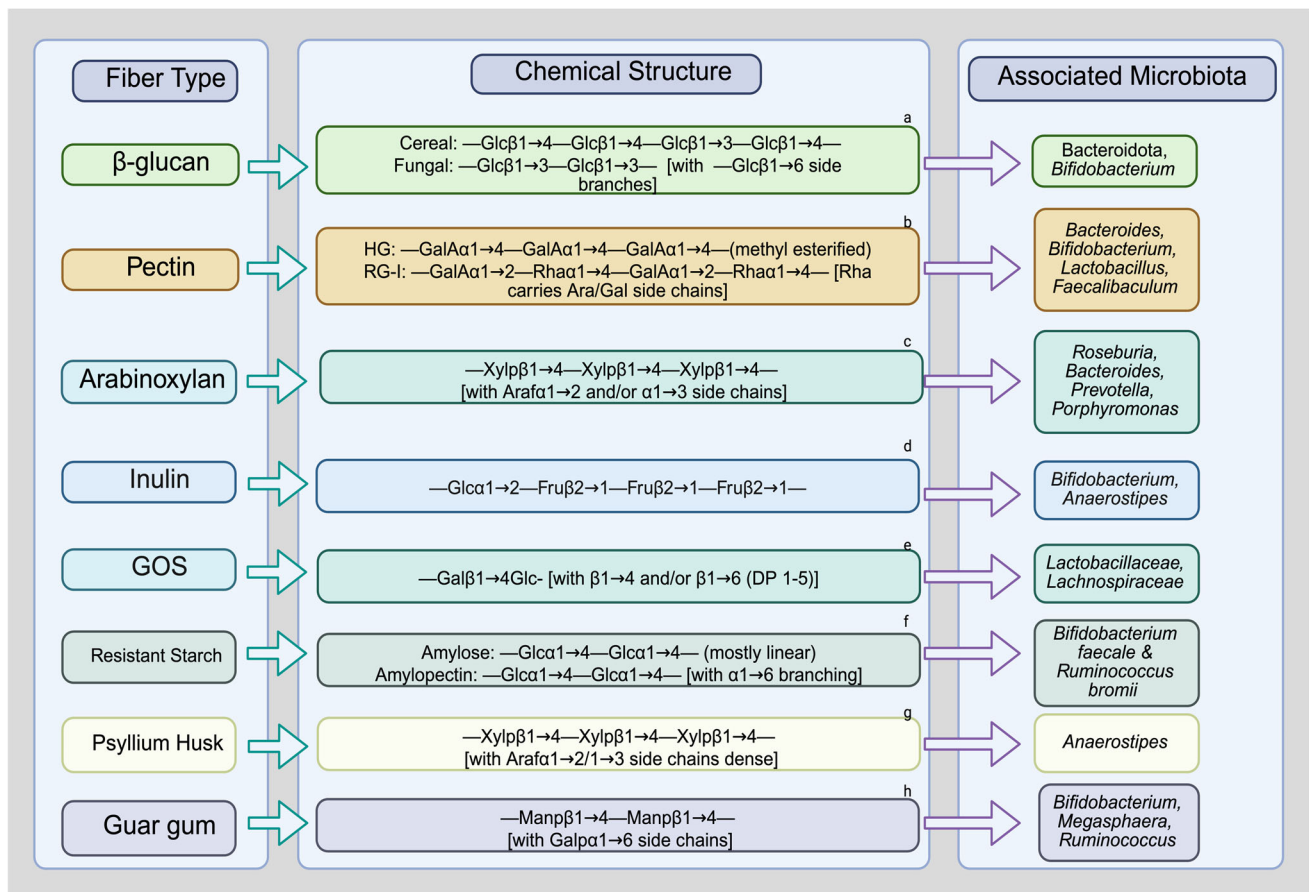


Figure 3. Dietary fiber and associated microbial profiles. Abbreviations: Ara, arabinose; Gal, galactose; Glc, glucose; Manp, mannopyranose; Rha, rhamnose; GalA, galacturonic acid; HG, homogalacturonan; RG-I, rhamnogalacturonan I; Xylp, Xylopyranoside; Arafa, Arabinofuranosyl. Sources: a [161], b [162], c [163], d [164], e [165], f [166], g [167], h [168].

4. Health Implications of Fiber–Microbiota Interactions

DF modulates the health in various ways. Fiber alters gut health by influencing gut microbiota and SCFA output. Microbial-derived metabolites connect fiber intake to metabolic health, and fiber microbiota interactions modulate immune function by influencing Treg balance and inflammatory signaling.

4.1. Gut Health

DF has been found to play a key role in regulating gut microbiota, particularly promoting the proliferation of beneficial Bacillota members, including *Faecalibacterium prausnitzii*, and *Roseburia*. These bacterial groups are major producers of SCFAs, such as butyrate, which support intestinal health by enhancing epithelial barrier integrity, reducing inflammation, and regulating host metabolism [169]. Disruption in the balance between the gut microbes and the intestinal mucosal barrier can cause dysbiosis and lead to intestinal inflammation [170]. Comparative studies show clear differences in gut microbiota between healthy and diseased individuals. Low DF intake has been linked to inflammatory bowel disease (IBD), autoimmune diseases, allergies, and ulcerative colitis. However, diet-IBD associations may be influenced by reverse causality, as dietary habits can change during the symptomatic pre-diagnostic period [133,171,172]. Prolonged lack of DF can damage the mucus barrier and increase mucin-degrading taxa such as *Akkermansia muciniphila*. When DF is absent, some gut bacteria switch to using mucin glycan. They do this by inducing expression of mucin-degrading enzymes, which can increase host vulnerability to

inflammation and infection susceptibility over time. Experimental evidence further shows that very low-fiber Western-diet feeding in mice increases penetrability of the inner mucus layer and lowers mucus growth rate. Using low-dose inulin (1%) prevented the increase in mucus penetrability, while *Bifidobacterium longum* can restore the mucus growth rate. These results suggest that bifidogenic or targeted probiotic strategies can improve specific aspects of mucus barrier function [173]. Fermentation also helps to maintain the oxygen level inside the gut. Beta-oxidation of butyrate by colonocytes consumes oxygen, promoting an anerobic milieu, and reduced butyrate can enable blooms of Pseudomonadota in a feedforward loop [174]. People with irritable bowel syndrome (IBS) often display an elevated Bacillota-to-Bacteroidota ratio and reduced levels of beneficial genera, such as *Lactobacillus* and *Bifidobacterium* [175]. Experimental studies show that fiber deprivation in animal models leads to increased levels of Pseudomonadota, compromised mucus barrier formation, and increased intestinal permeability. Supplementing *Bifidobacterium* or DF prevented those issues. In healthy individuals, fermentable fibers like fructans and GOS enhance *Bifidobacteria* and increase SCFAs such as butyrate in fecal samples [150]. The colonic luminal pH usually ranges from 6 to 7, varies along different regions of the colon, being lower in the ascending and transverse segments and higher in the descending and rectosigmoid regions. This pH gradient is closely influenced by microbial metabolism and diet. High-fat and alcohol-rich diets tend to elevate colonic pH, whereas fiber-rich diets lower pH by promoting SCFA production. Additionally, shifts in microbiota composition and metabolic activity can further modulate the colonic pH environment [176].

4.2. Metabolic Health

Both in vivo and in vitro studies have shown that DF beneficially shapes the gut microbiota, particularly by enriching beneficial Bacillota taxa. This, in turn, improves metabolic and inflammatory disorders, such as type 2 diabetes, obesity, and inflammatory bowel disease (IBD) [151]. Studies combining *Bacillus coagulans* with whole plant sugarcane fiber or green banana-derived RS have been shown to reduce intestinal inflammation and enhance the production of health-promoting SCFAs, which support gut barrier function and immune modulation [177]. Pomelo peel DF (PPDF) consists of SDF and IDF, which significantly reduced weight gain, fat accumulation in the liver and adipose tissues, and dyslipidemia markers. It influences the growth of *Bifidobacterium* and *Lactobacillus* while reducing the harmful *Staphylococcus* and *Corynebacterium*. PPDF can be utilized as a preventative measure for obesity [178]. Likewise, supplementation of β -glucan in a high-fat diet (HFD) has been shown to reduce adiposity, limit weight gain, and improve glucose tolerance compared to HFD supplemented with cellulose [179]. Controlled human studies support these microbiome-linked metabolic effects of DF beyond associative observations. In a 16-week randomized trial in prediabetes participants, a calorie-restricted legume-enriched diet produced greater reductions in low-density lipoprotein cholesterol (LDL-C), total cholesterol, and hemoglobin A1c than a calorie-restricted control diet. This diet also increased fiber-degrading species and changed bile acid and amino acid-related metabolites [180]. Likewise, a double-blind trial using type 3 RS from *Canna edulis* (20 g/day for 12 weeks) significantly reduced total cholesterol and LDL-C in mild hyperlipidemia. It also increased *Faecalibacterium* and *Agthobacter*, linking fibers to lipid improvements via microbiome remodeling [181]. In addition, marine-derived polysaccharides, including alginates, carrageenan, and funorans from seaweed, exhibit beneficial effects on serum lipid levels in rats. They lower serum cholesterol by dissolving in water, retaining cholesterol and other bioactive compounds, and reducing lipid absorption in the digestive tract [182]. Responses to DF are not uniform across people. In a large trial involving people with prediabetes, post hoc clustering indicated that DF improved glycemic control in some

clusters but not others. The same trial developed a lightGBM machine learning model to create a microbiome-based decision score that can help to predict who is more likely to get a glycemic benefit from fiber supplementation [183]. Collectively, high-fiber diets are associated with improved nutrient absorption and a lower risk of obesity and diabetes [153]. Those findings highlight the therapeutic potential of DF as a microbiome-targeted strategy for improving metabolic and inflammatory health.

4.3. Immune Modulation and Chronic Disease Prevention

The gastrointestinal tract is the body's largest immune organ, containing more than 70% of all immune cells. There is a significant connection between gut microbiota and the host's immune system. Fermentation of DF by gut microbiota produces SCFAs, such as acetate, propionate, and butyrate [175]. These SCFAs help to maintain immune homeostasis by promoting the differentiation of regulatory T cells (Tregs) through activation of G protein-coupled receptor 43 (GPR43) and by enhancing histone H3 acetylation. Maternal intake of a high-fiber diet during pregnancy and lactation has been shown to beneficially modulate the thymic microenvironment, inducing the expression of autoimmune regulator, a thymus-specific factor crucial for T cell maturation. This maternal DF intake elevates butyrate levels in offspring, which in turn enhances Treg count through GPR41. In contrast, high-fat diets are associated with early thymic involution, characterized by decreased thymocyte counts and increased T cell apoptosis [174]. Among different fibers, pectin has notable immunomodulatory properties. It influences microbial ecology by altering the Bacillota-to-Bacteroidota ratio and increasing SCFA levels in both fecal and systemic circulation. Functionally, pectin has been shown to reduce airway inflammation by modulating the activity of dendritic cells (DCs). Mechanistically, it can bind to toll-like receptor 2 (TLR2) on DCs and macrophages through electrostatic interactions, selectively inhibiting the pro-inflammatory TLR2-TLR1 pathway while maintaining the TLR2-TLR6 tolerogenic pathway [13].

Furthermore, modified citrus pectin has been reported to interact with immune cells such as T and B lymphocytes and natural killer cells. It has been shown to downregulate key inflammatory mediators, such as inducible nitric oxide synthase and cyclooxygenase-2, by inhibiting upstream regulators such as I κ B kinase, mitogen-activated protein kinase, and nuclear factor kappa B (NF- κ B) [13]. β -glucan modulates innate and adaptive immunity. It binds to pattern-recognition receptors such as dectin-1 and complement receptor 3 on macrophages, neutrophils, and dendritic cells, thereby improving their function. SCFAs from cereal β -glucans fermentation by gut microbiota, such as butyrate, promote regulatory/IL-10-producing T cells, support epithelial barrier integrity, and help control low-grade inflammation. Together, these immune and SCFAs effects help protect against infections and other chronic conditions [184–188]. Chronic systemic inflammation is linked with diseases such as cancer, heart disease, diabetes, and kidney disease. A fiber-rich diet reduces inflammation-related disease risk, but the effects vary by fiber type. For instance, IDF and cereal-derived fiber have been associated with reduced risk of CHD. In contrast, fruit-derived fiber, particularly pectin-rich sources, seems to be more effective in reducing the risk of gastrointestinal inflammatory conditions such as Crohn's disease [150].

5. Conclusions and Future Directions

The structure, conformation, and monosaccharide composition of DF are highly variable and are correlated with different responses of the gut microbiota. In general, fermentable fibers can enhance microbial fermentation and the production of beneficial metabolites, especially SCFAs. Those metabolites may have effects on the immune system, metabolism, and gastrointestinal function. Although there has been rapid progress

in DF-gut microbiome research, one of the most important knowledge gaps is the lack of a well-defined relationship between the structure of DF and consistent fermentation outcomes in humans. This is probably due to the effects of fiber structure, dietary habits, host factors, and baseline microbiome differences on fiber exposure, microbial functionality, and host-microbiota interactions. Future studies should focus on structure-based fiber interventions to modulate the gut microbiota, using standardized fiber characterization, incorporating dietary information and host genetic information with microbiome and metabolic outcomes.

Author Contributions: Conceptualization, S.D. and Y.W.; formal analysis, S.D. and C.J.F.; visualization, S.D. and C.J.F.; writing—original draft preparation, S.D.; writing—review and editing, S.D. and Y.W.; supervision, Y.W.; project administration, Y.W.; funding acquisition, Y.W. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the U.S. Department of Agriculture (USDA), National Institute of Food and Agriculture (NIFA), Capacity Building Grants (CBG) program, grant number 2024-38821-42214.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: No new data were created or analyzed in this study. Data sharing is not applicable to this article.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. EFSA NDA Panel. Scientific opinion on dietary reference values for carbohydrates and dietary fibre. *EFSA J.* **2010**, *8*, 1462. [\[CrossRef\]](#)
2. Fu, J.; Zheng, Y.; Gao, Y.; Xu, W. Dietary Fiber Intake and Gut Microbiota in Human Health. *Microorganisms* **2022**, *10*, 2507. [\[CrossRef\]](#)
3. Naumann, S.; Schweiggert-Weisz, U.; Eglmeier, J.; Haller, D.; Eisner, P. In Vitro Interactions of Dietary Fibre Enriched Food Ingredients with Primary and Secondary Bile Acids. *Nutrients* **2019**, *11*, 1424. [\[CrossRef\]](#)
4. Kaoutari, A.E.; Armougom, F.; Gordon, J.I.; Raoult, D.; Henrissat, B. The abundance and variety of carbohydrate-active enzymes in the human gut microbiota. *Nat. Rev. Microbiol.* **2013**, *11*, 497–504. [\[CrossRef\]](#)
5. So, D.; Whelan, K.; Rossi, M.; Morrison, M.; Holtmann, G.; Kelly, J.T.; Shanahan, E.R.; Staudacher, H.M.; Campbell, K.L. Dietary fiber intervention on gut microbiota composition in healthy adults: A systematic review and meta-analysis. *Am. J. Clin. Nutr.* **2018**, *107*, 965–983. [\[CrossRef\]](#)
6. Parizadeh, M.; Arrieta, M.-C. The global human gut microbiome: Genes, lifestyles, and diet. *Trends Mol. Med.* **2023**, *29*, 789–801. [\[CrossRef\]](#) [\[PubMed\]](#)
7. Cui, S.W.; Wu, Y.; Ding, H.; Delcour, J.A.; Poutanen, K. *The Range of Dietary Fibre Ingredients and a Comparison of Their Technical Functionality*; Woodhead Publ Ltd.: Cambridge, UK, 2013; Volume 237, pp. 96–119.
8. Ibrahim, O.; Menkovska, M. Dietary Fibers-Classification, Properties, Analysis and Function: A Review. *Adv. Biosci. Biotechnol.* **2022**, *13*, 527–544. [\[CrossRef\]](#)
9. Dhingra, D.; Michael, M.; Rajput, H.; Patil, R.T. Dietary fibre in foods: A review. *J. Food Sci. Technol.* **2012**, *49*, 255–266. [\[CrossRef\]](#)
10. Carlsen, H.; Pajari, A.M. Dietary fiber—A scoping review for Nordic Nutrition Recommendations 2023. *Food Nutr. Res.* **2023**, *67*. [\[CrossRef\]](#)
11. Sharma, S.K.; Sangita, B.; Manisha, M.; Kumar, D.A.; Gupta, R.K.; Mangal, A.K. Utilization of Food Processing By-products as Dietary, Functional, and Novel Fiber: A Review. *Crit. Rev. Food Sci. Nutr.* **2016**, *56*, 1647–1661. [\[CrossRef\]](#)
12. Salvatore, S.; Battagaglia, M.S.; Murone, E.; Dozio, E.; Pensabene, L.; Agosti, M. Dietary Fibers in Healthy Children and in Pediatric Gastrointestinal Disorders: A Practical Guide. *Nutrients* **2023**, *15*, 2208. [\[CrossRef\]](#)
13. Blanco-Pérez, F.; Steigerwald, H.; Schülke, S.; Vieths, S.; Toda, M.; Scheurer, S. The Dietary Fiber Pectin: Health Benefits and Potential for the Treatment of Allergies by Modulation of Gut Microbiota. *Curr. Allergy Asthma Rep.* **2021**, *21*, 43. [\[CrossRef\]](#)
14. Perry, J.; Wu, Y. A Review of Physiological Effects of Soluble and Insoluble Dietary Fibers. *J. Nutr. Food Sci.* **2016**, *6*, 2. [\[CrossRef\]](#)
15. Chawla, R.; Patil, G. Soluble dietary fiber. *Compr. Rev. Food Sci. Food Saf.* **2010**, *9*, 178–196. [\[CrossRef\]](#)
16. Slavin, J. Fiber and prebiotics: Mechanisms and health benefits. *Nutrients* **2013**, *5*, 1417–1435. [\[CrossRef\]](#) [\[PubMed\]](#)

17. Wang, W.; Fan, Z.; Yan, Q.; Pan, T.; Luo, J.; Wei, Y.; Li, B.; Fang, Z.; Lu, W. Gut microbiota determines the fate of dietary fiber-targeted interventions in host health. *Gut Microbes* **2024**, *16*, 2416915. [\[CrossRef\]](#)
18. Jovanovski, E.; Nguyen, M.; Kurahashi, Y.; Komishon, A.; Li, D.; Hoang Vi Thanh, H.; Khayyat, R.; Jenkins, A.L.; Khan, T.A.; Zurbau, A.; et al. Are all fibres created equal with respect to lipid lowering? Comparing the effect of viscous dietary fibre to non-viscous fibre from cereal sources: A systematic review and meta-analysis of randomised controlled trials. *Br. J. Nutr.* **2023**, *129*, 1180–1192. [\[CrossRef\]](#) [\[PubMed\]](#)
19. Feng, Y.; Jin, Q.; Liu, X.; Lin, T.; Johnson, A.; Huang, H. Advances in understanding dietary fiber: Classification, structural characterization, modification, and gut microbiome interactions. *Compr. Rev. Food Sci. Food Saf.* **2025**, *24*, e70092. [\[CrossRef\]](#) [\[PubMed\]](#)
20. Stevenson, L.; Phillips, F.; O'Sullivan, K.; Walton, J. Wheat bran: Its composition and benefits to health, a European perspective. *Int. J. Food Sci. Nutr.* **2012**, *63*, 1001–1013. [\[CrossRef\]](#)
21. Prasadi, N.P.V.; Joye, I.J. Dietary Fibre from Whole Grains and Their Benefits on Metabolic Health. *Nutrients* **2020**, *12*, 3045. [\[CrossRef\]](#)
22. Demuth, T.; Betschart, J.; Nyström, L. Structural modifications to water-soluble wheat bran arabinoxylan through milling and extrusion. *Carbohydr. Polym.* **2020**, *240*, 116328. [\[CrossRef\]](#)
23. Chiozzi, V.; Eliopoulos, C.; Markou, G.; Arapoglou, D.; Agriopoulou, S.; El Enshasy, H.A.; Varzakas, T. Biotechnological Addition of β -Glucans from Cereals, Mushrooms and Yeasts in Foods and Animal Feed. *Processes* **2021**, *9*, 1889. [\[CrossRef\]](#)
24. Alemayehu, G.F.; Forsido, S.F.; Tola, Y.B.; Amare, E. Nutritional and Phytochemical Composition and Associated Health Benefits of Oat (*Avena sativa*) Grains and Oat-Based Fermented Food Products. *Sci. World J.* **2023**, *2023*, 2730175. [\[CrossRef\]](#) [\[PubMed\]](#)
25. Ciudad-Mulero, M.; Fernández-Ruiz, V.; Matallana-González, M.C.; Morales, P. Chapter Two—Dietary fiber sources and human benefits: The case study of cereal and pseudocereals. In *Advances in Food and Nutrition Research*; Ferreira, I.C.F.R., Barros, L., Eds.; Academic Press: Cambridge, MA, USA, 2019; Volume 90, pp. 83–134.
26. Dynkowska, W. Rye (*Secale cereale* L.) arabinoxylans: Molecular structure, physicochemicals properties and the resulting pro-health effects. *Plant Breed. Seed Sci.* **2020**, *81*, 19–38. [\[CrossRef\]](#)
27. Bai, J.; Ren, Y.; Li, Y.; Fan, M.; Qian, H.; Wang, L.; Wu, G.; Zhang, H.; Qi, X.; Xu, M.; et al. Physiological functionalities and mechanisms of β -glucans. *Trends Food Sci. Technol.* **2019**, *88*, 57–66. [\[CrossRef\]](#)
28. Song, H.; Han, L.; Zhang, Z.; Li, Y.; Yang, L.; Zhu, D.; Wang, S.; He, Y.; Liu, H. Structural properties and bioactivities of pectic polysaccharides isolated from soybean hulls. *LWT* **2022**, *170*, 114079. [\[CrossRef\]](#)
29. Redondo-Cuenca, A.; Villanueva-Suárez, M.J.; Rodríguez-Sevilla, M.D.; Mateos-Aparicio, I. Chemical composition and dietary fibre of yellow and green commercial soybeans (*Glycine max*). *Food Chem.* **2007**, *101*, 1216–1222. [\[CrossRef\]](#)
30. Chivero, P.; Gohtani, S.; Ikeda, S.; Nakamura, A. The structure of soy soluble polysaccharide in aqueous solution. *Food Hydrocoll.* **2014**, *35*, 279–286. [\[CrossRef\]](#)
31. Chauhan, S.; Kaur, H.; Aggarwal, R.; Kaur, P.; Bains, K. Exploring the impact of cooking techniques and storage conditions on resistant starch levels in mung beans and its effect upon blood glucose level and lipid profile in vivo. *Front. Nutr.* **2024**, *11*, 1424112. [\[CrossRef\]](#) [\[PubMed\]](#)
32. Huong, N.T.M.; Ngoc, H.P.; Hung, P.V. Varying amylose contents affect the structural and physicochemical characteristics of starch in mung bean. *Int. J. Food Prop.* **2021**, *24*, 737–748. [\[CrossRef\]](#)
33. Azizah, A.; Zainon, H. Effect of processing on dietary fiber contents of selected legumes and cereals. *Malays. J. Nutr.* **1997**, *3*, 131–136.
34. Njoroge, D.M.; Kinyanjui, P.K.; Makokha, A.O.; Christiaens, S.; Shpigelman, A.; Sila, D.N.; Hendrickx, M.E. Extraction and characterization of pectic polysaccharides from easy- and hard-to-cook common beans (*Phaseolus vulgaris*). *Food Res. Int.* **2014**, *64*, 314–322. [\[CrossRef\]](#) [\[PubMed\]](#)
35. Shiga, T.M.; Lajolo, F.M.; Filisetti, T.M. Cell wall polysaccharides of common beans (*Phaseolus vulgaris* L.). *Food Sci. Technol.* **2003**, *23*, 141–148. [\[CrossRef\]](#)
36. Zhu, Y.; Feng, X.; Guo, J.; Wang, L.; Guo, X.; Zhu, X. A review of extraction, purification, structural properties and biological activities of legumes polysaccharides. *Front. Nutr.* **2022**, *9*, 1021448. [\[CrossRef\]](#) [\[PubMed\]](#)
37. Nakamura, A.; Ohboshi, H.; Sakai, M.; Nomura, K.; Nishiyama, S.; Ashida, H. Extraction of water-soluble polysaccharides from kidney beans and examination of their protein dispersion and stabilization properties under acidic conditions. *Food Res. Int.* **2021**, *144*, 110357. [\[CrossRef\]](#) [\[PubMed\]](#)
38. Ovodova, R.G.; Golovchenko, V.V.; Popov, S.V.; Popova, G.Y.; Paderin, N.M.; Shashkov, A.S.; Ovodov, Y.S. Chemical composition and anti-inflammatory activity of pectic polysaccharide isolated from celery stalks. *Food Chem.* **2009**, *114*, 610–615. [\[CrossRef\]](#)
39. Raffo, A.; Sinesio, F.; Moneta, E.; Nardo, N.; Peparaio, M.; Paoletti, F. Internal quality of fresh and cold stored celery petioles described by sensory profile, chemical and instrumental measurements. *Eur. Food Res. Technol.* **2006**, *222*, 590–599. [\[CrossRef\]](#)
40. Lara-Espinoza, C.; Carvajal-Millán, E.; Balandrán-Quintana, R.; López-Franco, Y.; Rascón-Chu, A. Pectin and Pectin-Based Composite Materials: Beyond Food Texture. *Molecules* **2018**, *23*, 942. [\[CrossRef\]](#)

41. Salamon, A.; Szafrńska, A.; Baryga, A.; Diowski, A.; Szymczyk, K.; Kowalska, H. Assessment of the Possibility of Using Sugar Beet Pulp with Molasses as By-Product for Enriching Flour and Production of Bread with Pro-Health Properties. *Appl. Sci.* **2024**, *14*, 10570. [\[CrossRef\]](#)
42. Lin, J.; Lei, H.; Han, Z.; Zeng, X.-A. Conformational flexibility and molecular weight influence the emulsification performance of pectin: A comparative study of sugar beet pectin and citrus pectin. *Food Hydrocoll.* **2024**, *146*, 109272. [\[CrossRef\]](#)
43. Voragen, A.G.J.; Coenen, G.-J.; Verhoef, R.P.; Schols, H.A. Pectin, a versatile polysaccharide present in plant cell walls. *Struct. Chem.* **2009**, *20*, 263–275. [\[CrossRef\]](#)
44. Subramani, R.; Pushparaj, C.; Ganesan, A. Kinetic modelling of Okra and *Gracilaria corticata* hydrocolloid mucilage polysaccharides. *J. Res. Innov. Food Sci. Technol.* **2024**, *13*, 17–22. [\[CrossRef\]](#)
45. Dantas, T.L.; Alonso Buriti, F.C.; Florentino, E.R. Okra (*Abelmoschus esculentus* L.) as a Potential Functional Food Source of Mucilage and Bioactive Compounds with Technological Applications and Health Benefits. *Plants* **2021**, *10*, 1683. [\[CrossRef\]](#)
46. Du, B.; Nie, S.; Peng, F.; Yang, Y.; Xu, B. A narrative review on conformational structure characterization of natural polysaccharides. *Food Front.* **2022**, *3*, 631–640. [\[CrossRef\]](#)
47. Farooq, U.; Malviya, R.; Sharma, P.K. Extraction and characterization of okra mucilage as pharmaceutical excipient. *Acad. J. Plant Sci.* **2013**, *6*, 168–172.
48. Golovchenko, V.V.; Khramova, D.S.; Ovodova, R.G.; Shashkov, A.S.; Ovodov, Y.S. Structure of pectic polysaccharides isolated from onion *Allium cepa* L. using a simulated gastric medium and their effect on intestinal absorption. *Food Chem.* **2012**, *134*, 1813–1822. [\[CrossRef\]](#) [\[PubMed\]](#)
49. Jaime, L.; Mollá, E.; Fernández, A.; Martín-Cabrejas, M.A.; López-Andréu, F.J.; Esteban, R.M. Structural Carbohydrate Differences and Potential Source of Dietary Fiber of Onion (*Allium cepa* L.) Tissues. *J. Agric. Food Chem.* **2002**, *50*, 122–128. [\[CrossRef\]](#)
50. Zdunek, A.; Pieczywek, P.M.; Cybulska, J. The primary, secondary, and structures of higher levels of pectin polysaccharides. *Compr. Rev. Food Sci. Food Saf.* **2021**, *20*, 1101–1117. [\[CrossRef\]](#) [\[PubMed\]](#)
51. Rascón-Chu, A.; Martínez-López, A.L.; Carvajal-Millán, E.; Ponce de León-Renova, N.E.; Márquez-Escalante, J.A.; Romo-Chacón, A. Pectin from low quality ‘Golden Delicious’ apples: Composition and gelling capability. *Food Chem.* **2009**, *116*, 101–103. [\[CrossRef\]](#)
52. Lattimer, J.M.; Haub, M.D. Effects of Dietary Fiber and Its Components on Metabolic Health. *Nutrients* **2010**, *2*, 1266–1289. [\[CrossRef\]](#)
53. Galant, A.L.; Luzio, G.A.; Widmer, W.W.; Cameron, R.G. Compositional and structural characterization of pectic material from Frozen Concentrated Orange Juice. *Food Hydrocoll.* **2014**, *35*, 661–669. [\[CrossRef\]](#)
54. Nile, S.H.; Park, S.W. Total, soluble, and insoluble dietary fibre contents of wild growing edible mushrooms. *Czech J. Food Sci.* **2014**, *32*, 302–307. [\[CrossRef\]](#)
55. Zhu, F.; Du, B.; Bian, Z.; Xu, B. Beta-glucans from edible and medicinal mushrooms: Characteristics, physicochemical and biological activities. *J. Food Compos. Anal.* **2015**, *41*, 165–173. [\[CrossRef\]](#)
56. Sari, M.; Prange, A.; Lelley, J.I.; Hambitzer, R. Screening of beta-glucan contents in commercially cultivated and wild growing mushrooms. *Food Chem.* **2017**, *216*, 45–51. [\[CrossRef\]](#)
57. Akter, A.; Sobuj, M.K.A.; Islam, M.S.; Chakroborty, K.; Tasnim, N.; Ayon, M.H.; Hossain, M.F.; Rafiquzzaman, S.M. Seaweed polysaccharides: Sources, structure and biomedical applications with special emphasis on antiviral potentials. *Future Foods* **2024**, *10*, 100440. [\[CrossRef\]](#)
58. Abasalizadeh, F.; Moghaddam, S.V.; Alizadeh, E.; Akbari, E.; Kashani, E.; Fazljou, S.M.B.; Torbati, M.; Akbarzadeh, A. Alginate-based hydrogels as drug delivery vehicles in cancer treatment and their applications in wound dressing and 3D bioprinting. *J. Biol. Eng.* **2020**, *14*, 8. [\[CrossRef\]](#)
59. Premarathna, A.D.; Tuvikene, R.; Fernando, P.H.P.; Adhikari, R.; Perera, M.C.N.; Ranaheewa, T.H.; Howlader, M.M.; Wangchuk, P.; Jayasooriya, A.P.; Rajapakse, R.P.V.J. Comparative analysis of proximate compositions, mineral and functional chemical groups of 15 different seaweed species. *Sci. Rep.* **2022**, *12*, 19610. [\[CrossRef\]](#)
60. Cotas, J.; Pacheco, D.; Araujo, G.S.; Valado, A.; Critchley, A.T.; Pereira, L. On the Health Benefits vs. Risks of Seaweeds and Their Constituents: The Curious Case of the Polymer Paradigm. *Mar. Drugs* **2021**, *19*, 164. [\[CrossRef\]](#) [\[PubMed\]](#)
61. Yao, W.; Gong, Y.; Li, L.; Hu, X.; You, L. The effects of dietary fibers from rice bran and wheat bran on gut microbiota: An overview. *Food Chem. X* **2022**, *13*, 100252. [\[CrossRef\]](#) [\[PubMed\]](#)
62. Chen, Z.; Li, S.; Fu, Y.; Li, C.; Chen, D.; Chen, H. Arabinoxylan structural characteristics, interaction with gut microbiota and potential health functions. *J. Funct. Foods* **2019**, *54*, 536–551. [\[CrossRef\]](#)
63. Cheng, W.; Sun, Y.; Fan, M.; Li, Y.; Wang, L.; Qian, H. Wheat bran, as the resource of dietary fiber: A review. *Crit. Rev. Food Sci. Nutr.* **2022**, *62*, 7269–7281. [\[CrossRef\]](#)
64. Jefferson, A.; Adolphus, K. The Effects of Intact Cereal Grain Fibers, Including Wheat Bran on the Gut Microbiota Composition of Healthy Adults: A Systematic Review. *Front. Nutr.* **2019**, *6*, 33. [\[CrossRef\]](#)

65. Leschonski, K.P.; Mortensen, M.S.; Hansen, L.B.S.; Krogh, K.B.R.M.; Kabel, M.A.; Laursen, M.F. Structure-dependent stimulation of gut bacteria by arabinoxylo-oligosaccharides (AXOS): A review. *Gut Microbes* **2024**, *16*, 2430419. [[CrossRef](#)]
66. Müller, M.; Hermes, G.D.A.; Emanuel, E.C.; Holst, J.J.; Zoetendal, E.G.; Smidt, H.; Troost, F.; Schaap, F.G.; Damink, S.O.; Jocken, J.W.E.; et al. Effect of wheat bran derived prebiotic supplementation on gastrointestinal transit, gut microbiota, and metabolic health: A randomized controlled trial in healthy adults with a slow gut transit. *Gut Microbes* **2020**, *12*, 1704141. [[CrossRef](#)] [[PubMed](#)]
67. Rasane, P.; Jha, A.; Sabikhi, L.; Kumar, A.; Unnikrishnan, V.S. Nutritional advantages of oats and opportunities for its processing as value added foods—A review. *J. Food Sci. Technol.* **2015**, *52*, 662–675. [[CrossRef](#)] [[PubMed](#)]
68. Khorasaniha, R.; Olof, H.; Voisin, A.; Armstrong, K.; Wine, E.; Vasanthan, T.; Armstrong, H. Diversity of fibers in common foods: Key to advancing dietary research. *Food Hydrocoll.* **2023**, *139*, 108495. [[CrossRef](#)]
69. Cerletti, C.; Esposito, S.; Iacoviello, L. Edible Mushrooms and Beta-Glucans: Impact on Human Health. *Nutrients* **2021**, *13*, 2195. [[CrossRef](#)]
70. Dong, J.-I.; Yu, X.; Dong, L.-e.; Shen, R.-I. In vitro fermentation of oat β -glucan and hydrolysates by fecal microbiota and selected probiotic strains. *J. Sci. Food Agric.* **2017**, *97*, 4198–4203. [[CrossRef](#)]
71. US Food and Drug Administration. *Food Labeling: Health Claims; Oats and Coronary Heart Disease*; US Food and Drug Administration: Silver Spring, MD, USA, 1997; Volume 62.
72. Sárossy, Z.; Tenkanen, M.; Pitkänen, L.; Bjerre, A.-B.; Plackett, D. Extraction and chemical characterization of rye arabinoxylan and the effect of β -glucan on the mechanical and barrier properties of cast arabinoxylan films. *Food Hydrocoll.* **2013**, *30*, 206–216. [[CrossRef](#)]
73. Knudsen, K.E.B.; Lærke, H.N. REVIEW: Rye Arabinoxylans: Molecular Structure, Physicochemical Properties and Physiological Effects in the Gastrointestinal Tract. *Cereal Chem.* **2010**, *87*, 353–362. [[CrossRef](#)]
74. Ounnas, F.; Privé, F.; Salen, P.; Gaci, N.; Tottey, W.; Calani, L.; Bresciani, L.; López-Gutiérrez, N.; Hazane-Puch, F.; Laporte, F.; et al. Whole Rye Consumption Improves Blood and Liver n-3 Fatty Acid Profile and Gut Microbiota Composition in Rats. *PLoS ONE* **2016**, *11*, e0148118. [[CrossRef](#)]
75. Dongowski, G.; Huth, M.; Gebhardt, E.; Flamme, W. Dietary Fiber-Rich Barley Products Beneficially Affect the Intestinal Tract of Rats. *J. Nutr.* **2002**, *132*, 3704–3714. [[CrossRef](#)] [[PubMed](#)]
76. Ain, H.B.U.; Saeed, F.; Khan, M.A.; Niaz, B.; Rohi, M.; Nasir, M.A.; Tufail, T.; Anbreen, F.; Anjum, F.M. Modification of barley dietary fiber through thermal treatments. *Food Sci. Nutr.* **2019**, *7*, 1816–1820. [[CrossRef](#)] [[PubMed](#)]
77. Mio, K.; Goto, Y.; Matsuoka, T.; Komatsu, M.; Ishii, C.; Yang, J.; Kobayashi, T.; Aoe, S.; Fukuda, S. Barley β -glucan consumption improves glucose tolerance by increasing intestinal succinate concentrations. *npj Sci. Food* **2024**, *8*, 69. [[CrossRef](#)]
78. Wang, Y.; Ames, N.P.; Tun, H.M.; Tosh, S.M.; Jones, P.J.; Khafipour, E. High Molecular Weight Barley β -Glucan Alters Gut Microbiota Toward Reduced Cardiovascular Disease Risk. *Front. Microbiol.* **2016**, *7*, 129. [[CrossRef](#)]
79. Lante, A.; Canazza, E.; Tessari, P. Beta-Glucans of Cereals: Functional and Technological Properties. *Nutrients* **2023**, *15*, 2124. [[CrossRef](#)]
80. US Food and Drug Administration. *CFR-Code of Federal Regulations Title 21*; US Food and Drug Administration: Washington, DC, USA, 2018.
81. EFSA Panel on Dietetic Products, Nutrition and Allergies (NDA). Scientific Opinion on the substantiation of a health claim related to barley beta-glucans and lowering of blood cholesterol and reduced risk of (coronary) heart disease pursuant to Article 14 of Regulation (EC) No 1924/2006. *EFSA J.* **2011**, *9*, 2470. [[CrossRef](#)]
82. Nandan, A.; Koirala, P.; Dutt Tripathi, A.; Vikranta, U.; Shah, K.; Gupta, A.J.; Agarwal, A.; Nirmal, N. Nutritional and functional perspectives of pseudocereals. *Food Chem.* **2024**, *448*, 139072. [[CrossRef](#)] [[PubMed](#)]
83. Wefers, D.; Bunzel, M. Characterization of Dietary Fiber Polysaccharides from Dehulled Common Buckwheat (*Fagopyrum esculentum*) Seeds. *Cereal Chem.* **2015**, *92*, 598–603. [[CrossRef](#)]
84. Valido, E.; Stoyanov, J.; Gorreja, F.; Stojic, S.; Niehot, C.; Kieft-de Jong, J.; Llanaj, E.; Muka, T.; Glisic, M. Systematic Review of Human and Animal Evidence on the Role of Buckwheat Consumption on Gastrointestinal Health. *Nutrients* **2022**, *15*, 1. [[CrossRef](#)]
85. Tas, A.A.; Shah, A.U. The replacement of cereals by legumes in extruded snack foods: Science, technology and challenges. *Trends Food Sci. Technol.* **2021**, *116*, 701–711. [[CrossRef](#)]
86. Nakamura, A.; Furuta, H.; Maeda, H.; Takao, T.; Nagamatsu, Y. Structural Studies by Stepwise Enzymatic Degradation of the Main Backbone of Soybean Soluble Polysaccharides Consisting of Galacturonan and Rhamnogalacturonan. *Biosci. Biotechnol. Biochem.* **2002**, *66*, 1301–1313. [[CrossRef](#)]
87. Pérez-López, E.; Cela, D.; Costabile, A.; Mateos-Aparicio, I.; Rupérez, P. In vitro fermentability and prebiotic potential of soyabean Okara by human faecal microbiota. *Br. J. Nutr.* **2016**, *116*, 1116–1124. [[CrossRef](#)]
88. Fan, H.; Zhang, Y.; Swallah, M.S.; Wang, S.; Zhang, J.; Fang, J.; Lu, J.; Yu, H. Structural Characteristics of Insoluble Dietary Fiber from Okara with Different Particle Sizes and Their Prebiotic Effects in Rats Fed High-Fat Diet. *Foods* **2022**, *11*, 1298. [[CrossRef](#)]

89. Zhihui, D.; Juan, W. Comparison of nutrient components of mung bean hull and peeled mung bean. *Mod. Food Sci. Technol.* **2010**, *26*, 656–659.
90. Guillon, F.; Champ, M.M.J. Carbohydrate fractions of legumes: Uses in human nutrition and potential for health. *Br. J. Nutr.* **2002**, *88*, 293–306. [CrossRef] [PubMed]
91. Hou, D.; Zhao, Q.; Chen, B.; Ren, X.; Yousaf, L.; Shen, Q. Dietary supplementation with mung bean coat alleviates the disorders in serum glucose and lipid profile and modulates gut microbiota in high-fat diet and streptozotocin-induced prediabetic mice. *J. Food Sci.* **2021**, *86*, 4183–4196. [CrossRef] [PubMed]
92. Weng, J.; Zhu, Y.; Wen, A.; Qin, L. Butyric acid generation from kidney beans mediated by gut microbiota based on the butyryl-CoA:acetate CoA-transferase pathway. *Food Biosci.* **2024**, *57*, 103520. [CrossRef]
93. Kilua, A.; Chihiro, H.; Han, K.-H.; Homma, K.; Fukuma, N.; Kamitani, T.; Suzuki, T.; Fukushima, M. Whole kidney bean (*Phaseolus vulgaris*) and bean hull reduce the total serum cholesterol, modulate the gut microbiota and affect the caecal fermentation in rats. *Bioact. Carbohydr. Diet. Fibre* **2020**, *24*, 100232. [CrossRef]
94. Zhao, D.; Cao, J.; Jin, H.; Shan, Y.; Fang, J.; Liu, F. Beneficial impacts of fermented celery (*Apium graveolens* L.) juice on obesity prevention and gut microbiota modulation in high-fat diet fed mice. *Food Funct.* **2021**, *12*, 9151–9164. [CrossRef]
95. Nordic Sugar. *Sugar Beet Fibre: Physiological Effects & Clinical Studies*; Nordic Sugar: Copenhagen, Denmark, 2012.
96. Masarweh, C.; Maldonado-Gomez, M.; Paviani, B.; Bhattacharya, M.; Weng, C.-Y.; Suarez, C.; Ehlers-Cheang, S.; Stacy, A.; Castillo, J.; Krishnakumar, N.; et al. Generation of novel prebiotic oligosaccharide pools from fiber drives biological insight in bacterial glycan metabolism. *Appl. Environ. Microbiol.* **2025**, *91*, e0207724. [CrossRef]
97. Wu, D.-T.; Nie, X.-R.; Gan, R.-Y.; Guo, H.; Fu, Y.; Yuan, Q.; Zhang, Q.; Qin, W. In vitro digestion and fecal fermentation behaviors of a pectic polysaccharide from okra (*Abelmoschus esculentus*) and its impacts on human gut microbiota. *Food Hydrocoll.* **2021**, *114*, 106577. [CrossRef]
98. Lu, S.; Flanagan, B.M.; Mikkelsen, D.; Williams, B.A.; Gidley, M.J. In vitro fermentation of onion cell walls and model polysaccharides using human faecal inoculum: Effects of molecular interactions and cell wall architecture. *Food Hydrocoll.* **2022**, *124*, 107257. [CrossRef]
99. Yang, J.-S.; Mu, T.-H.; Ma, M.-M. Extraction, structure, and emulsifying properties of pectin from potato pulp. *Food Chem.* **2018**, *244*, 197–205. [CrossRef]
100. Pastuszevska, B.; Antushevich, H.; Tusnio, A.; Taciak, M. Potato dietary fibre—Preliminary characterization of the properties and nutritional effects—A review. *Pol. J. Food Nutr. Sci.* **2009**, *59*, 205–210.
101. Muir, J.G.; O'Dea, K. Measurement of resistant starch: Factors affecting the amount of starch escaping digestion in vitro. *Am. J. Clin. Nutr.* **1992**, *56*, 123–127. [CrossRef] [PubMed]
102. Richter, C.; Fulgoni, K.; Fulgoni, V.L., 3rd; Johnson, B.; Kijek, M.; Maniscalco, S.; Psota, T. Assessment of the unique nutrient contribution of white potatoes in the diet and the nutrient implications of replacing Refined and Whole Grains with Starchy Vegetables. *Front. Nutr.* **2025**, *12*, 1692564. [CrossRef] [PubMed]
103. Bush, J.R.; Baisley, J.; Harding, S.V.; Alfa, M.J. Consumption of SolnulTM Resistant Potato Starch Produces a Prebiotic Effect in a Randomized, Placebo-Controlled Clinical Trial. *Nutrients* **2023**, *15*, 1582. [CrossRef]
104. Harvard, T.H. Chan School of Public Health. Brussels Sprouts. Available online: <https://nutritionsource.hsph.harvard.edu/food-features/brussels-sprouts/> (accessed on 1 March 2026).
105. US Department of Agriculture. *Brussels Sprouts, Raw—Components—Foundation*; US Department of Agriculture: Washington, DC, USA, 2024.
106. Enkhmaa, B.; Surampudi, P.; Anuurad, E.; Feingold, K.R.; Ahmed, S.F.; Anawalt, B. Lifestyle Changes: Effect of Diet, Exercise, Functional Food, and Obesity Treatment on Lipids and Lipoproteins. In *Endotext*, Updated ed.; MDText.com, Inc.: South Dartmouth, MA, USA, 2018.
107. Humblot, C.; Bruneau, A.; Sutren, M.; Lhoste, E.F.; Doré, J.; Andrieux, C.; Rabot, S. Brussels sprouts, inulin and fermented milk alter the faecal microbiota of human microbiota-associated rats as shown by PCR-temporal temperature gradient gel electrophoresis using universal, *Lactobacillus* and *Bifidobacterium* 16S rRNA gene primers. *Br. J. Nutr.* **2005**, *93*, 677–684. [CrossRef]
108. Koutsos, A.; Tuohy, K.M.; Lovegrove, J.A. Apples and cardiovascular health—Is the gut microbiota a core consideration? *Nutrients* **2015**, *7*, 3959–3998. [CrossRef]
109. Koutsos, A.; Lima, M.; Conterno, L.; Gasperotti, M.; Bianchi, M.; Fava, F.; Vrhovsek, U.; Lovegrove, J.A.; Tuohy, K.M. Effects of Commercial Apple Varieties on Human Gut Microbiota Composition and Metabolic Output Using an In Vitro Colonic Model. *Nutrients* **2017**, *9*, 533. [CrossRef] [PubMed]
110. Hamid, S.; Sharma, K.; Kumar, K.; Thakur, A. Types and Cultivation of Citrus Fruits. In *Citrus Fruits and Juice: Processing and Quality Profiling*; Gupta, A.K., Kour, J., Mishra, P., Eds.; Springer Nature: Singapore, 2024; pp. 17–43.
111. Sharma, R.; Nanda, R.; Bhagat, N. Citrus Flavours. In *Citrus Fruits and Juice: Processing and Quality Profiling*; Springer Nature: Singapore, 2024; pp. 275–299.

112. Mansi; Monika; Gupta, A.K.; Naik, B.; Kumar, V.; Jha, A.K. Role of Citrus Juice Sacs. In *Citrus Fruits and Juice: Processing and Quality Profiling*; Gupta, A.K., Kour, J., Mishra, P., Eds.; Springer Nature: Singapore, 2024; pp. 259–273.
113. Pratiksha; Adhikary, M. Industrial Production of Citrus By-products and Its Processing Techniques. In *Citrus Fruits and Juice: Processing and Quality Profiling*; Gupta, A.K., Kour, J., Mishra, P., Eds.; Springer Nature: Singapore, 2024; pp. 391–417.
114. Beukema, M.; Faas, M.M.; de Vos, P. The effects of different dietary fiber pectin structures on the gastrointestinal immune barrier: Impact via gut microbiota and direct effects on immune cells. *Exp. Mol. Med.* **2020**, *52*, 1364–1376. [[CrossRef](#)]
115. Hotchkiss, A.T.; Chau, H.K.; Strahan, G.D.; Nuñez, A.; Simon, S.; White, A.K.; Dieng, S.; Heuberger, E.R.; Yadav, M.P.; Hirsch, J. Structure and composition of blueberry fiber pectin and xyloglucan that bind anthocyanins during fruit puree processing. *Food Hydrocoll.* **2021**, *116*, 106572. [[CrossRef](#)]
116. Lin, Z.; Pattathil, S.; Hahn, M.G.; Wicker, L. Blueberry cell wall fractionation, characterization and glycome profiling. *Food Hydrocoll.* **2019**, *90*, 385–393. [[CrossRef](#)]
117. Guglielmetti, S.; Fracassetti, D.; Taverniti, V.; Del Bo', C.; Vendrame, S.; Klimis-Zacas, D.; Arioli, S.; Riso, P.; Porrini, M. Differential Modulation of Human Intestinal Bifidobacterium Populations after Consumption of a Wild Blueberry (*Vaccinium angustifolium*) Drink. *J. Agric. Food Chem.* **2013**, *61*, 8134–8140. [[CrossRef](#)]
118. Aida, F.M.N.A.; Shuhaimi, M.; Yazid, M.; Maaruf, A.G. Mushroom as a potential source of prebiotics: A review. *Trends Food Sci. Technol.* **2009**, *20*, 567–575. [[CrossRef](#)]
119. Cheung, P.C.K. Mini-review on edible mushrooms as source of dietary fiber: Preparation and health benefits. *Food Sci. Hum. Wellness* **2013**, *2*, 162–166. [[CrossRef](#)]
120. Morales, D.; Rutkevski, R.; Villalva, M.; Abreu, H.; Soler-Rivas, C.; Santoyo, S.; Iacomini, M.; Smiderle, F.R. Isolation and comparison of α - and β -D-glucans from shiitake mushrooms (*Lentinula edodes*) with different biological activities. *Carbohydr. Polym.* **2020**, *229*, 115521. [[CrossRef](#)]
121. Kozarski, M.; Klaus, A.; van Griensven, L.; Jakovljevic, D.; Todorovic, N.; Wan-Mohtar, W.A.A.Q.I.; Vunduk, J. Mushroom β -glucan and polyphenol formulations as natural immunity boosters and balancers: Nature of the application. *Food Sci. Hum. Wellness* **2023**, *12*, 378–396. [[CrossRef](#)]
122. Vetter, J. Chitin content of cultivated mushrooms *Agaricus bisporus*, *Pleurotus ostreatus* and *Lentinula edodes*. *Food Chem.* **2007**, *102*, 6–9. [[CrossRef](#)]
123. Zhao, J.; Hu, Y.; Qian, C.; Hussain, M.; Liu, S.; Zhang, A.; He, R.; Sun, P. The Interaction between Mushroom Polysaccharides and Gut Microbiota and Their Effect on Human Health: A Review. *Biology* **2023**, *12*, 122. [[CrossRef](#)] [[PubMed](#)]
124. Peñalver, R.; Lorenzo, J.M.; Ros, G.; Amarowicz, R.; Pateiro, M.; Nieto, G. Seaweeds as a Functional Ingredient for a Healthy Diet. *Mar. Drugs* **2020**, *18*, 301. [[CrossRef](#)] [[PubMed](#)]
125. Gotteland, M.; Riveros, K.; Gasaly, N.; Carcamo, C.; Magne, F.; Liabeuf, G.; Beattie, A.; Rosenfeld, S. The Pros and Cons of Using Algal Polysaccharides as Prebiotics. *Front. Nutr.* **2020**, *7*, 163. [[CrossRef](#)] [[PubMed](#)]
126. Sender, R.; Fuchs, S.; Milo, R. Revised Estimates for the Number of Human and Bacteria Cells in the Body. *PLoS Biol.* **2016**, *14*, e1002533. [[CrossRef](#)]
127. Bhattacharya, T.; Ghosh, T.S.; Mande, S.S. Global Profiling of Carbohydrate Active Enzymes in Human Gut Microbiome. *PLoS ONE* **2015**, *10*, e0142038. [[CrossRef](#)]
128. American Society for Microbiology. FAQ: Human Microbiome. Available online: <https://www.ncbi.nlm.nih.gov/books/NBK562894/> (accessed on 9 December 2024).
129. Onyango, S.O.; Juma, J.; De Paepe, K.; Van de Wiele, T. Oral and Gut Microbial Carbohydrate-Active Enzymes Landscape in Health and Disease. *Front. Microbiol.* **2021**, *12*, 653448. [[CrossRef](#)] [[PubMed](#)]
130. Venter, C.; Meyer, R.W.; Greenhawt, M.; Pali-Schöll, I.; Nwaru, B.; Roduit, C.; Untersmayr, E.; Adel-Patient, K.; Agache, I.; Agostoni, C.; et al. Role of dietary fiber in promoting immune health—An EAACI position paper. *Allergy* **2022**, *77*, 3185–3198. [[CrossRef](#)]
131. Jaeger, J.W.; Brandt, A.; Gui, W.; Yergaliyev, T.; Hernández-Arriaga, A.; Muthu, M.M.; Edlund, K.; Elashy, A.; Molinaro, A.; Möckel, D.; et al. Microbiota modulation by dietary oat beta-glucan prevents steatotic liver disease progression. *JHEP Rep.* **2024**, *6*, 100987. [[CrossRef](#)]
132. Wang, M.; Wichienchot, S.; He, X.; Fu, X.; Huang, Q.; Zhang, B. In vitro colonic fermentation of dietary fibers: Fermentation rate, short-chain fatty acid production and changes in microbiota. *Trends Food Sci. Technol.* **2019**, *88*, 1–9. [[CrossRef](#)]
133. Zhang, F.; Fan, D.; Huang, J.-l.; Zuo, T. The gut microbiome: Linking dietary fiber to inflammatory diseases. *Med. Microecol.* **2022**, *14*, 100070. [[CrossRef](#)]
134. Xiao, M.; Zhang, C.; Duan, H.; Narbad, A.; Zhao, J.; Chen, W.; Zhai, Q.; Yu, L.; Tian, F. Cross-feeding of bifidobacteria promotes intestinal homeostasis: A lifelong perspective on the host health. *npj Biofilms Microbiomes* **2024**, *10*, 47. [[CrossRef](#)]
135. Auer, E.; Lazuka, A.; Huguenin-Bizot, B.; Jehmlich, N.; Déjean, S.; Lombard, V.; Henrissat, B.; O'Donohue, M.; Hernandez-Raquet, G. Horizontal metaproteomics and CAZymes analysis of lignocellulolytic microbial consortia selectively enriched from cow rumen and termitegut. *ISME Commun.* **2024**, *3*, 134. [[CrossRef](#)]

136. Qu, L.; Zhang, R.; Chu, Z.; Cai, J.; He, Y.; Zhang, X.; Liu, J.; Xie, X.; Cao, Y. Gut microbiota: A key player for soluble dietary fiber in regulating inflammatory disease. *J. Adv. Res.* **2025**, *in press*. [\[CrossRef\]](#)
137. Fusco, W.; Lorenzo, M.B.; Cintoni, M.; Porcari, S.; Rinninella, E.; Kaitsas, F.; Lener, E.; Mele, M.C.; Gasbarrini, A.; Collado, M.C.; et al. Short-Chain Fatty-Acid-Producing Bacteria: Key Components of the Human Gut Microbiota. *Nutrients* **2023**, *15*, 2211. [\[CrossRef\]](#)
138. Prado, S.B.R.D.; Minguzzi, B.T.; Hoffmann, C.; Fabi, J.P. Modulation of human gut microbiota by dietary fibers from unripe and ripe papayas: Distinct polysaccharide degradation using a colonic in vitro fermentation model. *Food Chem.* **2021**, *348*, 129071. [\[CrossRef\]](#) [\[PubMed\]](#)
139. Mansuy-Aubert, V.; Ravussin, Y. Short chain fatty acids: The messengers from down below. *Front. Neurosci.* **2023**, *17*, 1197759. [\[CrossRef\]](#) [\[PubMed\]](#)
140. Frost, G.; Sleeth, M.L.; Sahuri-Arisoylu, M.; Lizarbe, B.; Cerdan, S.; Brody, L.; Anastasovska, J.; Ghourab, S.; Hankir, M.; Zhang, S.; et al. The short-chain fatty acid acetate reduces appetite via a central homeostatic mechanism. *Nat. Commun.* **2014**, *5*, 3611. [\[CrossRef\]](#) [\[PubMed\]](#)
141. Van-Wehle, T.; Vital, M. Investigating the response of the butyrate production potential to major fibers in dietary intervention studies. *npj Biofilms Microbiomes* **2024**, *10*, 63. [\[CrossRef\]](#) [\[PubMed\]](#)
142. Recharla, N.; Geesala, R.; Shi, X.-Z. Gut Microbial Metabolite Butyrate and Its Therapeutic Role in Inflammatory Bowel Disease: A Literature Review. *Nutrients* **2023**, *15*, 2275. [\[CrossRef\]](#) [\[PubMed\]](#)
143. Wrzosek, L.; Miquel, S.; Noordine, M.L.; Bouet, S.; Chevalier-Curt, M.J.; Robert, V.; Philippe, C.; Bridonneau, C.; Cherbuy, C.; Robbe-Masselot, C.; et al. Bacteroides thetaiotaomicron and Faecalibacterium prausnitzii influence the production of mucus glycans and the development of goblet cells in the colonic epithelium of a gnotobiotic model rodent. *BMC Biol.* **2013**, *11*, 61. [\[CrossRef\]](#) [\[PubMed\]](#)
144. Price, C.E.; Valls, R.A.; Ramsey, A.R.; Loeven, N.A.; Jones, J.T.; Barrack, K.E.; Schwartzman, J.D.; Royce, D.B.; Cramer, R.A.; Madan, J.C.; et al. Intestinal Bacteroides modulates inflammation, systemic cytokines, and microbial ecology via propionate in a mouse model of cystic fibrosis. *mBio* **2024**, *15*, e0314423. [\[CrossRef\]](#) [\[PubMed\]](#)
145. Nielson, B.T.; Schmidt, A.W.; Venkataraman, A.; Kim, K.S.; Waldron, C.; Schmidt, T.M. Dynamics of Human Gut Microbiota and Short-Chain Fatty Acids in Response to Dietary Interventions with Three Fermentable Fibers. *mBio* **2019**, *10*, e02566-18. [\[CrossRef\]](#) [\[PubMed\]](#)
146. Kjølbæk, L.; Benítez-Páez, A.; Gómez del Pulgar, E.M.; Brahe, L.K.; Liebisch, G.; Matysik, S.; Rampelli, S.; Vermeiren, J.; Brigidi, P.; Larsen, L.H.; et al. Arabinoxylan oligosaccharides and polyunsaturated fatty acid effects on gut microbiota and metabolic markers in overweight individuals with signs of metabolic syndrome: A randomized cross-over trial. *Clin. Nutr.* **2020**, *39*, 67–79. [\[CrossRef\]](#) [\[PubMed\]](#)
147. Cronin, P.; Joyce, S.A.; O'Toole, P.W.; O'Connor, E.M. Dietary Fibre Modulates the Gut Microbiota. *Nutrients* **2021**, *13*, 1655. [\[CrossRef\]](#)
148. Cheng, J.; Guo, M.; Wang, C. Chapter 3—Dietary fiber and dietary fiber-rich foods. In *Functional Foods*, 2nd ed.; Guo, M., Ed.; Woodhead Publishing: Cambridge, UK, 2025; pp. 55–103.
149. Ross, F.C.; Patangia, D.; Grimaud, G.; Lavelle, A.; Dempsey, E.M.; Ross, R.P.; Stanton, C. The interplay between diet and the gut microbiome: Implications for health and disease. *Nat. Rev. Microbiol.* **2024**, *22*, 671–686. [\[CrossRef\]](#) [\[PubMed\]](#)
150. Ma, W.; Nguyen, L.H.; Song, M.; Wang, D.D.; Franzosa, E.A.; Cao, Y.; Joshi, A.; Drew, D.A.; Mehta, R.; Ivey, K.L.; et al. Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. *Genome Med.* **2021**, *13*, 102. [\[CrossRef\]](#)
151. Sun, Y.; Zhang, S.; Nie, Q.; He, H.; Tan, H.; Geng, F.; Ji, H.; Hu, J.; Nie, S. Gut firmicutes: Relationship with dietary fiber and role in host homeostasis. *Crit. Rev. Food Sci. Nutr.* **2023**, *63*, 12073–12088. [\[CrossRef\]](#)
152. Guan, Z.-W.; Yu, E.-Z.; Feng, Q. Soluble Dietary Fiber, One of the Most Important Nutrients for the Gut Microbiota. *Molecules* **2021**, *26*, 6802. [\[CrossRef\]](#)
153. Rodriguez, C.I.; Isobe, K.; Martiny, J.B.H.; Cope, E.K. Short-term dietary fiber interventions produce consistent gut microbiome responses across studies. *mSystems* **2024**, *9*, e0013324. [\[CrossRef\]](#)
154. Inman, M. How Bacteria Turn Fiber into Food. *PLoS Biol.* **2011**, *9*, e1001227. [\[CrossRef\]](#)
155. Luis, A.S.; Briggs, J.; Zhang, X.; Farnell, B.; Ndeh, D.; Labourel, A.; Baslé, A.; Cartmell, A.; Terrapon, N.; Stott, K.; et al. Dietary pectic glycans are degraded by coordinated enzyme pathways in human colonic Bacteroides. *Nat. Microbiol.* **2018**, *3*, 210–219. [\[CrossRef\]](#) [\[PubMed\]](#)
156. Ze, X.; Duncan, S.H.; Louis, P.; Flint, H.J. *Ruminococcus bromii* is a keystone species for the degradation of resistant starch in the human colon. *ISME J.* **2012**, *6*, 1535–1543. [\[CrossRef\]](#) [\[PubMed\]](#)
157. Healey, G.; Murphy, R.; Butts, C.; Brough, L.; Whelan, K.; Coad, J. Habitual dietary fibre intake influences gut microbiota response to an inulin-type fructan prebiotic: A randomised, double-blind, placebo-controlled, cross-over, human intervention study. *Br. J. Nutr.* **2018**, *119*, 176–189. [\[CrossRef\]](#)

158. Lai, H.; Li, Y.; He, Y.; Chen, F.; Mi, B.; Li, J.; Xie, J.; Ma, G.; Yang, J.; Xu, K.; et al. Effects of dietary fibers or probiotics on functional constipation symptoms and roles of gut microbiota: A double-blinded randomized placebo trial. *Gut Microbes* **2023**, *15*, 2197837. [\[CrossRef\]](#)
159. Yasukawa, Z.; Inoue, R.; Ozeki, M.; Okubo, T.; Takagi, T.; Honda, A.; Naito, Y. Effect of Repeated Consumption of Partially Hydrolyzed Guar Gum on Fecal Characteristics and Gut Microbiota: A Randomized, Double-Blind, Placebo-Controlled, and Parallel-Group Clinical Trial. *Nutrients* **2019**, *11*, 2170. [\[CrossRef\]](#)
160. Hoffmann Sardá, F.A.; Giuntini, E.B.; Oliveira, A.; Souza, G.S.; Prado, S.B.R.; Taddei, C.R.; Tadini, C.C.; Bittinger, K.; Bushman, F.D.; Menezes, E.W.; et al. Baseline intestinal microbiota composition influences response to a real-world dietary fiber intervention. *npj Biofilms Microbiomes* **2025**, *11*, 203. [\[CrossRef\]](#)
161. Bobade, H.; Gupta, A.; Sharma, S. Chapter 20—Beta-glucan. In *Nutraceuticals and Health Care*; Kour, J., Nayik, G.A., Eds.; Academic Press: Cambridge, MA, USA, 2022; pp. 343–358.
162. Caffall, K.H.; Mohnen, D. The structure, function, and biosynthesis of plant cell wall pectic polysaccharides. *Carbohydr. Res.* **2009**, *344*, 1879–1900. [\[CrossRef\]](#)
163. Wang, J.; Bai, J.; Fan, M.; Li, T.; Li, Y.; Qian, H.; Wang, L.; Zhang, H.; Qi, X.; Rao, Z. Cereal-derived arabinoxylans: Structural features and structure–activity correlations. *Trends Food Sci. Technol.* **2020**, *96*, 157–165. [\[CrossRef\]](#)
164. Alonso-Allende, J.; Milagro, F.I.; Aranaz, P. Health Effects and Mechanisms of Inulin Action in Human Metabolism. *Nutrients* **2024**, *16*, 2935. [\[CrossRef\]](#)
165. Ignatova, I.; Arsov, A.; Petrova, P.; Petrov, K. Prebiotic Effects of α - and β -Galactooligosaccharides: The Structure-Function Relation. *Molecules* **2025**, *30*, 803. [\[CrossRef\]](#) [\[PubMed\]](#)
166. Zhu, J.; Bai, Y.; Gilbert, R.G. Effects of the Molecular Structure of Starch in Foods on Human Health. *Foods* **2023**, *12*, 2263. [\[CrossRef\]](#)
167. Fischer, M.H.; Yu, N.; Gray, G.R.; Ralph, J.; Anderson, L.; Marlett, J.A. The gel-forming polysaccharide of psyllium husk (*Plantago ovata* Forsk). *Carbohydr. Res.* **2004**, *339*, 2009–2017. [\[CrossRef\]](#)
168. Mudgil, D.; Barak, S.; Khatkar, B.S. Guar gum: Processing, properties and food applications-A Review. *J. Food Sci. Technol.* **2014**, *51*, 409–418. [\[CrossRef\]](#)
169. Ríos-Covián, D.; Ruas-Madiedo, P.; Margolles, A.; Gueimonde, M.; De Los Reyes-gavilán, C.G.; Salazar, N. Intestinal short chain fatty acids and their link with diet and human health. *Front. Microbiol.* **2016**, *7*, 185. [\[CrossRef\]](#)
170. Ma, W.-w.; Huang, Z.-Q.; Liu, K.; Li, D.-Z.; Mo, T.-L.; Liu, Q. The role of intestinal microbiota and metabolites in intestinal inflammation. *Microbiol. Res.* **2024**, *288*, 127838. [\[CrossRef\]](#) [\[PubMed\]](#)
171. Li, A.; Gao, S.; Li, B.; Zheng, Y.; Zhang, L.; Li, K.; Liu, Y.; Qin, X. Characterization of physical and chemical properties of dietary fiber from grain bran and its regulation of gut microbiota and metabolite to prevent colitis. *Food Chem.* **2024**, *456*, 140043. [\[CrossRef\]](#)
172. Meyer, A.; Agrawal, M.; Savin-Shalom, E.; Wong, E.C.L.; Levinson, C.; Gold, S.; Narula, N.; Colombel, J.F.; Carbonnel, F. Impact of diet on inflammatory bowel disease risk: Systematic review, meta-analyses and implications for prevention. *EClinicalMedicine* **2025**, *86*, 103353. [\[CrossRef\]](#) [\[PubMed\]](#)
173. Schroeder, B.O.; Birchenough, G.M.H.; Ståhlman, M.; Arike, L.; Johansson, M.E.V.; Hansson, G.C.; Bäckhed, F. Bifidobacteria or Fiber Protects against Diet-Induced Microbiota-Mediated Colonic Mucus Deterioration. *Cell Host Microbe* **2018**, *23*, 27–40.e27. [\[CrossRef\]](#)
174. Makki, K.; Deehan, E.C.; Walter, J.; Bäckhed, F. The Impact of Dietary Fiber on Gut Microbiota in Host Health and Disease. *Cell Host Microbe* **2018**, *23*, 705–715. [\[CrossRef\]](#) [\[PubMed\]](#)
175. Liu, H.; Liu, H.; Liu, C.; Shang, M.; Wei, T.; Yin, P. Gut Microbiome and the Role of Metabolites in the Study of Graves' Disease. *Front. Mol. Biosci.* **2022**, *9*, 841223. [\[CrossRef\]](#)
176. Pihelgas, S.; Ehala-Aleksejev, K.; Adamberg, S.; Kazantseva, J.; Adamberg, K. The gut microbiota of healthy individuals remains resilient in response to the consumption of various dietary fibers. *Sci. Rep.* **2024**, *14*, 22208. [\[CrossRef\]](#)
177. Shinde, T.; Perera, A.P.; Vemuri, R.; Gondalia, S.V.; Karpe, A.V.; Beale, D.J.; Shastri, S.; Southam, B.; Eri, R.; Stanley, R. Synbiotic Supplementation Containing Whole Plant Sugar Cane Fibre and Probiotic Spores Potentiates Protective Synergistic Effects in Mouse Model of IBD. *Nutrients* **2019**, *11*, 818. [\[CrossRef\]](#) [\[PubMed\]](#)
178. Ni, J.; Shangguan, Y.; Jiang, L.; He, C.; Ma, Y.; Xiong, H. Pomelo peel dietary fiber ameliorates alterations in obesity-related features and gut microbiota dysbiosis in mice fed on a high-fat diet. *Food Chem. X* **2023**, *20*, 100993. [\[CrossRef\]](#)
179. Howard, E.J.; Meyer, R.K.; Weninger, S.N.; Martinez, T.; Wachsmuth, H.R.; Pignitter, M.; Auñón-Lopez, A.; Kangath, A.; Duszka, K.; Gu, H.; et al. Impact of Plant-Based Dietary Fibers on Metabolic Homeostasis in High-Fat Diet Mice via Alterations in the Gut Microbiota and Metabolites. *J. Nutr.* **2024**, *154*, 2014–2028. [\[CrossRef\]](#) [\[PubMed\]](#)
180. Wu, X.; Tjahyo, A.S.; Volchanskaya, V.S.B.; Wong, L.H.; Lai, X.; Yong, Y.N.; Osman, F.; Tay, S.L.; Govindharajulu, P.; Ponnalagu, S.; et al. A legume-enriched diet improves metabolic health in prediabetes mediated through gut microbiome: A randomized controlled trial. *Nat. Commun.* **2025**, *16*, 942. [\[CrossRef\]](#)

181. Miao, T.; Zhang, X.; Zhang, C.; Wu, J.; Zhu, Y.; Xiao, M.; Zhang, N.; Zhong, Y.; Liu, Y.; Lin, Y.; et al. Type 3 resistant starch from *Canna edulis* reduce lipid levels in patients with mild hyperlipidemia through altering gut microbiome: A double-blind randomized controlled trial. *Pharmacol. Res.* **2024**, *205*, 107232. [[CrossRef](#)] [[PubMed](#)]
182. Jiménez-Escrig, A.; Sánchez-Muniz, F.J. Dietary fibre from edible seaweeds: Chemical structure, physicochemical properties and effects on cholesterol metabolism. *Nutr. Res.* **2000**, *20*, 585–598. [[CrossRef](#)]
183. Song, D.; Feng, G.; Ma, Y.; Shi, Y.; Qian, C.; Wang, C.; Xu, J.; Li, Y.; Wang, X.; Fan, N.; et al. Gut microbiome predicts personalized responses to dietary fiber in prediabetes: A randomized, open-label trial. *Nat. Commun.* **2025**, *16*, 11506. [[CrossRef](#)]
184. De Marco Castro, E.; Calder, P.C.; Roche, H.M. β -1,3/1,6-Glucans and Immunity: State of the Art and Future Directions. *Mol. Nutr. Food Res.* **2021**, *65*, e1901071. [[CrossRef](#)]
185. Kim, C.H.; Park, J.; Kim, M. Gut microbiota-derived short-chain Fatty acids, T cells, and inflammation. *Immune Netw.* **2014**, *14*, 277–288. [[CrossRef](#)]
186. Goodridge, H.S.; Wolf, A.J.; Underhill, D.M. β -glucan recognition by the innate immune system. *Immunol. Rev.* **2009**, *230*, 38–50. [[CrossRef](#)]
187. Daou, C.; Zhang, H. Oat Beta-Glucan: Its Role in Health Promotion and Prevention of Diseases. *Compr. Rev. Food Sci. Food Saf.* **2012**, *11*, 355–365. [[CrossRef](#)]
188. El Khoury, D.; Cuda, C.; Luhovyy, B.L.; Anderson, G.H. Beta glucan: Health benefits in obesity and metabolic syndrome. *J. Nutr. Metab.* **2012**, *2012*, 851362. [[CrossRef](#)]

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