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REVIEW ARTICLE

Barley's Prebiotic Potential: Role in Gut Health and Microbiome Modulation

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ABSTRACT

In animals, the gastrointestinal tract is essential for digestion, nutrient utilization, and immune function. Any disruption in its function can lead to metabolic challenges that negatively influence health and productivity. In animal production, barley is frequently utilized as a feed component for ruminants, poultry, and aquaculture. Barley (*Hordeum vulgare)* is a valuable cereal grain consumed globally, rich in functional ingredients, especially fiber, beta glucan, flavonoids and phenolic acids and can significantly reduce gastrointestinal (GI) dysfunction and reduce inflammation by reducing oxidative stress across gastrointestinal tract (GIT). Different varieties of barley and its form used in studies are highland barley (HB), black barley, fermented also extract and roasted barley, fermented barley bran, barley leaf, low molecular weight barley and fiber bound polyphenols from HB. β-glucan is a soluble dietary fiber which produce prebiotics effects, it increases intestinal bacteria which produce short chain fatty acids (SCFAs) in return promote gut health. Barley is an excellent substrate for the production of grain-derived probiotics and prebiotics. It also improves gut bacteria profile, intestinal fermentability, regulates intestinal microbiome, and has gastroprotective, prebiotic, and probiotic effects. This review aims to summarize all studies conducted in the previous five years on the preventive effect of barley on the GIT. These studies have shown inclusion of barley in the diet promotes GI health and reduces various diseases linked.

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INTRODUCTION

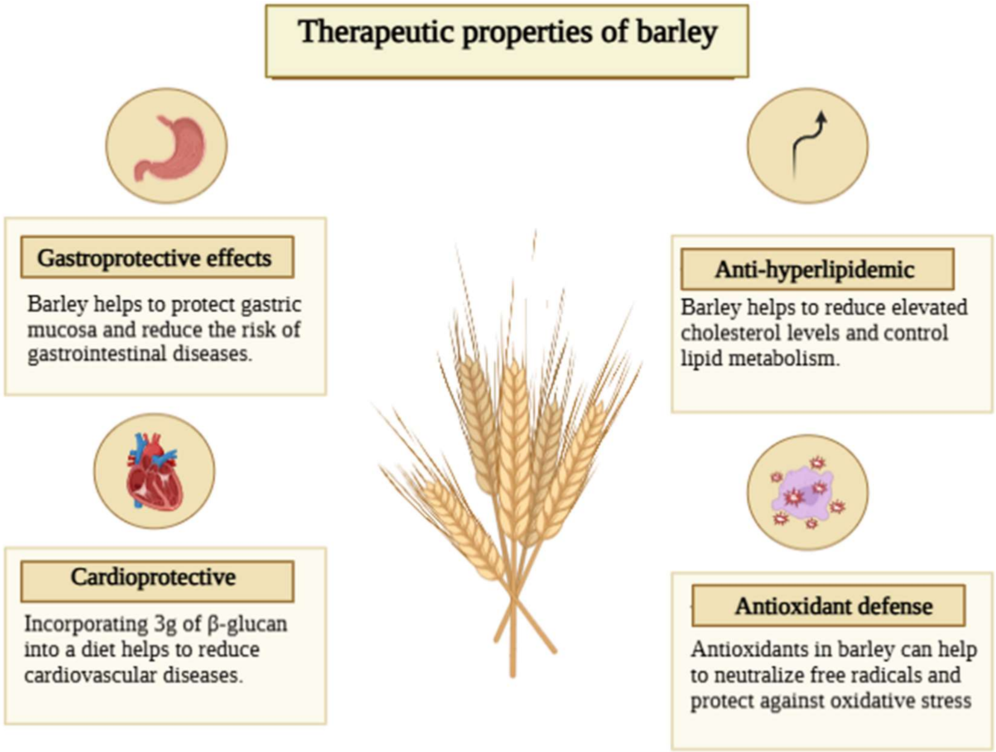
The gut microbiota is a complex community of microorganisms essential for immune regulation and maintaining physiological balance. Live bacteria have gained growing attention as potential therapeutics for intestinal disorders, as they can prevent pathogen colonization and promote a healthy microbial composition in the gut (Pan *et al.*, 2022). Moreover, the gut microbiome participates in cellular and tissue communication and regulates the animal's overall metabolic processes (Balasubramanian & Liu, 2024). In both human and veterinary medicine, the significance of gut health is growing, as well as balanced intestinal microbiota in domestic animals promotes overall health, growth, and performance (Chowdhary *et al.*, 2025). Maintaining the balance between harmful and beneficial microorganisms highlights the role of gut's defense system in preventing gastrointestinal tract (GIT) health. The luminal microbiota must be tolerated by the GIT, but the defense system needs to shield the GI mucosa from pathogenic agents and potentially hazardous food allergens (Mio *et al.*, 2021). GI system of mammals is inhabited by trillions of microorganisms, also their composition and variety within the gut microbiome are essential for controlling host immunity, preventing the proliferation of harmful microorganisms and enhancing the absorption of nutrients (Feng *et al.*, 2022). In animals, the gut environment supports a highly diverse microbial ecosystem essential for maintaining physiological homeostasis. The microbial structure is shaped by host genetics and external factors such as diet, habitat conditions, stress, and management systems. Alterations in the normal microbial balance, or dysbiosis, can predispose animals to gastrointestinal and immunological problems, ultimately affecting their welfare and productivity (Barathan *et al.*, 2024). Moreover, dysbiosis is continuously developing, encompassing alterations in the diversity and composition of the microbiome, as well as functional changes in the production of microbial metabolites (Suchodolski, 2022). Dysbiosis, along with various other stressors, triggers an inflammatory response resulting in increased intestinal permeability or gut leakage (Ducatelle *et al.*, 2023). Consequently, the examination of gut microbiota composition and microbial metabolites establishes a mechanistic connection between barley consumption and the health advantages.

Efficient utilization of feed ingredients is a key determinant of growth and productivity in animal production systems. With rising demand for conventional grains, the exploration of alternative feed ingredients has gained importance for supporting sustainable and efficient production (Ibrahim *et al.*, 2023). The rising global population has increased pressure on animal production systems to supply sufficient high-quality protein. Climate variability, drought, and reduced agricultural land availability have further challenged conventional feed production. Vertical farming systems offer a controlled method for producing reliable livestock feed, commonly using cereal grains such as barley (Crump *et al.*, 2024). Barley is widely used as a feed ingredient across various animal production systems. Fermented barley products are increasingly recognized as functional feed ingredients due to their potential to enhance growth performance, product quality, and gut health in animals (Badea & Wijekoon., 2021).

The cereal barley is bulky in dietary fiber, particularly beta-glucan (β-glucan). During colonic fermentation, β-glucan is known to produce a significant amount of butyric acid. It has been suggested that the colon serves as a medium for the nutritional effects of fiber through the microbiota by increasing the process for producing short chain fatty acids (SCFAs) (primarily acetic, propionic, and butyric acids) (Kaur *et al.*, 2024). β-glucan is mostly found in the cell walls of the aleurone layer and starchy endosperm of barley grains, with the endosperm accounting for the majority of the total β-glucan content (Kumar *et al.*, 2025). Butyric acid is the predominant energy source for colonocytes, with propionic acid following closely behind. Both are strongly implicated in systems that reduce the inflammatory response (particularly gut inflammation, such as in inflammatory bowel disease (IBD) and colitis) through modulation of pro-inflammatory cytokines and promotion of anti-inflammatory pathways (Teixeira *et al.*, 2017). Dietary highland barley, whole grain barley, and β-glucan boosted barley can all affect the structure and composition of gut flora. Furthermore, a large amount of metabolites of the gut microbiota (SCFAs), can be produced, which is beneficial to host health (Li *et al.*, 2022). β-glucan, which is made up of β (1-3) and (1-4) glycosidic polymers, is abundant in barley. Barley β-glucan acts through two major mechanisms: the first inhibits reabsorption of bile acid, and the second stimulates outflow of fecal bile acid. The secondary mechanism refers to the impact of byproducts generated in the GIT as a result of β-glucan fermentation originating from the gut microbiota (Mio *et al.*, 2021). A clinical trial demonstrated that consuming sixty grams of whole barley (WB) daily for 4 weeks boosted the number and variety of several different genera of gut bacteria (Cortijo-Alfonso *et al.*, 2024). Barley leaves have a long past of use in conventional Chinese medicine due to its benefits on gastroprotective effects, anti-inflammatory properties, and lipid lowering properties. They are also rich in insoluble dietary fiber. In colon by gut microbiota, insoluble dietary fiber is digested more than the soluble dietary fiber, yet it has a significant physiological advantage on fecal bulking (Tian *et al.*, 2021).

Highland barley (HB), also known as hull-less barley, is a common dish in China, Japan, Pakistan, Nepal, and Afghanistan (Lu *et al.*, 2023). HB is a hull-less barley cultivar that is primarily found in highland areas. Globally, HB is the fourth most produced cereal and has high nutritional fiber content. HB has a significant phytochemical content, mainly including phenolic compounds, polyphenol, lipids, and other components. These phytochemicals have been shown to improve a variety of chronic diseases associated with lipid metabolism (Li *et al.*, 2022). The composition of intestinal microorganisms can be altered by dietary polyphenols, which are then catabolized by the microbes to produce bioactive metabolites (Wang *et al.*, 2022). Fig. 1 represents therapeutic benefits of barley. Furthermore, several studies have revealed that HB has a substantial ability to reduce the severity of elevated cholesterol levels, control lipid metabolism, reduce oxidative stress and reduce the damaged area of the liver (Li *et al.*, 2022). This review aims to summarize all studies conducted in the previous five years on the preventive effect of barley on the GIT. Barley also improves gut bacteria profile, intestinal fermentability, regulates intestinal microbiome, and has gastroprotective, prebiotic, and probiotic effects.

Barley production and consumption: Agriculture is regarded as the backbone of the economy in emerging countries, playing a vital role in economic growth. It has long been the primary source of essential food crop production (Mithu *et al.*, 2025). Agricultural trade is essential for connecting agricultural production with market demand in the context of global economic development and food safety (Li Qing, 2024). Barley is a valuable crop with various uses, including human consumption, animal feed, and industrial raw materials. With rising consumer interest in health and wellness, the food industry is exploring ways to enhance nutritional quality by incorporating functional ingredients that provide added health benefits (Albaayit *et al.*, 2024). Barley cultivation occurs on all continents, but varies widely by region. Europe has the largest barley cultivation area and production. In 2021, Europe had the biggest barley cultivation area on the continent, totaling 22,525,713 hectares. Between 2015 and 2021, Europe accounted for 60.7% of global barley production (Soare *et al.*, 2023). Among many varieties of barley, HB is particularly important especially in Asia region and used as a dietary staple and gained popularity due to its high β-glucan and polyphenol content improving human health (Chen *et al.*, 2021). China produces more than 60% of the world's HB, particularly in highland regions such as west



Barley helps to protect gastric mucosa and reduce the risk of gastrointestinal diseases.

Barley helps to reduce elevated cholesterol levels and control lipid metabolism.

Incorporating 3g of β-glucan into a diet helps to reduce cardiovascular diseases.

Antioxidants in barley can help to neutralize free radicals and protect against oxidative stress

Fig. 1: Therapeutic benefits of barley.

Sichuan, Tibet, southwest Gansu, northwest Yunnan, and Qinghai (~0.27 million hectares of cultivated area) (Lu *et al.*, 2023). In 2020, Qinghai cultivated 82,730 ha of HB and produced 191,700 tons, whereas Tibet cultivated 138,790 ha and produced 790,500 tons of highland barley. Furthermore, Gannan cultivated 11,210 hectares of HB in 2020, yielding 34,949 tons of total yields. Ganzi cultivated 5853 hectares of HB annually, yielding 18,614 tons of HB (Gan *et al.*, 2023). Barley is being grown on 975 hectares in Ethiopia's highlands. The study analyzed secondary data from the USDA and found that barley productivity increased by 0.5 MT/ha from 2014 to 2023. Household consumption of barley has increased from 1975 metric tons (MT) in 2014 to 2475 MT in 2023. Furthermore, imports have risen from 31 metric tons (MT) in 2014 to 50 MT in 2023. Ethiopia's government is increasing barley production to address the demand and supply discrepancy (Beyene, 2024). In 2017, Iran imported around 1.3 million tons. A study was conducted in Iran to increase barley production by combining fertilizers (deficit irrigation and nitrogen). During the study period, the Reyhane 0-3 barley cultivar outperformed Iran's average barley output of 3.07 Mg ha−1 with 75% full irrigation and nitrogen fertilizer treatments of 140 and 210 kg $^{\text{ha-1}}$, respectively. The study found that, in comparison to other commonly grown cultivars in the area, the Reyhane 0-3 barley cultivar absorbed more nitrogen in grain than straw. Consider using 25% deficit irrigation with 140 kg N ha^{-1} for sustainable barley production in semi-arid areas (Naghdyzadegan Jahromi *et al.*, 2023).

Barley is often used in the making of beer, one of the world's most popular alcoholic beverages. In 2022, over 1.89 billion hectoliters of beer were produced worldwide. That year, China produced the most beer, with over 360 million hectoliters. The United States and Brazil placed second and third, respectively. Barley is processed into cereals such as bread, noodles, pasta, muffins, cakes, cookies, and biscuits. Barley has immense potential for use in a range of cereal-based recipes as a partial or total substitution for existing grains such as wheat, maize, rice, and oats (Lukinac & Jukić, 2022). Ground pearled barley is used throughout the Middle East and North Africa to produce flatbread, soups, and cereal. In Western countries, pearled barley is used as flaked, whole, or ground for breakfast cereals, porridge, soups, stews, infant feeding, and baking flour blends (Fernandes *et al.*, 2018).

Nutritional composition and feed value of barley: Starch, dietary fiber and crude protein are the highest constituents of barley. Together, these three ingredients account for almost 90% of grain's dry matter. The low molecular weight sugars, ether extract, and ash that make up the remaining portion of barley grain are minor components. In barley, the two main non-starch polysaccharides are cellulose and pentosans (Biel & Jacyno, 2013). Barley contains soluble fiber called β-glucans, which may lower cholesterol (Raj *et al.*, 2023). Compared to most other grains, whole grain HB was found to contain higher quantities of β-glucans, phenolics, tocols, and phytosterols. Because of its unique nutritional composition and bioactive components, whole grain HB and its extracts have been shown to have potential health-promoting properties, such as the ability to prevent cardiovascular disease, obesity, diabetes, and cancer, as well as have gut-protecting and anticarcinogenic effects (Li *et al.*, 2022). The endosperm exhibited very significant amounts of catechins and hydroxybenzoic acid along with a very high content of β-glucan content (Mart *et al.*, 2021). One of the investigations found significant chemical variations between spring and winter barley types. Winter barley cultivars contain the most β-glucan, which functions as an antinutritional factor for animals with monogastric systems (Alijošius *et al.*, 2016). Wholegrain barley exhibited a lower amylose/amylopectin ratio than peeled and pearled barley grains. The cereal industry may take advantage of the middling fraction's high β-glucan concentration as a health-promoting component (Sullivan *et al.*, 2010). Barley includes fiber, phenolic acids, flavonoids, phytosterols, alkylresorcinols, benzoxazinoids, lignans, and folate. It also contains β-glucan and total tocopherols. Among the 64 chemicals detected in barley, one study discovered 27 anthocyanins, 9 flavanols, 9 flavone glycosides, and 19 phenolic acids and aldehydes (Zeng *et al.*, 2020). The nutritional profile of barley including the bioactive components mentioned in Table 1. The most common phenolics found in HB included bound forms of ferulic acid, naringin, and catechin. These varieties exhibit hypoglycemic effect by inhibiting α-glucosidase and α-amylase, boosting glucose intake, glycogen build-up, and glycogen synthase 2 (GYS2) activity, and decreasing glucose-6-phosphatase (G6Pase) and phosphoenolpyruvate carboxykinase (PEPCK) activities (Deng *et al.*, 2020). Cooked whole-grain, HB is a source of bio accessible phenolic acids (Drawbridge *et al.*, 2021). The malting method resulted in barley lipids containing 51.74% linoleic acid, 19.94% oleic acid, and 18.53% palmitic acid (Özcan *et al.*, 2018). The major phytochemical constituents of barley are shown in Fig. 2.

Table 1: Nutritional composition of barley.

Components		Percentages	Citations
Carbohydrates		55-60%	(Soare *et al.*, 2023; Kaur *et al.*, 2024)
Protein		9.5-14%	
Fat		2-3%	
Cellulose		4-7%	
Fiber		11.7-16.5%	
Ash		2-3%	
Ca		350.7–975.5mg/kg	(Guo *et al.*, 2020)
P		3032.75mg/kg	
Fe		6.32–93.7mg/kg	
Cu		3.64–6.02mg/kg	
Zn		16.8–30.3mg/kg	
Mn		14.49–20.29mg/kg	
Se		0.007–0.323mg/kg	
Vitamin E		19.20-54.56µg/g	(Ghulam Muhu Din Ahmed *et al.*, 2025)
β-glucan		3.2-4.6%	(Biel *et al.*, 2020)
Total essential amino acid		31.6-32.9g/100 g	(Kaur *et al.*, 2024)
Total anthocyanin		158-353.5mg/100 g	(Zeng *et al.*, 2020)
Ferulic acid		270mg/g	(Raj *et al.*, 2023)
Phenolic acid	Free form	4.6-23mg/g	
	Conjugated form	86-198mg/g	
	Bound form	133-523mg/g	
Pro-anthocyanins		15.8-131.8mg/g	
Tocol		40-151mg/g	
Sterols		761mg/g	

Anti-inflammatory properties of barley in animal nutrition: Barley has gained significant importance due to its anti-inflammatory effects. β-glucan, phenolics, and lutonarin (LN) are the primary components in barley that contribute to its anti-inflammatory properties. These substances play significant role in regulating the immune system and lowering systemic inflammation (Eid *et al.*, 2023).

Polyphenol-mediated anti-inflammatory effects: Polyphenols are secondary metabolites that have the potential to be advantageous because of their high antioxidant characteristics, which include scavenging reactive oxygen species (ROS) and free radicals (Gönül Geyik *et al.*, 2023). Plant polyphenols, such as epigallocatechin-3-gallate (EGCG), are naturally occurring dietary compounds rich in catechol and galloyl groups that enable multiple noncovalent interactions (Wu *et al.*, 2025). Barley polyphenols, including ferulic acid, catechin, and proanthocyanidins, possess comparable structural features that allow them to interact with various biomolecules and metal ions. These interactions contribute not only to the formation of stable complexes and antioxidant networks but also to modulating biological functions, such as anti-inflammatory and lipid-lowering activities (Jin *et al.*, 2022).

Polyphenol-based surface functionalization offers a flexible strategy for developing multifunctional therapeutic systems. Through their strong antioxidant and anti-inflammatory properties, these structures can be tailored to respond to oxidative or inflammatory environments, thereby enhancing cellular protection and tissue recovery (He *et al.*, 2025). Barley contains various phenolic compound flavonoids that plays important role to reduce inflammation. The free phenolic extracts of the four barley varieties contained a polyamine that was tentatively identified as N1, N8-dicaffeoyl spermidine. This polyamine was found in relatively high abundance when compared to the phenolic acids and has additional anti-inflammatory and antioxidant properties (Drawbridge *et al.*, 2021). Gallic acid, a polyphenol, can improve the effectiveness of chronic colitis via a complex mechanism that affects gut microbiota, intestinal barrier integrity, and inflammatory responses (Tian *et al.*, 2025). Barley seedling (BS) extracts are reported to possess anti-inflammatory and antioxidant properties. BS extract contains the flavonoid (LN), which has several types of known bioactivities. LN inhibited the proinflammatory cytokines production including (IL-6, TNF-α), inflammatory enzymes (COX-2, iNOS), and lipopolysaccharide-induced inflammatory pathways. LN may be an effective and secure therapy for physiological inflammation (Yang *et al.*, 2021). Moreover, the anti-obesity properties of tea polyphenols can be better understood by looking at their potential to reduce intestinal inflammation and improve the treatment of obesity (Tian *et al.*, 2024). Consuming a diet high in instant soluble barley melanoidins may have the preventive benefits against chronic inflammatory disorders by lowering oxidative stress and inflammation (Ogilvie, 2021; Antonietti *et al.*, 2022).

Anti-inflammatory effects of others component (β-glucan, arabinoxylans, etc.): The most common crop among Tibetans, HB has the highest amount of β-glucan of any crop. HBBG (β-glucan from highland barley) can

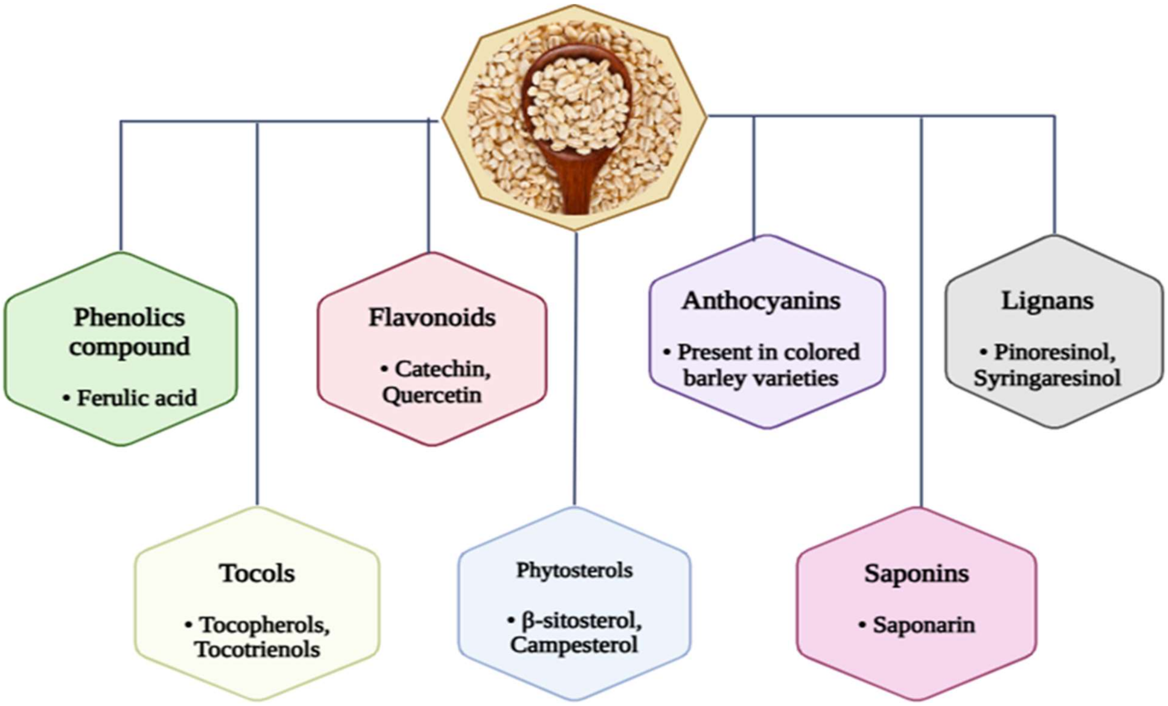


Fig. 2: Phytochemical profile of barley.

improve intestinal health and alleviate GI disorders. A study conducted on mice found that HBBG regulated the structure of the gut flora while maintaining an equilibrium of anti- and pro-inflammatory cytokines (Chen *et al.*, 2021). Additionally, barley bran extracts have been shown to enhance lymphocyte proliferation, phagocytosis, and pinocytosis in macrophages, while inhibiting tumor cell proliferation. These actions have immunomodulatory effects and may reduce systemic inflammation (Ghulam Muhu Din Ahmed *et al.*, 2025). Insoluble dietary fiber obtained from barley leaves reduces inflammation by modifying the gut microbiota composition and boosting the synthesis of metabolites derived from the microbiota (Tian *et al.*, 2021). The immune system was stimulated by higher β-glucan barley flour as it modulated the gut microbiota, leading to an increase in SCFA concentration (Mio *et al.*, 2021). One of the study showed that Co-fermented wholegrain quinoa with black barley may help reduce chronic inflammation and metabolic disorders resulting from a consumption of Western-style diet (Lin *et al.*, 2024).

Food applications of barley and its functional components relevant to animal health: A number of factors have contributed to the recent rise in consumer demand for health-benefitting products. More than any other functional food, probiotic-based foods are becoming more prominent (Durukan *et al.*, 2024). In an attempt to produce mixed chapattis and cookies, hulless barley genotype (BHS 352) was used in combination with wheat flour (C 306 & HS 490). According to their research, barley can significantly increase the nutritional value of wheat biscuits and chapattis by increasing their β-glucan concentration, phenolic content, and antioxidant activity. Incorporating barley flour into widely consumed wheat-based products may help people improve their health (Narwal *et al.*, 2017). Due to its increased level of β-glucan soluble fiber and certain cancer-preventive compounds, barley is considered a particularly nutritious cereal grain. Additionally, research shows that bread made with a blend of wheat and barley flour has appropriate sensory qualities. By modifying the insulin and glycemic response, the β-glucan found in barley flour can enhance the quality of bread (Shaveta *et al.*, 2019). Food applications of barley are presented in Table 2.

Prebiotic effect of barley and its role in modulating animal gut microbiota: A prebiotic is a non-digestible food component that benefits the host by promoting the growth and/or activity of specific beneficial bacteria in the digestive tract, thereby supporting microbial balance (Zhu *et al.*, 2021). Probiotics exert a variety of beneficial effects, including the restoration of intestinal microbial balance and the stimulation of enzymatic activity, both of which contribute to improved nutrient absorption (Dar *et al.*, 2022). One advantage of prebiotics over probiotics is that they stimulate bacteria that are already naturally present in the GI and are therefore well-adapted to that environment (Kassymbekova & Strochkov, 2025). To maintain a healthy microbial balance in the body, probiotics encourage the growth and activity of particular microorganisms in the GIT, mainly *Lactobacilli* and *Bifidobacteria* (Jin Yu Chieng & Yan Pan, 2022). By boosting the number and activity of *Lactobacilli* and *Bifidobacteria*, prebiotic dietary manipulation of the gut microbiota seeks to improve health (Rashid *et al.*, 2023). Prebiotics promote the growth and activity of our GI flora, which further improves our health, and are fermentable by our GI microbiota (Alqahtani *et al.*, 2024). Certain strains have a unique ability to survive harsh conditions within the host. Even as they pass through the acidic environment of the stomach and the presence of bile salts,

Table 2: Food applications of barley

Food product	Component	Main findings	Reference
Barley tea	Hulled barley	More common in Japan and Korea. It includes minerals, tocols, phytates, dietary fiber, and phenolics.	(Baik *et al.*, 2014)
Flour dough balls	WG barley	Barley flour was fermented with different species of lactobacilli. Dietary fiber in barley acts as a prebiotic for probiotic bacteria.	(Suman and Sreeja *et al.*, 2019)
Barley bread	Whole barley flakes	The inclusion of 15% barley flakes decreased bread volume. Adding flakes produced bread with a desirable texture and flavor.	(Lukinac *et al.*, 2022)
Pasta	Barley flour	Pasta made from whole grains and high-fiber cereals like barley contained 4.3-5.0% β-glucan and 15.2-16.1% fiber.	(Izydorczyk and Dexter *et al.*, 2015)
Cookies/biscuits	Barley flour	Replacement or partial addition of wheat flour to barley flour enhances the functionality of cookies by containing phenolic compounds, antioxidant activity, β-glucan, and dietary fiber.	(Drakos *et al.*, 2019)

they remain viable and active (Dablool *et al.*, 2024). Probiotics are live, non-pathogenic microorganisms used as dietary supplements to provide health benefits. They help maintain a balanced intestinal microbial flora by colonizing the gut and preventing the growth of harmful pathogens. Regular intake of probiotics has been shown to help reduce anxiety and manage chronic psychological stress (Arsène, 2021). Probiotic bacteria play a key role in balancing and supporting healthy gut function, helping to prevent age-related dysbiosis (Yu *et al.*, 2024). Prebiotics and probiotics are essential for maintaining the intestinal flora and enhancing host health. Dietary prebiotics are metabolized by various colonic bacteria to produce beneficial metabolites, particularly SCFAs, which enhance intestinal function and luminal contents while favorably impacting host physiology as a whole (Ashaolu, 2020; Coniglio *et al.*, 2023). The by-products of prebiotic processing possess immunomodulatory and anti-inflammatory effects, indicating to a potential therapeutic use for a number of pathological conditions (Guarino *et al.*, 2020).

According to research study, the thermally treated digesta of germinated HB, particularly for those that were extruded, followed by those that were steamed, microwaved, and baked, stimulated the growth of *Lactobacillus plantarum* and *L. Delbruck* in a dose-dependent way. The prebiotic impact was positively linked with the total dietary fiber level, according to a Pearson correlation analysis (Huang *et al.*, 2021). HBBG has prebiotic potential, and co-microencapsulating it with probiotic bacteria may enhance its protective effects during digestion (Yuan *et al.*, 2023). A study conducted on broilers revealed that supplementing male broiler diets with up to 30% barley with prebiotics reduced feed intake while not affecting their characteristics or slaughtering weight (Rehman *et al.*, 2020). High-glucan barley flour exerts a prebiotic effect which improves the immunological system of high-fat mice. This effect was detected in IgA secretion and IL-10 production, among other immunological activities, even in factors where higher fat diet damaged the immune system (Mio *et al.*, 2021). Studies compared LMW-BG with HMW-BG to analyze their effects on cecal fermentation, glucose, and lipid metabolism. While LMW-BG specifically increased bacterial populations of Bacteroides and Bifidobacterium as well as SCFAs (acetate, and propionate) in caecum, HMW-BG specifically inhibited fat absorption and reduced abdominal deposit fat (Aoe *et al.*, 2021). According to one of the research study, Xylo oligosaccharides, or XOS, from pretreatment barley straw may generate interesting prebiotic substrates that, when fermented by the gut microbiota, form SCFAs. These products can be used in a variety of ways as nutraceutical components (Álvarez *et al.*, 2023). Because butyric acid producing bacteria break down dietary fiber to make butyric acid, functional barley may work as a prebiotic, boosting BAPB and subsequently butyric acid in the intestine (Akagawa *et al.*, 2021). Supplementing the diet with chlorella (unicellular green microalga known for its high nutrient density and bioactive constituents) and germinated barley can have an effect on certain blood and biochemical parameters (Al-Baroodi & Al-Attar, 2021).

Recent studies show a positive effect of different varieties of barley and its form used in studies are highland barley, black barley, fermented also extract and roasted barley, fermented barley bran, barley leaf, low molecular weight barley and fiber bound polyphenols have different effect on gut health. Rats given a high-fat diet could have their body weight successfully controlled. Supplementing with black barley fermented with *Lactobacillus* reduced hepatic steatosis and oxidative stress while improving liver function (Zhu *et al.*, 2021). It may manage high fat diet (HFD)-induced intestinal microbiota dysbiosis by boosting microbial diversity, raising the relative abundance of *Bacteroidetes*, decreasing the *Firmicutes/Bacteroidetes* ratio, and enriching specific intestinal probiotics (such as *Akkermansia*) (Li & Wang, 2023). A study conducted to examine the possible gut microbiota modulatory effect of partly milled highland barley (PHB) and determine whether it can control blood glucose levels and abnormal lipid levels in mice administered a HFD (high-fat diet). For mice given a HFD, HB consumption produced positive results. Major decreases in fasting and postoperative blood glucose levels, suppression of lipid droplet aggregation in the liver, improvement of colon damage, and recovery of intestinal flora ratio have all been reported. It had no apparent effect on plasma lipid levels, body weight, and the weight of adipose tissue (Li *et al.*, 2022).

Another study was conducted to examine the preventive effects of β-glucan extracted from HB on the GIT treatment with β-glucan may minimize ethanol-induced damage to the stomach mucosa and lesions, lowering the gastric ulcer index. In vehicle animals, β-glucan therapy lowered malondialdehyde levels and boosted superoxide dismutase and catalase activity in the stomach, reducing oxidative stress (Chen *et al.*, 2019). The prebiotic impact of barley consumption on gut health is illustrated in Fig. 3.

Another study investigated the possible gastro-protective effects of saccharification on indomethacin (INDO)-induced gastric ulcers in rats by utilizing triple fermented *H. vulgare* extract (FBe) from *Weissella ciboria* and *Saccharomyces cerevisiae*. The outcome of this investigation demonstrates that oral FBe administration had anti-inflammatory benefits and strengthened the body's immune system, which contributed to beneficial gastro-protective effects (Lim *et al.*, 2019). In another study, the effects of melanoidins from barley malts on the bacteria in the gut was investigated. SCFAs (acetate, propionate, and butyrate) are continuously produced as a result of fermentation of melanoidins by gut microbes in the colon. Sustained SCFA production is beneficial because it preserves intestinal epithelial integrity, supports metabolic and immunological balance, and maintains a stable colonic environment. Significantly different gut microbiota profiles were seen in response to increased melanoidins, which also promoted sustained SCFA production. Mice that consumed the highest levels of melanoidin showed a considerable rise in *Bifidobacterium* spp. and *Akkermansia* spp. Long-term ingestion of melanoidin malt increases beneficial bacteria such as *Bifidobacterium*, *Akkermansia*, and *Lactobacillus*. The *Lactobacillus* population didn't vary substantially between groups that received 0% or 100% melanoidin malts. The gut microbiota responds differentially to diverse types of melanoidin-rich diets (Aljahdali *et al.*, 2020). Study is conducted to check the impact on growth outcomes, nutritional utilization, and GIT development of broilers. Birds fed diets with coarse barley (CB) and WB showed higher weight gain and digestibility of dry matter, nitrogen, calcium, gross energy, and ileal digestible energy than birds on Fine Barley (FB) diets. Feed per gain was lower in birds fed WB diets than in birds fed FB diets. The birds given CB had a higher fat digestibility than the bird's fed FB and WB. But supplemental protease had no influence on growth performance or nutrient utilization. This is probably because the basal diet's beneficial inherent protein digestibility and well-balanced digestible amino acid composition help to promote healthy growth (Tari *et al.*, 2022). The objective of this study was to determine the effect of graded WB feeding on broiler chicken growth rate, carcass efficiency, GIT morphology, and function. Aside from increased butyrate concentrations in the caecum and decreased digesta viscosity in the broiler ileum, there were no variations in ammonia nitrogen concentrations among the groups fed low-, medium-, and high-whole barley diets. The high amount of WB in the food resulted in increased Lactobacillus spp. in ileal contents and improved ileum shape (Viliene *et al.*, 2022). Incorporating 3g of β-glucan per day into the diet can reduce the occurrence of hyperlipidemia and cardiovascular disease (CVD). The accepted health claim for β-glucan and normal blood LDL cholesterol, as well as the presence of tocols (tocotrienols) and phenolic compounds linked to health benefits, highlight the need to promote the development of food items including oat and barley grain or flour as an ingredient (Biel *et al.*, 2020). In this study, the researchers wanted to see if insoluble dietary fiber from barley leaves (BLIDF) could reduce gut inflammation by modifying the intestinal microbiota in mice with DSS-induced colitis. Feeding BLIDF reduced DSS-induced acute colitis symptoms, as well as IL-6, TNF-α, and IL-1β levels in the colon and sserum of affected mice. Results shows that BLIDF lowers inflammation by changing the composition of the gut microbiota and enhancing the production of microbiome-derived metabolites (Tian *et al.*, 2021). Many studies suggest the inclusion of barley in a diet to promote gut health as mentioned in the Table 3. The synergistic effects of other components of barley are presented in Fig. 4.

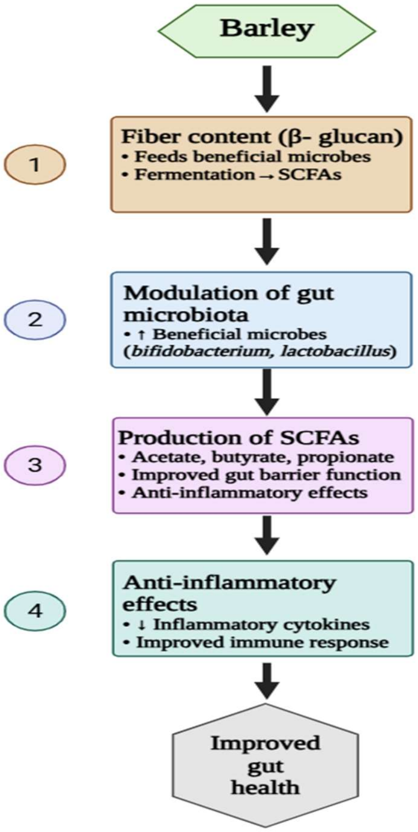


Fig. 3: Prebiotic mechanism of barley β-glucan on gut health of animal.

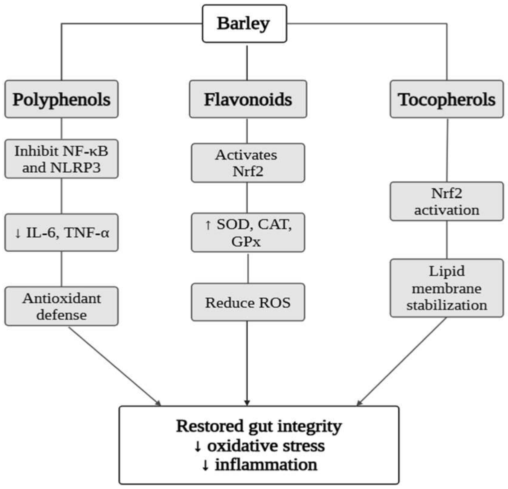


Fig. 4: Synergistic effects of barley components. (Tian *et al.*, 2025; Krawczyk *et al.*, 2023; Luo *et al.*, 2023; Altanam *et al.*, 2025) NF-κB (nuclear factor kappa-light-chain-enhancer of activated B cells), NLRP3 (NOD-like receptor family pyrin domain-containing 3), IL-6 (interleukin-6), TNF-α (tumor necrosis factor-alpha), Nrf2 (nuclear factor erythroid 2–related factor 2), SOD (superoxide dismutase), CAT (catalase), GPx (glutathione peroxidase), ROS (reactive oxygen species).

Table 3: Studies on barley inclusion and gut health outcomes in human and animals

Study object	Barley type/study objective	Methodology	Duration	Result / conclusion	References
Mice	The impact of eating melanoidins from barley malts on intestinal flora.	Mice were randomized into 5 groups. Dosage: Group 1 and 5 contains Melanoidin-free malts and Melanoidin-rich malts respectively. While group 2, 3 & 4 receives 75 %, 50%, 25% of melanoidin free malts & 25 %, 50%, 75 % of melanoidin rich malts respectively.	25 days	• ↑ Melanoidins alter gut microbiota and promote SCFA production. • ↓ *Dorea*, *Alisitpes*, and *Oscillibacter* ↑ *Lactobacillus*, *Parasutterella*, *Akkermansia*, *Barnesiella*, and *Bifidobacterium*. • Highest melanoidin intake group resulted in ↑ *Bifidobacterium* and *Akkermansia* spp. showing strong prebiotic potential.	(Aljahdali *et al.*, 2020)
Broiler chickens	To determine how feeding graded amounts of WB affects carcass and growth performance, as well as GI morphology and function.	800 male chickens were randomly divided and assigned into 4 treatment groups: 1. No- WB 2. Low- WB (4 %, 8 %, 15 %) 3. Medium- WB (6 %, 12 %, 20%) 4. High-WB (8 %, 16 %, 25 %)	35 days	• ↑ Feed conversion ratio (treatments diluted with WB). • ↑ Butyrate content (in caecum) • ↓ Digesta viscosity (in ileum) of broilers fed low-WB, medium-WB, and high-WB diets. • Diets high in WB resulted in • ↑ *Lactobacillus* spp. in ileal contents and better ileum morphology. The use of graded levels of WB in diets seems to promote GIT development.	(Viliene *et al.*, 2022)
Mice	HGB was tested for its prebiotic effects on the natural immune system of mice on a high-fat diet.	Rats were randomly assigned into 2 groups 1. Control group (cellulose supplemented diet with 50% fat energy diet 2. HGB group (Waxy hulled barley "White Fiber" flour)	90 days	In the group treated with HGB • ↑ sIgA concentrations in the Cecal pouch • ↑ IL-10 and pIgR gene expression levels • ↑ Propionate and lactate levels (in cecum), positively associated with IL-10 expression level. • ↑ in expression levels of the IL-10 gene HGB intake: • ↑ Microbiome count, such as *Bifidobacterium* and *Lactobacillus*.	(Mio, Otake, *et al.*, 2021)
Mice	A comparison of low molecular weight barley β-glucan (LMW-BG) and high molecular weight β-glucan (HMW-BG) for glucose, lipid metabolism and cecal fermentation.	Mice were randomly assigned to 3 groups 1. Control group 2. LMW-BG (due to the fact that LMW-BG diet comprised 33.6% accessible carbohydrate and 4.2% protein, the protein and carbohydrate amounts were modified with casein and dextrinized maize starch.) 3. Freeze dried, 68.4 % of maize starch was combined with 31.6 % of dissolved HMW-BG and added to an experimental diet.	61 days	• ↓ in both BG groups, blood leptin, total and LDL cholesterol levels, and the mRNA level of sterol regulatory element-binding protein-1c. • HMW-BG inhibited fat absorption and decreased abdominal fat deposits. • LMW-BG increased bacterial counts of *Bifidobacteria* and *Bacteroides*, also increasing total SCFAs (acetate and propionate) in the caecum. In LMW-BG group: ↑ mRNA expression of neurogenin 3 LMW-BG acts as a prebiotic, affecting glucose and lipid metabolism, but HMW-BG's high viscosity in the GIT is responsible for its unique effects.	(Aoe *et al.*, 2021)
Human study (Japanese population)	To explore the connection between barley intake and gut microbiome profiles among Japanese individuals.	94 individuals were divided into two groups depending on the rate of median barley intake: 1. High (47 participants): 3.5-28g /1000 kcal 2. Low (47 participants): 0-3.5g /1000 kcal	Cross sectional study	• ↑ *Lactobacillus*, *Faecalibacterium*, *Bacteroides*, *Prevotella*, and *Akkermansia* bacteria was observed in the group that consumed high amounts of barley. • The link between barley consumption and *Bifidobacterium* remained significant even after adjusting for disease and dietary patterns, while the association with *Butyricicoccus* persisted after controlling for disease. There was a direct correlation between barley consumption and *Bifidobacterium* and *Butyricicoccus*.	(Matsuoka *et al.*, 2022)
Mice	To investigate if Tibetan highland barley fiber (T-fiber) has the potential to reduce obesity caused by a high-fat diet (HFD) and also its regulatory effects on gut microbiota.	60 mice were randomized into 5 groups: 1. Normal-chow diet group 2. HFD Group. 3. HFD (Group with a low dose of T-fiber) (LTF) 4. HFD (Group with a medium-dose of T-fiber) (MTF). 5. Group with high-dose T-fiber (HTF)	15 weeks	• ↑ Acetic acid, propionic acid, butyric acid in the MTF and HTF fed mice as compared to the mice in HFD group. • T-Fiber supplementation: • ↑ *Muribaculaceae, Akkermansiaceae*, and *Lachnospiraceae* NK4A136 groups • ↓ *Bacteroidaceae*, *Prevotellaceae*, *Rikenellaceae*, and *Alloprevotella*.	(Gan *et al.*, 2023)
Mice	To evaluate whether highland barley β-glucan (HBBG) can relieve ulcerative colitis (UC) in mice.	18 mice were divided into 3 groups: 1. Normal control group (regular chow, ultrapure water) 2. HBBG group (HBBG diet, 2% dextran sulphate sodium (DSS) water (day 1-7) and then ultrapure water 3. UC group (regular chow, 2% DSS water (day 1-7) and then ultrapure water day (7-14))	14 days	In HBBG group: • Shorter colons were observed compared to the NC group, but much longer than the UC group. • HBBG can enhance the relative transcriptional levels of genes that encode occluding, mucin2 (MUC2), and claudin-1, lowering gut permeability. HBBG maintained the balance of proinflammatory and anti-inflammatory cytokines and altered the	(M. Chen *et al.*, 2021)

				composition of the gut flora.	
Mice	To investigate whether BLIDF can alleviate intestinal inflammation in DSS-induced colitis in rats by modulating the gut microbiota.	For experiment 1: 24 mice divided into 3 groups (4 in each) 1. CT group (control diet) 2. CT+DSS group (control diet) 3. BLIDF+DSS group (Adding BLIDF powder (1.52%) to the control diet) In experiment 2: 16 mice were administered antibiotics. A mixture of antibiotics contains ampicillin, metronidazole, and neomycin was incubated in drinking water for 14 days before being separated into 2 groups: CT+DSSab BLIDF+DSSab groups (mixing 1.52 % powder of BLIDF with the standard diet).	28 days	In CT+DSS group: • Inflammatory lesions (such as notable and included goblet cell reduction, crypt structural abnormalities, inflammatory cell buildup, body weight loss, elevated DAI scores, and colon shortening were all observed as key outcomes. BLIDF resulted: • ↓ Colon inflammation symptoms induced by DSS • Levels of IL-10, TGF-β, and IFN-γ were present in both the colon tissue and serum of rats with colitis. BLIDF supplementation: • ↓ *Akkermansia* • ↑ *Parasutterella*, *Erysipelatoclostridium*, and *Alistipes* • DSS treatment increased occludin and mucin2 expression while decreasing claudin-1 expression in mouse colons. Antibiotics reduced the intestinal flora, removing BLIDF's anti-colitis benefits. The analysis of microbiota-derived metabolites showed that BLIDF feeding can restore the DSS-induced decline in SCFAs and secondary bile acids in mouse feces.	(Tian *et al.*, 2021)
Mice	The impact of β-glucan derived from HB on the GIT.	All mice were randomly assigned to a control group and β-glucan groups receiving 8, 16, 32, or 64 mg/kg (based on body weight). The β-glucan groups were treated daily via gavage for two weeks.	4 weeks	• β-glucan groups benefit in the colon of mice, ↑the colon index, colon length, and total SCFAs (butyrate, acetate, and propionate) levels while ↓ pH levels in colon and caecum.	(H. Chen *et al.*, 2019)
Mice	To evaluate the effect of partly milled highland barley (PHB) to influence gut microbiota.	Mice were randomly assigned to five groups: 1. Group fed diet low-fat (normal chow) 2. Group fed HFD control (MC) 3. Low-dose group of an HFD (10% PHB) 4. Middle-dose group that was fed an HFD (20% PHB) 5. High-dose group (30% PHB) was fed an HFD.	12 weeks	• Mucosal structure of the ileum tissues improved. • In contrast to the MC group, low- and middle-dose PHB treatment reduced inflammation, while high-dose PHB treatment produced an equivalent level of suppression of inflammation as the normal group. • Intestinal flora's imbalance was restored. • ↑ The average amount of beneficial bacteria, including *Lactobacillus* and *Bifidobacterium*.	(S. Li *et al.*, 2022)
Human fecal microflora (vitro study)	This study aims to explore the MGO scavenging potential of fiber-bound polyphenols from HB during colonic fermentation and their role in reducing MGO-induced damage to gut microbes.	Six healthy 3 female and 3male. Experimental groups are: 1. Dephenolized insoluble dietary fiber (IDF) 2. HBBP-IDF 3. MGO group 4. MGO + dephenolized IDF group 5. MGO + HBBP-IDF group 6. MGO + catechin group (positive control)	24 hrs.	• Catechin and dephenolized IDF, HB containing fiber bound polyphenols raise the concentration of total SCFAs. MGO, HBBP-IDF may have a modulatory effect on the gut flora, improvement in SCFA production.	(J. Li *et al.*, 2024)
Human study	Consumption of fiber-rich barley boosts BAPB levels in the gut and raises butyric acid concentrations in feces.	18 healthy adults consumed granola with functional barley (BARLEY max®) daily for four weeks.	4 weeks	• Proportion of BAPB ↑ significantly after the intake. • ↑ Fecal butyric acid concentration from 0.99 mg/g feces before intake to 1.43 mg/g after intake.	(Akagawa *et al.*, 2021)
Rats	Investigate the gastroprotective effects of fermented barley extract (FBe) from *H. vulgare*.	48 rats were divided into 6 groups. The oral administration of FBe extract (100, 200, and 300 $^{\text{mg kg}^{-1}}$) half an hour before to the oral administration of indomethacin (INDO) (25 mg kg^{-1})	6 weeks	• ↓ Stomach mucosal injury was observed with FBe therapy. By ↑ glutathione (GSH) levels and superoxide dismutase (SOD) activity. Oral FBe administration had anti-inflammatory benefits and strengthened the body's defense system.	(Lim *et al.*, 2019)
Mice	This study investigates the effect of consumption of roasted barley flour on lipid metabolism and fermentation barley β-glucan in gut.	32 rats were separated into four groups. 1. Control group (Co) BF 2. Untreated barley flour (BF) group 3. Roasted barley flour (R1) group. 4. Roasted barley flour (R2) group AIN-93G diet with 5% dietary fiber (supplemented with cellulose). R1, R2, and BF groups received the same diet.	12 weeks	• Mice fed R1, R2 had ↑ of SCFAs in their cecum than mice fed untreated barley flour. The prebiotic action contributed to enhanced improvements in lipid metabolism.	(Mio, Yamanaka, *et al.*, 2021)
Mice	Examined the impact of barley-derived arabinoxylan on intestinal fermentability and GLP-1 secretion.	Mice were randomized into 3 groups 1. Control group (C) 2. β-glucan free barley diets (bgl) 3. High β-glucan barley diets (BF) AIN-93G diet were supplemented with arabinoxylan given to bgl and BF groups	12 weeks	• BF and bgl had higher GLP-1 concentrations at 60 minutes. Both barley groups had ↑ acetic acid and total SCFAs in their cecum contents, whereas the bgl group had higher concentrations of butyric acid.	(Mio *et al.*, 2022)

Mice	Fermented black barley was investigated for its preventive effects on gut microbiota and metabolic dysbiosis.	Mice were separated into 3 groups: 1. Normal control (NC) group 2. smoking(S) group 3. Smoking + fermented black barley-fed group (SB) SB group received oral administration of 100 μL/10 g BW per day of black barley fermentation broth.	12 weeks	• FBB increased abundances Ruminococcin and Oscillopsia at the genus. • ↓ Abundances of *Turicibacter*, *Lactobacillus*, and *Bifidobacterium* modulating the diversity of the gut microbiome.	(Zhong *et al.*, 2022)
Mice	Examined the effects of BL supplementation before or during CR (*Citrobacter rodentium*) infestation to determine its mode of action.	Mice were randomized into 4 groups (6 per group) 1. CD (chow diet) + CR 2. BL (barley leaf) + CR 3. duCR (BL chow before CR infection) 4. beCR (CD before infection) The beCR group received BL chow before CR infection and then switched to CD, whereas the duCR group received BL chow during the infection. CD+CR and BL+CR groups received CD and an isocaloric diet with 2.5% BL, respectively.	4 weeks	• BL+CR and beCR interventions markedly lowered levels of IL-6, IL-12, and MCP-1 were observed. BL pretreatment alleviated the dysbiosis of the gut microbiota by ↓*Proteobacteria* and ↑*Lactobacillus*	(Feng *et al.*, 2022)
Mice	Epicatechin (EC) and β-glucan (BG) from HB improved hyperlipidemia by restoring gut barrier function and microbiota balance.	Mice were separated into 11 groups. 1. Model group (M) 2. Low dosage of 150 mg/kg (ECL, BGL and EC + BGL) 3. High dosage 250 mg/kg (ECH, BGH and EC + BGH) 4. Positive control group 0.03 % LOV 5. Normal mice (N) low fat diet (LFD) 6. Whole grain diet groups (MWHB and NWHB) HFD and LFD with 25g whole grain barley.	12 weeks	• The combination of EC and BG synergistically activated Peroxisome Proliferator-Activated Receptor Alpha (PPARα), improved colonic barrier function, enhanced the comparative prevalence of *Lactobacillus* and *Desulfovibrio*, and improved short-chain fatty acid levels.	(Liu *et al.*, 2024)
Mice	To examine how dietary fiber from oat bran (OB), barley flour (BF), hi-maize amylose (HMA), and wheat bran (WB) alters gut microbiota composition and optimizes energy and glucose balance.	Rats were divided into 2 groups: 1. Obese rats received an HFD with four plant-based fiber supplements. 2. Lean rats previously on a chow diet were switched to a high-fat diet supplemented with 10% WB or BF.	12 weeks	10% BF and WB: • ↓ bw and obesity • ↑ Cecal butyrate, and enriched SCFA-producing bacteria, including *Lactobacillus* and *Lachnospiraceae* UCG-001. • WB and BF also elevated portal taurodeoxycholic acid (TDCA) compared to HFD rats.	(Martinez *et al.*, 2023)
Mice	To evaluate the role of barley vinegar on constipation by modulating gut microbiota and SCFAs levels.	30 rats were randomly divided into 5 groups (6 in each group). 1. Blank group (ND) 2. Model group (Mod) 3. Low dose (LD), medium dose (MD), high dose (HD) with 0.5, 1, 2 mL/kg/day doses of barley vinegar. ND and Mod group were given normal feed.	10 days	• Barley vinegar improved constipation by restoring gut microbiota balance and increasing SCFA levels. Liquid Chromatography-Mass Spectrometry (LC-MS) metabolomics confirmed its impact on intestinal metabolites in constipated mice.	(Li *et al.*, 2023)
Mice	To examine the impact of whole grain highland hull-less barley (WHLB) on gut microbial profiles using denaturing gradient gel electrophoresis (DGGE).	72 rats were randomized into 4 groups (18 per group). 1. Negative control (NC) 2. Blank control (BC) 3. High dose (HD), LD group were given 489.5, 100 g/kg of WHLB. NC fed standard diet and BC fed HFD.	4 to 8 weeks	• WHLB altered gut microbial profiles, with dominant bands varying by dose and time. Fecal and cecal microbiota were similar but had different dominant bacteria. • DGGE identified 19 bands from *Firmicutes* and *Bacteroidetes* and two unclassified bacteria. WHLB increased *Lactobacillus gasseri*, Uncultured *Prevotella* sp., and *Clostridium* sp.	(Xia *et al.*, 2024)
Mice	To investigate the effects of barley β-glucan on intestinal microbiota and metabolic byproduct succinate through microbiome and metabolome profiling.	Mice were divided into 4 groups (4 per group) 1. Normal diet + β-glucan rich barley (BF) 2. Normal diet + β-glucan free barley flour (BGL) 3. Middle fat diet with BF 4. Middle fat diet with BGL A normal experimental diet or a middle-fat diet (25% fat from lard) was used. BGL or BF flour was added equally, creating four groups.	8 weeks	Barley β-glucan: • ↑ Bacteroides, Parasutterella, and succinate, regardless of diet. It also enhanced succinate-producing bacteria and altered glucose metabolism.	(Mio *et al.*, 2024)
Mice	To investigate how barley polysaccharides (BP) inhibit colorectal cancer and promote beneficial gut microbiota through distinct pathways.	Mice were assigned into 4 separate groups. 1. Control group 2. Pseudo-germ-free groups: BP-ABX (barley polysaccharide-fed), BPf-ABX (given fermentation products), and CC-ABX (colorectal cancer model). BP-	8 weeks	• BP directly promotes protective metabolites and inhibits cancer pathways to reduce inflammation. It also enriches beneficial gut bacteria (*Colidextribacter*, *Bilophila*), strengthens the intestinal barrier, and increases metabolites like L-Glutamic acid, further inhibiting cancer pathways (Nuclear receptor, Apoptosis).	(Zhang *et al.*, 2024)

		ABX, BPf-ABX groups administrated 300 mg/kg of BP daily by gavage.			
Broiler chicken	To investigate the effects of high doses of oats and barley supplemented with external glucanase on gut health and microbiome in jejunum content (JC), jejunum mucosa, and cecal matter.	308 broilers were assigned to three groups with five pens of 24 each, fed a corn-soybean, barley, or oat diet. Barley and oat were included at 40% and 20%, respectively, in all feeding phases.	40 days	• Ten chickens were slaughtered in each treatment to measure intestinal viscosity and cecal SCFA levels, and microbiota composition. Despite glucanase, the barley diet increased ileal viscosity and small intestine microbial diversity but reduced cecal diversity and SCFA content. • Barley also increased *Bacteroidetes* and decreased *Firmicutes* in JC and CC. Oats had minimal effects.	(Rawash *et al.*, 2023)
Mice	To examine the impact of varying ratios of inulin soluble dietary fiber (ISDF) and barley leaf insoluble dietary fiber (BLIDF) on intestinal microbiota and glycolipid metabolism in obese mice.	Rats were divided into 7 groups 1. HFD, BLIDF, ISDF 2. I3S1DF, I2S2DF, I1S3DF (insoluble/soluble 3:1, 1:1, 1:3) 4. MIX (ISDF + BLIDF + insoluble/ soluble 3:6:1).	8 weeks	• All fiber groups, except MIX, reduced blood glucose markers. • BLIDF, ISDF, I3S1DF, and I2S2DF improved glucose tolerance and lowered IL-6, while BLIDF and I1S3DF boosted SOD activity. I3S1DF and I1S3DF improved serum lipids. All treatments enhanced gut microbiota balance.	(Ren *et al.*, 2024)
Mice	To study the effects of HB, whole grain HB (WGHB), HB bran (HBB) on hyperlipidemia and hepatic inflammation.	50 rats were allocated into 5 groups (10 per group) NC, HB, HBB, WGHB, HFCD (high-fat and cholesterol diet). The XT108C experimental diet was mixed with HB, HBB, and WGHB diets for the respective groups.	9 weeks	HB and HBB: • ↓ Triglycerides (TG), total cholesterol (TC), low-density lipoprotein cholesterol (LDL-C), aspartate aminotransferase (AST), and alanine aminotransferase (ALT) • ↑ Good cholesterol HDL-C (high-density lipoprotein). HBB improved gut microbiota: • ↑ *Bacteroidetes/Firmicutes* ratio, *Lactobacillus*, and *Akkermansia muciniphila*. • ↓ *Proteobacteria* and *Shigella*.	(Li & Wang, 2023)
Mice	To examine the effect of dietary fiber derived from young barley leaves (YB) on gut and immune system function.	2 groups control and YB groups. The specialized diet (modified) replaced casein (CE) in the experimental diet (AIN-93G) with dietary fiber obtained from YB leaves. The adjusted experimental diet, which contains 64.5% df, was changed to match the original AIN-93G diet.	4 weeks	YB feeding gut microbiota composition shifted, with increased *Lachnospiraceae*, mainly butyrate-producing species. Fecal butyrate levels increased. In mice fed with YB the number of intestinal immunoglobulin A-positive (IgA+) plasma cells increased.	(Chudan *et al.*, 2024)
Mice	To evaluate the effects of whole highland barley (WHB) supplementation on preventing atherosclerosis progression and improving gut microbiota balance.	Rats were divided into 3 groups (10 per group). HFD, HFD with 30 % WHB, HFD with 30% RFD (refined highland barley).	18 weeks	• WHB showed reduced atherosclerotic plaque formation, lower serum tumor necrosis factor-alpha (TNF-α). • HB supplementation restored gut microbiota balance by increasing *Lachnospiraceae*, *Lactobacillus*, *Muribaculaceae*, and *Bifidobacterium.*	(Wu *et al.*, 2023)
Human study	Examining the gut microbiota of non-obese people who eat a lot of barley.	A total of 185 people were participated in the barley and intestinal environment cohort research. Participants were categorized into: 1. High barley consumption groups (non-obese individuals as responders while obese individuals as non-responders) 2. Low barley consumption group	Cross-sectional study	• Respondents consumed more fermented foods, including natto (fermented soybeans), compared to non-respondents. • Responders had ↑ *Butyricicoccus* and *Subdoligranulum* in their intestines. Natto contains *Bacillus subtilis*, a glycolytic bacterium, as well as *Butyricicoccus* and *Subdoligranulum*, which produce butyrate. This suggests that fiber breakdown and butyrate synthesis may be enhanced in the digestive tract of barley responders.	(Maruyama *et al.*, 2024)
Mice	To investigate the hypoglycemic effects of HBG on rats with type 2 diabetes (T2D), as well as if these effects are associated with gut microbiota alteration.	Mice were put into two groups: normal control (NC; n = 8) and high-fat diet (HFD; n = 24). 1. NC group (chow diet) with citric acid buffer. 2. Group of high-fat, high-sugar diet group induced with STZ (HFD) Rats with T2D were randomized into 4 separate groups: 1. Group NC received a basal diet. 2. Group of DC (diabetes control) followed the HFD. 3. low-dose HBG (L-HBG) group received HFD supplemented with HBG. 4. High-dose HBG (H-HBG) group received HFD-adjusted HBG.	8 weeks	• After 4 weeks of HBG intervention, mice in the H-HBG group had significantly higher amounts of three SCFAs (butyric acid, acetic and propionic) than animals in the DC group. Mice in the L-HBG group also showed an increasing trend. • ↓ *Bacteroidota* and *Proteobacteria* abundance in mice with T2D in the H-HBG group. • ↑ *Firmicutes*, *Actinobacteria*, and *Verrucomicrobia* abundance compared to mice in the DC group. • In the H-HBG group ↑ *Lachnospiraceae*, *Erysipelotrichaceae*, *Akkermansiaceae*, and *Prevotellaceae*.	(Zang *et al.*, 2023)

Conclusions: Cereal barley is a valuable crop and bulky in dietary fiber (β-glucan), arabinoxylans and many other functional components (phenolic acid, flavonoids) that improve intestinal fermentability. Barley leaves have a long past of use in conventional Chinese medicine due to its benefits on gastroprotective effects, anti-inflammatory properties, and lipid lowering properties. Its inclusion in animal diet suggests potential contribution in diet to improve overall health. Its potential impact along with promoting gut health is further increased by its variety in food products, including whole grains and flours to beverages and bakery items. Even with these positive outcomes, there is currently a lack of human studies, and it is unclear how individual gut microbiota variations, barley processing methods, and variety affect prebiotic effectiveness. Future research should give priority to long-term clinical trials, molecular insights, and practical application in food industry.

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Author contribution: Uswa Khawar: Conceptualization, Data collection, Methodology, Writing original draft. Sadia Zahid: Data collection, Writing – review & editing. Rehma Gulzar: Writing – review & editing. Gholamreza Abdi: Conceptualization, Writing – review & editing. Doha M. Al-Nouri: Writing – review & editing. Isam A. Mohamed Ahmed: Writing – review & editing. Muhammad Mobashar: Writing – review & editing. Rana Muhammad Aadil: Conceptualization, Data collection, Methodology, Writing – review & editing, Supervision.

Abbreviations:

HB	Highland barley or hulless barley
WB	Whole barley
HGB	High β-glucan barley
T-fiber	Tibetan highland barley fiber
HFD	High fat diet
HBBG	Highland barley β-glucan
NC	Normal control
UC	Ulcerative colitis
LMW-BG	low molecular weight barley β-glucan
BLIDF	Insoluble dietary fiber from barley leaves
DAI	Disease activity index
PHB	Partly milled highland barley
MGO	Methylglyoxal
HMW-BG	high molecular weight β-glucan
IDF	Insoluble dietary fiber
HBBP	Bound polyphenols from highland barley
BAPB	Butyric acid producing bacteria
INDO	Indomethacin
FBe	Fermented barley extract
DSS	Dextran sulphate sodium
BF	Barley flour
GLP-1	glucagon-like protein 1
BW	Body weight
BL	Barley leaf
SCFAs	Short chain fatty acids
EC	Epicatechin
LOV	Lovastatin
PPARα	Peroxisome Proliferator-Activated Receptor Alpha
GI	gastrointestinal

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