

Review

Unlocking the Potential of High-Amylose Starch for Gut Health: Not All Function the Same

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Abstract: High-amylose starch has unique functional properties and nutritional values in food applications. This type of starch is generally resistant to enzymatic digestion in the gastrointestinal tract, and contains an increased fraction of resistant starch (RS), which is a type of dietary fiber. The digestion and fermentation of high-amylose starch in the gut are of current research interest, as the processes are related to its nutritional functionality. This review summarizes recent *in vitro* and *in vivo* studies on the digestion and fermentation of high-amylose starches from different botanical sources and those that have been obtained by modifications. The RS content and fermentation properties are compared among high-amylose starches. This review aims to provide a current understanding of the relationship between high-amylose starch structures and fermentation-related nutritional properties. The results of these studies suggest that both modifications and food processing of high-amylose starch result in distinct fermentation products and nutritional properties. The review provides insight into the potential future applications of diverse high-amylose starches as bioactive compounds to modulate colonic fermentation.

Keywords: high-amylose starch; fermentation; digestion; dietary fiber; starch structure



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1. Introduction

Cereal grains contain a unique blend of bioactive components, including nondigestible carbohydrates, vitamins, minerals, phytochemicals, and antioxidants. Nondigestible carbohydrates have been shown to impact the host by altering the composition of the gut microbiota and modulating cellular differentiation and apoptosis in the colon [1]. There is growing evidence that nondigestible carbohydrates could potentially prevent or manage chronic health conditions such as diabetes and obesity [2–4]. Starch is the most common type of carbohydrate in the diet and is found in grain-based staple foods, such as white bread, noodles, pasta and tortillas, etc. However, these foods often contain a large fraction of highly digestible starch [5–7], and can lead to a rapid increase in blood sugar levels. In the management of diabetes, maintaining blood glucose levels within a safe range is crucial. Therefore, there has been an increasing interest in starches that are resistant to the action of digestive enzymes.

High-amylose starches have gained popularity because of their high resistance to enzymatic hydrolysis and their contribution to dietary fiber intake. A wide range of high-amylose types of major starch-containing food crops is now available, including wheat, maize, barley, potatoes, peas, etc. [8–10]. High-amylose starches are being intensively studied to evaluate their nutritional functionality. These starches are generally more resistant to enzymatic digestion in the gastrointestinal tract and contain a higher fraction of resistant starch (RS). Their nutritional effects are not limited to reducing glycaemic responses, but also depend on colonic fermentation, which produces important metabolites, in particular short-chain fatty acids (SCFAs). SCFAs play a crucial role in improving physical and mental

health by reducing precursors of colorectal cancer, regulating macronutrient metabolism, and altering hormone secretion [11].

Currently, the structural features of high-amylose starch can be manipulated through biological, chemical, and physical approaches. These approaches have expanded the range of available varieties for targeted nutritional functions. Recent studies have shown that high-amylose starch from food crops is a potential platform for delivering health benefits and addressing non-communicable diseases such as type 2 diabetes and obesity [9,12]. However, high-amylose starch with different structural features may have different nutritional properties, such as butyrate and gas production, due to individual variations in microbiota composition. Therefore, it is timely to review these advances and evaluate how the structural features of high-amylose starch impact its fermentation products. This mini-review critically evaluates (1) the structural features of high-amylose starch that confer resistance to enzymes, and (2) the effect of high-amylose starch structures on fermentation products and nutritional properties.

2. Structure and Unique Functional Properties of High-Amylose Starch

2.1. Multilevel Structure

Starch is a complex polymer made up of glucose molecules, which can be divided into two types: amylose and amylopectin. Amylose is mostly linear with rare branches, while amylopectin has a higher percentage of branch points (approximately 5%) [13]. In wild-type starch, amylose typically makes up about 25% of the starch, but the typical amylose contents of starches are dependent on botanical sources, varying from 6 to 33% in seeds of cereals [8]. Starch with a higher proportion of amylose than the wild type is referred to as high-amylose starch. Starch has multiple levels of structure, from the lowest level, individual chains, to the highest level, starch deposition in grains. The structural features that are responsible for the unique properties of high-amylose starch have been widely studied at multiple length scales (such as the lower proportion of short chains, the appearance of intermediate amylopectin with elongated chains, the lower degree of branching, and the increased fraction of V-type polymorph, etc.) However, the effects of these structural features on digestion resistance, fermentation products, and nutritional values need to be carefully evaluated in order to fully exploit their potential applications.

At the level of individual chains, high-amylose starches obtained through biological approaches, such as the suppression of starch branching enzymes and soluble starch synthases, generally have an increased proportion of relatively long chains with the degree of polymerization (DP) greater than ~30 [9,14,15]. Additionally, these starches may also show a decrease in relatively short chains, with DP between ~10 and ~20, and an increase in very short chains with DP less than ~10. These changes in chain length and distribution can affect the properties of high-amylose starch and its potential applications.

Individual chains are linked by α -(1–6) glycosidic bonds to form the whole starch molecules. In high-amylose starch, whole starch molecules typically have a lower degree of branching. Furthermore, high-amylose starch may contain less-branched amylopectin with extra-long chains and branched amylose. Such whole starch molecules are usually referred to as intermediate materials. The intermediate amylopectin or amylose cannot be unambiguously classified using the ratio of large-to-small whole starch molecules, or long-to-short individual chains. These structural features cannot be easily characterized using traditional methods, such as iodine colorimetry. The method tends to overestimate the amylose content of high-amylose starch due to interference from amylopectin–iodine complexes. The interference can be significant for high-amylose starches in which amylopectin has extra-long chains. However, an experimental two-dimensional (2D) distribution has been developed to better understand the complex structure of high-amylose starch [16].

High-amylose starch exhibits unique structural features at higher levels, including semicrystalline lamellae and granules. The location of amylose in starch granules is still a topic of debate, but it is generally accepted that amylose is located tangentially to the radial orientation of amylopectin chains. The distribution of amylose is not even within the starch

granules, and the periphery of the granules was proposed to contain a higher amylose content than the core of the granules [17]. Increased amylose content in high-amylose content impacts the interactions among starch molecules. For example, the glucan chains in high-amylose wheat starches (HAWS) are organized differently and are relatively more mobile compared to high-amylose maize starch (HAMS) with the same apparent amylose content [18]. The difference was proposed to be due to the greater proportion of very long chains/branches in HAWS compared to HAMS. The finding emphasizes the important role of molecular structure in determining the higher-level structure of high-amylose starch.

High-amylose starches tend to have amylopectin double helices packed into hexagonal unit cells, resulting in B-type crystallinity in the X-ray diffraction pattern. B-type crystallinity has a diffraction singlet at 17° and peaks at approximately 5.5° Bragg angles (2θ). In contrast, wild-type cereal starch typically exhibits A-type crystallinity, which is characterized by a main diffraction doublet at 17° and 18° 2θ . Monoclinic unit cells in the A-type starch are relatively more compact and bind less water as compared to B-type unit cells. Additionally, lower granular crystallinity and increased fraction of V-type polymorph were generally found in high-amylose starches, compared to wild-type starch. The long chains of amylopectin and chains near branching points are less likely to form double helices, but along with amylose, they can constitute the amorphous region of granules [19]. The increased fractions of amylose and long chains of amylopectin lead to reduced crystallinity [20–24]. The reduction could be accompanied by the conversion of A-type into B-type crystallinity, which is dependent on the extent of amylose content elevation. The less regular order in high-amylose starches can also be observed by small-angle X-ray scattering patterns, in which the characteristic 9 to 10 nm repeat structure becomes weaker [18,22,25]. Similarly, when viewed under polarized light, the Maltese cross pattern tends to diminish in high-amylose starches [18,26], likely due to a less orderly organization on the light wavelength scale of several hundred nanometers.

The granular shape of high-amylose starch tends to be asymmetrical and deformed, while native wild-type starch generally has spherical and angular shapes. Wheat starch granules with increased amylose content become crescent-shaped and shrunken [23,24,26,27]. Elongated and filamentous granules were reported in wheat starch with very high apparent amylose content ($>90\%$), whereas such granules were not found in wheat starch with lower levels of amylose content. Additionally, the size A-type granules (large lenticular granules) of wheat starch decrease with increasing amylose content levels [23]. Elongated and filamentous granules were also observed in high-amylose starch from maize and rice, possibly due to increased amylose interaction on the granular surface that causes granule agglomeration [28,29].

2.2. Unique Functional Properties

High-amylose starch has a range of unique properties that make it valuable in food and nutrition applications. Compared to regular starch, it has reduced water-holding capacity (in native granular form), increased melting temperature, limited granular swelling, reduced leachate during gelatinization, and improved gelling capacity of gelatinized starch. These properties make high-amylose starch useful for a variety of applications in food processing, medicine, and other industries.

In particular, high-amylose starch has low enzymatic digestibility, which confers various nutritional or physiological effects. These include increased intake of dietary fiber, improved glycemic control, reduced caloric value, and increased production of colonic SCFAs. High-amylose starch can also be used to encapsulate drugs and probiotics and formulate oral rehydration solutions, etc. The mechanisms and structural basis underlying the digestive resistance of high-amylose starch are discussed in detail in Section 3.

3. Enzymatic Resistance of High-Amylose Starch

High-amylose starch, also known as resistant starch type 2, generally fulfills the definition of dietary fiber by food regulatory agencies. Potential physiological benefits

of resistant starch have been recognized by agencies such as the European Food Safety Authority (EFSA), Food Standards Australia New Zealand (FSANZ), and the U.S. Food and Drug Administration (FDA). The multilevel structural features of high-amylose starches linked to digestive resistance have been extensively investigated. Previous (mostly in vitro) studies have generally found that amylose content is correlated with resistant starch content in the native granular form of starch as well as in foods (Table 1). Biological approaches appear to be the most effective at elevating the level of amylose content and, thus, digestive resistance, while physical and chemical techniques can only modify the starch properties to a limited extent (Table 1). The fundamental but rate-determining steps of the conversion of high-amylose starch into absorbable products (small sugars) have been reviewed elsewhere to link the multilevel structural features to digestibility [9]. The two fundamental steps are the diffusion or absorption of the enzyme onto the substrate and the catalytic event once digestive enzymes attach to the starch substrate.

Several structural features of high-amylose starches in their native or food-related forms can limit the enzyme attachment to the starch substrate. High-amylose starches often have an increased content of granular surface-bound proteins, such as high-amylose wheat starches [30] and high-amylose rice starches [31]. These proteins can have barrier effects that prevent or slow down enzyme binding to the substrate and reduce the digestion rate. High-amylose cereal starches have also been reported to have reduced interior surface area due to a lack of channels or pores [29,32]. The features of the interior surface play an important role in starch digestibility and the structure of its digestion residue [33–35]. Moreover, food processing of high-amylose cereal ingredients can result in the formation of a relatively integral food structure. This improved food structure integrity (a dense and less porous starch–protein matrix) is associated with the thermal stability of granule structures, and was found to limit the action of digestive enzymes [5].

After the adsorption of the enzymes onto the substrate, the glucan chains must fit into the active sites of enzymes before the breakdown of glycosidic linkages can occur. Multiple structural features have been proposed to limit the catalytic process. At the molecular level, long glucan chains in high-amylose starch are postulated to maintain the crystalline structure by extending through multiple crystals, contributing to the digestive resistance of high-amylose starches [36,37]. Furthermore, the amorphous packing of starch polymers with elongated branches has been shown to contribute to the digestive resistance of granular high-amylose wheat starch [38] and high-amylose maize starch [39]. At the submolecular level (<10 nm), the helical structure does not fit into the active site of α -amylases. The glucan chains of high-amylose starch tend to retain their helical structures during thermal processing [40]. Even if the helical structure is disrupted during thermal processing, the higher the proportion of long glucan chains, the faster and to the greater extent it retrogrades into complex structures [41]. During heating and chilling, more amylose or longer branch chains can complex with lipids to form amylose–lipid complexes [42]. These processes that limit the catalytic event are associated with increased amylose content levels.

Table 1. Resistant starch content of native and modified high-amylose starches.

Approach to Improve Amylose Content	Botanical Sources (Amylose Content, %)	Reference	Approach to Improve Amylose Content	Digestion Model Used	Resistant Starch Content (%)
Biological approach	Wheat (downregulated SS i1a: 34.0%→43.5%/downregulated SBE i1a: 33.3%→57.8%); food processing into pasta	[43]	Downregulated SSi1a or SBE i1a	In vitro model (pepsin, amyloglucosidase)	↑1.33% (downregulated SS i1a)/↑7.15% (downregulated SBE i1a)
	Wheat (bread wheat: 22.9%→55.7%/durum wheat: 24.4%→47.4%); milled	[26]	Downregulated SBE i1a	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑10.38% (bread wheat)/↑4.63% (durum wheat)

Table 1. *Cont.*

Approach to Improve Amylose Content	Botanical Sources (Amylose Content, %)	Reference	Approach to Improve Amylose Content	Digestion Model Used	Resistant Starch Content (%)
	Wheat (27.2%→84.2%)	[44]	Downregulated SBEs (IIa, IIb)	NA	↑36.00%
	Wheat (27.9%→44.9%)	[45]	Downregulated SBEs (IIa, IIb)	Resistant starch kit	↑5.50%
	Wheat (30.7%→50.0%)	[46]	Downregulated SBEs (IIa, IIb)	Resistant starch kit	↑2.43%
	Wheat (23.0%→31.4%); cooked	[15]	Downregulated SBE (IIa)	In vitro model (pancreatic alpha-amylase, glucoamylase)	↑
	Wheat (32.3%→61.8%)	[47]	Targeted mutagenesis of SBEIIa	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑13.30%
	Rice (19.6%→41.2%); cooked	[20]	Downregulated SBE IIb	In vitro model (simulated oral phase, gastric phase, and intestinal phase)	↑4.60%
	Rice (27.2%→64.8%)	[48]	Downregulated SBE I, SBE IIb	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑15.10%
Chemical approach	Rice (30.6%)	[49]	Acid and heat-moisture treatments (citric acid/lactic acid/acetic acid)	In vitro model (alpha-amylase, amyloglucosidase)	↑32.70% (citric acid) / ↑28.80% (lactic acid) / ↑26.70% (acetic acid)
	Waxy rice (0.0%→30.3%); cooked (before pullulanase debranching)	[50]	Enzymatic modification (pullulanase)	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑28.28%
	Rice (enzymatic modification: 42.7%→49.2%/heat-moisture treatment: 42.7%→43.2%/acid treatment: 42.7%→43.9%)	[51]	Enzymatic modification (pullulanase)/heat-moisture treatment/acid treatment (citric acid)	In vitro model (pepsin, alpha-amylase, amyloglucosidase)	↑6.26% (enzymatic modification) / ↑2.52% (heat-moisture treatment) / ↑10.77% (acid treatment)
	Maize (58.6%→58.5%)	[52]	Enzymatic modification (maltogenic alpha-amylase)	In vitro model (pancreatin, amyloglucosidase)	↑1.00%
	Wheat (26.2%→35.6%)	[53]	Annealing (50 °C, 96 h, 1:3 w/v)	In vitro model (saccharifying enzyme, pancreatic alpha-amylase)	↑4.61%
Physical approach	Maize (85.0%→83.7%)	[54]	Annealing (45 °C, 72 h, 1:2 w/v)	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑0.60%
	Maize (51.3%→49.1%)	[55]	Microwave (2450 MHz, 1.2 kW, 1 min)	In vitro model (pancreatin, amyloglucosidase)	↑14.10%
	Barley (23.1%→23.4%)	[56]	Heat-moisture treatment (110 °C, 2 h, 30% moisture content)	In vitro model (pancreatin, amyloglucosidase)	↑11.35%
	Quinoa (9.1%→16.4%)	[57]	Electron beam irradiation (8 kGy, 2 kGy/h)	In vitro model (pancreatin, amyloglucosidase)	↑23.50%
	Potato (25.0%→28.8%)	[58]	Sonication (28 kHz, 300 W, 30 min, 25 °C)	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑
	Lotus stem (41.9%→49.1%)	[59]	Sonication (20 kHz, 400 W, 35 min, 0 °C)	In vitro model (pancreatic alpha-amylase, amyloglucosidase)	↑7.99%

SBE: starch-branching enzyme; SS: starch synthases.

4. Colonic Fermentation of High-Amylose Starch and Nutritional Properties

The fermentation of high-amylose starch in the colon produces short-chain fatty acids, consisting primarily of acetate, propionate, and butyrate, which are absorbed by the colonic mucosa and can have various beneficial effects on the host [60,61]. This fermentation process has the potential to increase glucose tolerance and insulin sensitivity, decrease inflammation, and improve intestinal barrier integrity [62–64]. The nutritional properties of

high-amylose starch could be affected by its specific structural changes (e.g., the degree of cross-linking, the degree of substitution, and the degree of association with other molecules) due to chemical modifications [65,66] and its interactions with other food components [67]. The resistance of high-amylose starch against human digestive enzymes may be relevant to its resistance against microbial degradative enzymes, which may influence its fermentation rate and extent, as well as shifts in the microbiota and fermentation products (Figure 1). However, there is limited information on the role of multilevel structural features of high-amylose starches in determining their fermentation properties. In this section, previous results from in vitro fermentation models, in vivo studies, and dietary intervention studies are summarized to provide an overview of the fermentation properties and nutritional functionality of high-amylose starches with different structural features.

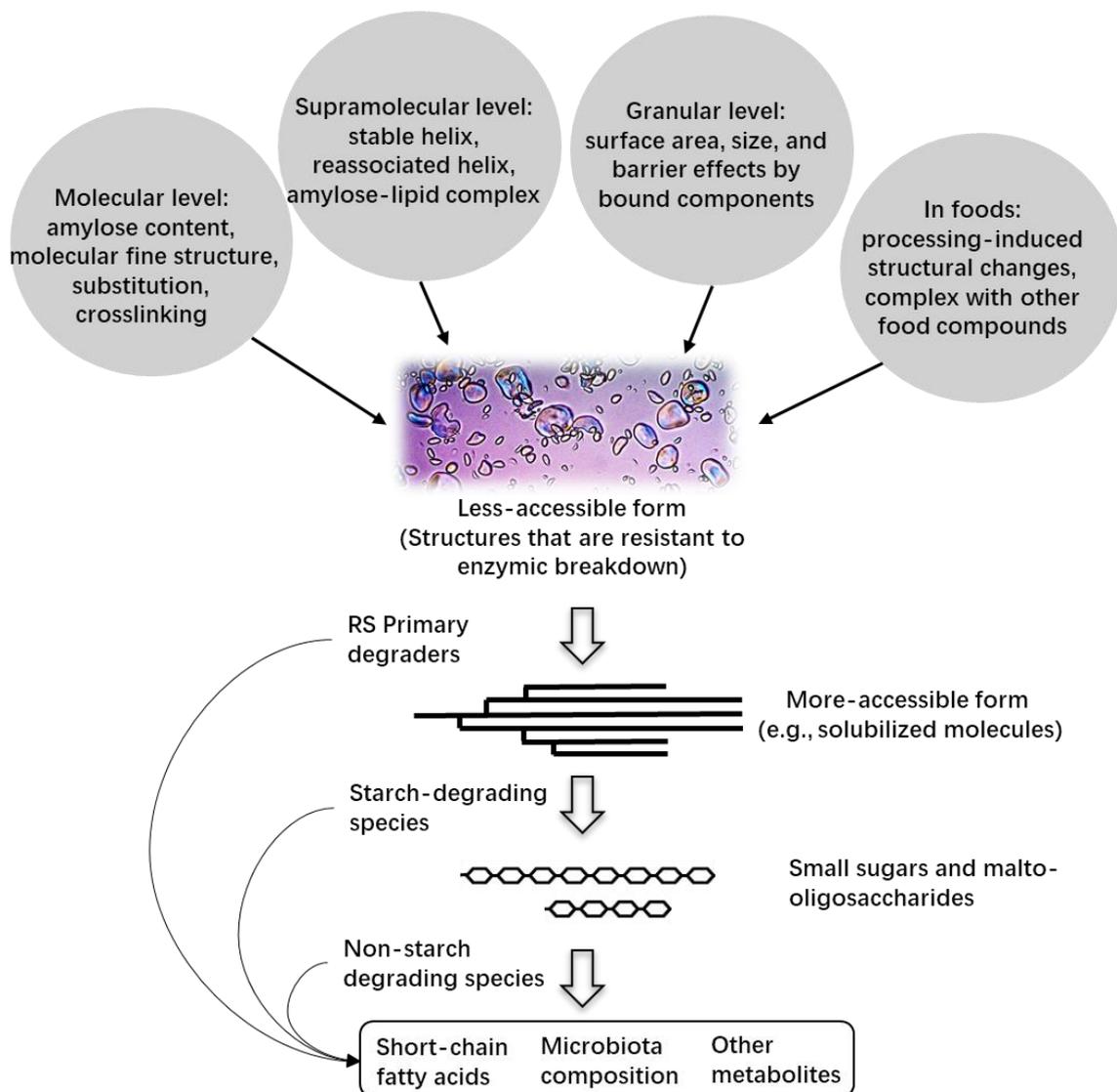


Figure 1. Schematic illustration of high-amylose starch (a type of resistant starch) fermented by the colonic microbiota. Primary degraders break down resistant starch (RS), releasing soluble starch molecules that can be used by starch-degrading species. This process may also increase the surface area of RS granules, allowing other starch-degrading species to access and utilize this energy source. Smaller sugars and malto-oligosaccharides released during the processes could support the growth of non-starch degrading species. The figure was adapted from [63].

4.1. In Vitro Studies and Animal Studies

Fermentation is a complex metabolic process by which organisms convert carbohydrates into various biochemicals. Two major groups of biochemicals that are produced by fermentation are short-chain fatty acids (SCFAs) and gases, while the most common volatile fatty acids produced during the fermentation of carbohydrates are acetate, propionate, and butyrate [68,69]. The relationship between starch structure and SCFA production is often a focus of the in vitro fermentation studies of high-amylose starches (Table 2). Starch with elevated amylose content leads to increased production of SCFAs [70–73] and significant changes in the relative abundance of specific bacterial populations [61,67,71–75]. Animal studies have consistently demonstrated that the levels and total amount of SCFAs produced during fermentation are higher when high-amylose starch is used compared to regular starch [76–86]. As shown in Table 2, there is also evidence that feeding animals high-amylose starch can increase the relative abundance of specific bacterial populations, such as *Bifidobacterium* and *Lactobacillus* [78,85]. This effect may be due to the indigestible fraction of high-amylose starch favoring the production of SCFAs, which in turn lowers the colonic pH. The resulting changes in pH create an environment conducive to the growth and reproduction of specific bacterial populations, such as RS primary degraders and starch-degrading species. High-amylose starch, especially with an amylose content of 93%, has been observed to exhibit a notable reduction in cumulative gas production at 72 h and the fastest rate of gas production during in vitro fermentation [61]. The result is consistent with the previous research on chemically modified high-amylose starch by cross-linking [74]. However, no significant effects on gas production were observed in propionylated starch [72,75]. Furthermore, the presence of ammonium, which is generally used as an indicator for protein fermentation, was also recorded in in vitro fermentation of high-amylose starch. As Bui et al. (2020) reported, there was no discernible difference in end-point NH_4^+ production among wheat starches varying in amylose content.

The fermentation properties of high-amylose starches also depend on the plant sources [79]. This may be due to differences in structural features controlled by starch biosynthesis in different plants, including those noted in Figure 1. Additionally, modifying high-amylose starch through chemical methods can further increase the production of specific SCFAs, with the production depending on the degree of substitution [72,82]. This may be because acetyl groups from acetylated starch were released by gut microbiota [87,88]. Lower pH created by acetylated starch is more conducive to the growth of SCFA-producing species. Another possible explanation is that improved starch resistance against the host enzymes can result in a greater proportion of undigested starch residues reaching the colon. Changes in in vitro fermentation properties were also reported in cross-linked high-amylose maize starches [74] and processed forms (cooked and cooked-cooled) [71].

The changing patterns of molecular structure in the in vitro fermentation by microbial enzymes were found to differ from those of the remnant starch obtained from in vitro digestion by pancreatic α -amylase [89]. This observation implies that molecular structural features that contribute to slow degradation during small intestinal digestion are not the same as those that affect colonic fermentation, likely due to the difference in enzyme types and combinations. However, the structural basis for resistant starch fermentability by gut microbiota was not fully understood. While there is a wealth of knowledge on the relationship between starch structural features and enzymatic breakdown, there are still gaps in our understanding of how these features impact the complex process of fermentation in the lower gut, which involves multiple amylolytic enzymes and other fiber-degrading mechanisms. More in-depth structural characterization throughout the digestion and fermentation processes of starches in relation to various RS-forming mechanisms will help to bridge the gaps [90,91].

Animal studies (Table 2) also showed changes in SCFA production and microbiota in the fecal matter of animals fed with high-amylose starch. Moreover, rats fed high-amylose starch have higher levels of fasting plasma glucagon-like peptide-1 (GLP-1) than those fed ordinary starch [84]. This hormone stimulates insulin secretion and regulates food intake,

which are crucial in the management of diabetes and obesity. High-amylose starch was also shown to inhibit colon cell proliferation in rats, potentially lowering the risk of colon cancer [92].

Table 2. Short-chain fatty acid (SCFA) and gas production and microbiota shift of high-amylose starches from in vitro fermentation and animal studies.

Fermentation Studies	Botanical Sources (Amylose Content, %)	Reference	Approach to Improve Amylose Content	Fermentation Models Used	Fermentation Properties (SCFA, Gas Production, and Microbiota Composition Changes)
	Maize (70%)	[84]	NA	In vivo fermentation model (7-week-old male rats)	Butyrate: ↑9.85 μmol per cecal content Acetate: ↑109.0 μmol per cecal content Propionate: ↑15.3 μmol per cecal content Total: ↑135.0 μmol per cecal content (cecal content, than low-amylose group)
	Maize (63.3%)	[86]	NA	In vivo fermentation model (4-week-old male rats)	Butyrate: ↑10.1 μmol/g wet matter Acetate: ↑40.0 μmol/g wet matter Propionate: ↑10.3 μmol/g wet matter Total: ↑58.9 μmol/g wet matter Bacteroidetes ↑ (cecal content, than low-amylose group)
	Maize (85%)	[76]	NA	In vivo fermentation model (adult male rats)	Butyrate: ↑26.0 μmol Acetate: ↑225.0 μmol Propionate: ↑21.0 μmol Total: ↑276.0 μmol (cecal content, than low-amylose group)
	Maize (85%)	[78]	NA	In vivo fermentation model (4-week-old pigs)	Butyrate: ↑ Acetate: ↑ Propionate: ↑ Total: ↑ Total anaerobes↑, Lactobacillus ↑ (colonic digesta, than low-amylose group)
	Maize (80%)	[85]	NA	In vivo fermentation model (ileal-cannulated pigs)	Butyrate: ↓0.7 μmol/g wet matter Acetate: ↓0.7 μmol/g wet matter Propionate: ↑1.49 μmol/g wet matter Total: ↑8.5 μmol/g wet matter Bifidobacterium ↑ (feces, than low-amylose group)
Animal models	High-amylose maize	[82]	NA	In vivo fermentation model (male rats)	Butyrate: ↑ Acetate: ↑ Propionate: ↑ Total: ↑ Proteobacteria↓, Bacteroidetes↑ (feces, than low-amylose group)
	High-amylose maize	[93]	NA	In vivo fermentation model (adult male rats)	Butyrate: ↑ Acetate: ↑ Propionate: ↑ Total: ↑ (feces, than low-amylose group)
	High-amylose maize	[81]	NA	In vivo fermentation model (5-week-old male rats)	Butyrate: ↑3.0 μmol/g feces Acetate: ↑17.7 μmol/g feces Propionate: ↑7.0 μmol/g feces Total: ↑28.9 μmol/g feces (than low-amylose group)
	High-amylose maize	[83]	NA	In vivo fermentation model (adult male rats)	Butyrate: ↑24.9 μmol Acetate: ↑120.2 μmol Propionate: ↑38.9 μmol Total: ↑184.8 μmol (cecal content, than low-amylose group)
	High-amylose wheat/high-amylose maize	[79]	NA	In vivo fermentation model (male rats)	Butyrate: ↑9.0 μmol (wheat)/↑4.0 μmol (maize) Acetate: ↑21.0 μmol (wheat)/↑8.0 μmol (maize) Propionate: ↑12.0 μmol (wheat)/↑3.0 μmol (maize) Total: ↑44.0 μmol (wheat)/↑17.0 μmol (maize) (colonic digesta, than low-amylose group)
	Wheat (25.5%→74.4%)	[27]	Downregulated SBEs (IIa, IIb)	In vivo fermentation model (4-week-old male rats)	Butyrate: ↓2.8 mmol/kg Acetate: ↑5.0 mmol/kg Propionate: ↑3.9 mmol/kg Total: ↑4.5 mmol/kg (cecal digesta, than low-amylose group)
	Wheat (27.9%→44.9%)	[45]	Downregulated SBEs (IIa, IIb)	In vivo fermentation model (8-week-old rats)	Butyrate: ↑11.7 μmol Acetate: ↑79.8 μmol Propionate: ↑28.2 μmol Total: ↑119.7 μmol (cecal content, than wild-type starch)

Table 2. Cont.

Fermentation Studies	Botanical Sources (Amylose Content, %)	Reference	Approach to Improve Amylose Content	Fermentation Models Used	Fermentation Properties (SCFA, Gas Production, and Microbiota Composition Changes)
	Rice (27.2%→64.8%)	[48]	Downregulated SBES (I, IIb)	In vivo fermentation model (feeding rats for four weeks)	Butyrate: ↑11.9 μmol/g dry feces Acetate: ↑60.5 μmol/g dry feces Propionate: ↑68.1 μmol/g dry feces Total: ↑140.6 μmol/g dry feces (feces, than wild-type starch) Butyrate: ↓4% Acetate: ↓6.4% Propionate: ↑7.9%
	Barley (41%)	[80]	NA	In vivo fermentation model (4-week-old pigs)	Total: ↑19 mMol/kg digesta sample NH ₃ : ↑1 mMol/kg digesta sample (colonic digesta, than low-amylose group) Butyrate: ↑12.0 μmol Acetate: ↑142.0 μmol Propionate: ↑9.0 μmol Total: ↑161.0 μmol (feces, than low-amylose group)
	High-amylose barley	[77]	NA	In vivo fermentation model (adult male rats)	
	High-amylose maize	[72]	Propionylated	In vitro fermentation model (bacteroides-dominated enterotype inocula)	Butyrate: ↓1.0 mM/50 mg dry feces Acetate: ↑0.2 mM/50 mg dry feces Propionate: ↑0.7 mM/50 mg dry feces Total: ↑2.4 mM/50 mg dry feces Bacteroidetes ↑ Gas production → (than unmodified starch) Butyrate: ↑ Acetate: ↑ Propionate: ↑ Total: ↑ (than low-amylose group) Butyrate: ↑2.4 mM Acetate: ↑1.8 mM Propionate: ↑2.7 mM Total: ↑7.4 mM (fermentation for 24 h, than unmodified starch) Butyrate: → Acetate: → Propionate: → Total: ↓0.6 mmol/g dry matter DMCV: ↑14 mL, R _{max} : ↓0.8 mL/h NH ₃ production: ↓ (fermentation for 146 h, than cooked and recrystallized group) Butyrate: ↓ Acetate: ↑ Propionate: ↑ Total: ↑ Firmicutes ↑, Bacteroidetes: ↓ Gas production → (fermentation for 24 h, than unmodified starch) Butyrate: ↓ Acetate: ↑ Propionate: → Total: ↓ Firmicutes/Bacteroidetes ratio: ↓ Gas production: ↓ (fermentation for 24 h, than unmodified starch) Butyrate: ↓ Acetate: ↓ Propionate: ↑ Total: ↓ DMCV: ↓10 mL/gDM, R _{max} : ↓ (fermentation for 48 h, than wild-type starch) Butyrate: ↓ Acetate: ↓ Propionate: ↓ Total: ↓ DMCV: ↓55 mL/g DM, R _{max} : ↓6.3 mL/h, NH ₄ ⁺ production: no difference (fermentation for 72 h, than wild-type starch)
	High-amylose maize; Cooked	[71]	NA	In vitro fermentation model (inoculum from human stool samples)	
	High-amylose maize	[70]	Debranched (pullulanase), recrystallization combined with HMT	In vitro fermentation model (inoculum from human stool samples)	
	High-amylose maize; cooked, recrystallized, and amylase digested	[75]	NA	In vitro fermentation model (inoculum from pig fecal samples)	
In vitro models	Maize (69.8%)	[73]	Propionylated	In vitro fermentation model (inoculum from human stool samples)	
	Maize (65.0%)	[74]	Chemical cross-linking	In vitro fermentation model (inoculum from human stool samples)	
	Wheat (32%→84%)	[67]	Downregulated SBES (IIa, IIb)	In vitro fermentation model (using wheat-based foods and inoculum from human stool samples)	
	Wheat (37%→93%)	[61]	Downregulated SBES (IIa, IIb)	In vitro fermentation model (inoculum from human stool samples)	

DMCV: the total cumulative gas values per gram dry matter; DM: dry matter; HMT: heat-moisture treatment; SCFA: short-chain fatty acids; R_{max}: the fastest rate of gas production. NA: not applicable.

4.2. Dietary Intervention Studies

Dietary intervention studies have shown the effects of high-amylose starch on glucose and insulin homeostasis and fecal composition (including SCFA content and microbial composition) (Table 3). High amylose from wheat, maize, barley, etc., has been shown

to improve the production of SCFAs [94–98]. It is important to note that the SCFA levels present in feces do not necessarily reflect those found in the colon. This is due to the fact that SCFAs are produced through the fermentation process in the large intestine, and the composition of the gut microbiome can vary greatly between the upper and lower sections of the colon. Furthermore, SCFAs can be absorbed and metabolized by the colonic epithelium and gut microbiota before the excursion within the feces, and therefore measuring SCFA levels in feces alone may not provide a complete understanding of SCFA production and metabolism throughout the entire colon.

There is conflicting evidence regarding the effects of resistant starch type 2 from high-amylose starch on acute postprandial responses and insulin resistance and/or sensitivity. There are several studies indicating that resistant starch type 2 from high-amylose starch can attenuate acute postprandial responses [96,97,99–108], while no effects were also reported [109–111]. While several studies concluded that high-amylose starch has no effects on insulin resistance and/or sensitivity [106,112,113], a limited extent of changes was reported [96,97,100,101,104,107,108,111,114]. The effect of high-amylose starch on glucose and insulin homeostasis was also evaluated previously, with the conclusion that there is insufficient evidence to conclude that it can improve insulin resistance and/or sensitivity [115]. In addition, high-amylose starches have been shown to have positive effects on bowel movement, increasing stool frequency and volume [94–96,102,104]. In particular, an increased concentration of butyrate was reported in the stool, which supports the growth of intestinal epithelial cells and creates a protective environment in the colon [95,96]. Similarly, a high-amylose starch-rich diet increased the abundance of SCFA-producing bacteria in the stool [94]. It should be noted that the information provided in Table 3, which is related to the variations in glucose levels, insulin levels, and glycemic responses, primarily in healthy subjects, is inadequate to yield a comprehensive understanding of the clinical significance of these changes. Additionally, the possible health implications of these observations, such as enhanced diabetes management or modified weight loss outcomes, are not adequately explored in the current studies. Future research is needed to bridge these gaps in knowledge, in order to gain a holistic understanding of the nutritional implication of these findings.

Table 3. Colonic fermentation of high-amylose starches and results from dietary intervention studies.

Botanical Sources		Reference	Modifications or Food Processing	Study Design	Results
Wheat	High-amylose wheat	[94]	Bread/biscuits with low-amylose wheat or low-amylose wheat refined, high-amylose wheat or high-amylose wheat refined	Healthy subjects (n = 80), random, double-blinded, 4-arm parallel	Fecal butyrate excretion: ↑38% (p < 0.05, refined high-amylose wheat vs. refined low-amylose wheat) Abundance of fecal SCFA-producing bacteria: ↑ <i>Roseburia inulinivorans</i> (p < 0.001) of refined high-amylose wheat than at baseline (week 0) Cumulative postprandial glycemic AUC (0 to 200 min): ↓0.18 mmol/L (p < 0.05) Cumulative blood glucose AUC (0 to 200 min): ↓75.53 mmol × min/L (p < 0.05) (than 100% wheat flour) Postprandial glycemic AUC: ↓25 mmol/L × 3 h (p < 0.001) Plasma glucose concentration: ↓33% Glycemic AUC response: ↓39% (p < 0.0001) Insulinemic AUC response: ↓24–30% (p < 0.05) (than low-amylose group) Whole-meal or refined flour did not affect the glycemic, insulinemic, or incretin response
	High-amylose maize flour (amylose content = 67%)	[105]	Cookies with high-amylose maize flour, low-amylose maize flour, or 100% wheat flour	Healthy men (n = 30), random, double-blinded	
	High-amylose wheat (amylose content = 74.3%)	[100]	Bread containing low-amylose wheat or low-amylose wheat refined, high-amylose wheat or high-amylose wheat refined	Healthy subjects (n = 20), random, double-blinded	
Maize	High-amylose maize (amylose content = 33%)	[96]	Muffins with low or high (RS2 20 g) amylose maize starch	Hypertriglyceridemia subjects (n = 23), random	Postprandial glucose area: ↓0.25 mmol × min/L SCFA concentrations in fecal water: ↑32% (p < 0.001) Overall postprandial plasma insulin concentration: ↓17% Postprandial insulin area: ↓62 pmol × min/L (p < 0.01) Frequency of bowel actions: ↑0.2 actions/day (than low-amylose group)

Table 3. Cont.

Botanical Sources	Reference	Modifications or Food Processing	Study Design	Results
High-amylose maize starch	[95]	Supplements containing HAMS (RS 30 g/day) or low-fiber content	Healthy subjects (n = 24), random	Fecal bulk: ↑22 g/day (p < 0.001) Fecal SCFA output: ↑2.32 mmol/day Fecal SCFA concentration: ↑5.3 mmol/L Fecal butyrate: SCFA ratio significantly 31% (p = 0.035) (than low-fiber supplement)
High-amylose maize starch	[102]	Breakfast with amylopectin starch plus cellulose, amylopectin starch plus lactulose, or high-amylose starch plus cellulose	Healthy subjects (n = 10), random, single-blinded	PPGR: ↓ Glucose tolerance: ↑ Non-esterified fatty acids concentrations: ↑ (high-amylose starch plus cellulose vs. amylopectin starch plus cellulose group)
High-amylose maize starch	[116]	Sachets containing waxy maize starch (Amioca) or HAMS (RS2 30 g/day)	Healthy subjects (n = 10), random, single-blinded	SCFA concentrations (acetate and propionate): ↑ (not colonic SCFAs) Plasma insulin response: ↓ No effect on Postprandial glycemic AUC, HOMA, and FBG than waxy maize starch Blood glucose incremental AUC: ↓44.4 mmol × min/L Insulin incremental AUC: ↓4.8 pmol × min/L (p < 0.05)
High-RS maize starch	[111]	Bread with or without HAMS	Healthy subjects (n = 15), random	Colonic fermentation in the late postprandial phase: ↑23.3 ± 4.5 ppm (breath H ₂) No effect on PPGR (than white wheat flour bread) PPGR: ↓
High-amylose maize starch (resistant starch content = 60%)	[112]	A test breakfast and lunch containing either 48 g RS or not	Healthy males (n = 10), random, single-blinded, cross-over	AUC C-peptide: ↑26,457 nmol/L 300 min AUC Insulin: ↑40,714 pmol/L 300 min (than breakfast and lunch without RS) PPGR: ↓80.9 mmol × min/L (p = 0.004) Mean GI: ↓30.07
High-amylose maize starch	[103]	Chinese steamed bun formulation containing either HAMS or not	Healthy females (n = 15), random, single-blinded	Incremental postprandial glycemic AUC values: ↓ (than wheat flour without HAMS) FSIVGTT: ↑in men (n = 11) Fecal SCFA output: ↑ No effect on HOMA and FBG (than waxy maize starch)
High-amylose maize	[110]	Sachets containing waxy maize starch (Amioca) or HAMS (RS2 15 or 30 g/day)	Obese subjects (n = 33), random, double-blinded	Fecal acetate: ↓6.87 μmol/L Fecal propionate: ↑0.82 μmol/L Fecal butyrate: ↑0.08 μmol/L (than bread without HAMS)
High-amylose maize starch	[97]	Bread with or without HAMS (RS2 12 g/day)	Obese subjects (n = 15), random, subject-blinded	HOMA for insulin resistance: ↓ (p = 0.029) Fasting insulin: ↓21 pmol/liter (p = 0.041) FBG: ↓ (p = 0.017)
High-amylose maize	[108]	Sachets containing waxy maize starch or HAMS (RS2 40 g/day)	Insulin-resistant subjects (n = 15), random, controlled	Postprandial glucose disposal: ↑65% (than waxy maize starch) Insulin resistant group (n = 14): insulin sensitivity after consuming HAMS 30 g/day ↑ (than HAMS 15 g/day); Insulin sensitive group (n = 9): no significant difference (p > 0.05)
High-amylose maize	[113]	Cookies containing waxy maize starch or HAMS (RS2 15 or 30 g/day)	Healthy and non-diabetic women (n = 51; 23 women completed all 3 arms), random, placebo-controlled, double-blinded, cross-over	Both groups: no significant differences in fasting glucose or insulin after consuming HAMS 15 or 30 g/day (than waxy maize starch)
High-amylose maize starch	[114]	Bagel containing only hard wheat flour or 60% substitution of HAMS (RS2 25 g/day)	Subjects at high risk of type 2 diabetes (n = 24), random, double-blinded	HOMA for insulin resistance: ↓ Insulin incremental AUC: ↓18.9% (p = 0.04) (than hard wheat flour)
High-amylose maize	[106]	Muffins with or without HAM (RS2 30 or 0 g/day)	Overweight, healthy adults (n = 18), randomized-controlled, parallel-arm, double-blinded	Postprandial glycemic AUC: ↓ Glucose homeostasis: ↑ Insulin change not observed (than muffins without HAM)
High-amylose maize starch	[107]	Muffin top containing modified HAMS (RS4) or not	Healthy adults (n = 12), random, double-blinded, controlled	Postprandial glycemic AUC: ↓33% (p = 0.037) Maximum glucose concentration: ↓8% Postprandial serum insulin incremental AUC: ↓38% (p < 0.001) (than control)
High-amylose maize	[101]	Sachets containing waxy maize starch or HAMS (RS2 40 g/day)	Insulin-resistant, obese subjects (n = 12), random, single-blinded	Insulin and C-peptide concentrations: ↑ Glucose effectiveness: ↓0.01/min (p = 0.06) (than waxy maize starch)
High-amylose maize starch	[99]	Soups with 50 g maltodextrin, whole grain (RS 27 g/day), high-amylose (RS 23 g/day), regular cornstarch, or no added starch	Healthy men (n = 17), random	Postprandial glycemic AUC: ↓ (than soups without added starch)

Table 3. Cont.

Botanical Sources		Reference	Modifications or Food Processing	Study Design	Results
Barley	High-amylose maize	[104]	Breakfast and lunch containing barley flour (more HAM) or white wheat flour (without HAM)	Healthy women ($n = 14$), random, single-blinded	Postprandial glycemic AUC: \downarrow 22% AUC of insulin: \downarrow 32% No effect on HOMA and FBG (than white wheat flour)
	High-starch amylose (amylose content = 42%)	[109]	Barley tortillas varying in fiber and/or starch composition	Healthy adults ($n = 12$), random, double-blinded	No significant difference in GI between the low-amylose and high-amylose groups No difference in the glucose iAUC or percentage change at 30 min between the low-amylose and high-amylose groups Insulin concentrations at 15–60 min: \uparrow all groups

AUC: area under the curve; GLP-1: glucagon-like peptide-1; GI: Glycemic index; HAMS: high-amylose maize starch; HOMA: homeostasis model assessment; FBG: fasting blood sugar level; FSIVGTT: frequently sampled intravenous glucose tolerance test for insulin sensitivity; PPGR: postprandial glucose response; SCFA: short chain fatty acids.

5. Conclusions

This mini-review highlights the fact that not all high-amylose starches (a type of resistant starch) are functionally similar, and the structural differences of high-amylose starch can impact its utilization by gut microbiota and, therefore, its fermentation properties and nutritional functionality. Because there are large inter-individual differences in the microbiome, it is unlikely that there is a single optimal structure and dosage of high-amylose starch that will be effective for all individuals. In addition, diet plays a significant role in shaping the composition of the gut microbiota [117], and changes in the microbiota can affect the fermentation of high-amylose starch. Therefore, future studies need a better understanding of how the structural features of high-amylose starch and those relevant to processing and modifications impact the gut microbiota, and the association between microbiota composition and fermentation products of high-amylose starch. This may allow the design of personalized resistant starch with desirable fermentability to promote certain microbiota groups for specific nutritional purposes. A better understanding of the link between starch structural features and beneficial nutritional functionality will also enable the selection of more nutritious grains at the stage of breeding and food processing.

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