

REVIEW ARTICLE

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# Asian fermented plant foods as modulators of gut microbiota and host health: current evidence and future perspectives—a narrative review

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## Abstract

Fermented plant foods, deeply rooted in cultural traditions, are gaining increasing attention for their potential to modulate the gut microbiome and improve host health. This review summarizes current data on the microbial composition, functional metabolites, and health effects of fermented plant foods commonly consumed in Asia, with a focus on fermented soybean foods (e.g., cheonggukjang, natto, and tempeh), and fermented vegetable foods (e.g., kimchi). Several bioactive compounds derived from fermentation modulate gut microbial composition and diversity, gut barrier integrity, and immune and inflammatory responses to help prevent and manage metabolic disorders, inflammatory bowel disease, and other gut-related disorders. Preclinical and animal studies have elucidated the mechanisms underlying these health effects. We highlight the importance of developing personalized dietary interventions, standardizing the production of fermented plant foods, and evaluating health effects using multi-omics approaches. These foods hold promise as microbiome-targeted interventions for maintaining and improving host health.

**Keywords** Gut microbiome, Fermented foods, Plant foods, Functional foods, Personalized nutrition

## Introduction

The human gastrointestinal tract harbors a large and dynamic community of microorganisms collectively referred to as the gut microbiota [1]. This complex ecosystem plays a crucial role in preserving host health through its involvement in various physiological processes such as nutrient metabolism, immune modulation, preservation of gut barrier integrity, and protection against pathogens [1–4]. Disruptions in the composition or function of the gut microbiota, commonly known as

dysbiosis, are associated with various chronic diseases such as obesity, type 2 diabetes (T2D), inflammatory bowel disease (IBD), and colorectal cancer [5, 6].

Among the environmental factors that shape the gut microbiome, diet has the most profound and modifiable influence [3, 7]. Short-term dietary changes can rapidly alter microbial composition, whereas long-term dietary patterns help determine the stability and diversity of the gut ecosystem [8, 9]. A high consumption of fiber- and polyphenol-rich diets increases gut microbial diversity and enriches beneficial taxa within *Ruminococcaceae* and *Lachnospiraceae* [10]. Conversely, a high intake of Western-style diets that are abundant in fats, sugars, and ultra-processed ingredients can reduce gut microbial richness and increase the abundance of pro-inflammatory species [11].

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Plant-based diets are rich in fiber, polyphenols, antioxidants, and unsaturated fats [12, 13], which can contribute to long-term weight maintenance and reduce insulin resistance, dyslipidemia, high blood pressure, and inflammation [14–18]. Several studies have uncovered the association between the consumption of plant-based foods and human health. According to a meta-analysis of 55 prospective cohort studies, higher adherence to a plant-based dietary pattern, including whole grains, vegetables, fruits, and legumes, was associated with a lower risk T2D, cardiovascular diseases, and cancer [19]. Moreover, plant-based diets may alter the composition and metabolic pathways of gut microbiota, influencing gut health [20]. For instance, the consumption of fruits and vegetables was inversely associated with the development of IBDs, such as ulcerative colitis and Crohn's disease [21].

The Asian population, particularly in South Korea, consumes more plant-based foods than Western populations, with approximately 78% of the Korean diet consisting of plant-based foods—though this proportion has slightly decreased over the past decade [22–25]. Furthermore, many Asians have traditionally stored and consumed plant foods through fermentation. In South Korea, fermented plant foods, such as fermented soybeans and cabbages, have been consumed for over 2000 years, rooted in the country's long-standing farming culture [26, 27]. This long history of fermentation has relied on naturally occurring microbial communities and the addition of specific starter cultures [28]. Lactic acid bacteria (LAB), including species belonging to *Lactobacillus*, *Lactococcus*, *Streptococcus*, and *Leuconostoc*, as well as fungi, including yeasts, contribute to the complex microbial ecosystems involved in plant-based fermentation [29].

Fermented foods are produced through controlled microbial growth and the enzymatic conversion of various food components [30]. Fermentation enhances digestibility and nutritional value, resulting in a rich source of functional microbes and microbial metabolites. Recent advances in high-throughput sequencing and metabolomics have enabled the detailed characterization of microbial communities and functional compounds present in fermented plant foods, shedding light on their potential roles in host health and physiology. For instance, a large longitudinal cohort study in the USA investigated the gut microbiome and metabolic markers associated with the consumption of fermented plants [31]. The consumption of fermented plant foods was associated with a higher abundance of several gut microbial taxa, such as *Bacteroides* spp., *Pseudomonas* spp., and *Dorea* spp., as well as elevated levels of conjugated linoleic acid, a metabolite with health-promoting properties [31]. It was hypothesized that the

production of conjugated linoleic acid may be attributed to microbial taxa associated with fermented plant intake, highlighting the interplay between diet, microbes, and bioactive metabolites.

Building on these insights, this review summarizes recent preclinical, clinical, and mechanistic research findings on the effects of fermented plant foods on gut microbial communities and their contributions to intestinal and systemic health.

## Microbial composition and functional metabolites in fermented plant foods

### Fermented soybean foods

Fermented soybean foods are widely consumed in East and Southeast Asia and are typically produced through the microbial fermentation of soybeans.

#### Cheonggukjang

Cheonggukjang is a traditional Korean short-term fermented soybean paste, produced by fermenting steamed soybeans for 2 to 3 days, traditionally using rice straw as a source of *Bacillus* species [32]. A recent study identified strains responsible for the production of tyramine, a biogenic amine (BA) [33]. Shotgun metagenomic sequencing revealed that *Bacillus* species, particularly *Bacillus piscis*, dominated the microbial community and correlated with tyrosine metabolism, suggesting its involvement in tyramine production. These results are consistent with those of previous studies finding *Bacillus thermoamylovorans* as dominant [34], reinforcing that *Bacillus* species form a conserved core microbiota in cheonggukjang. Glycine, glutamic acid, histidine, and tyrosine were the most abundant free amino acids, reflecting active microbial amino acid biosynthesis during fermentation [34]. Recent studies have suggested that the overall community structure can vary depending on the manufacturing methods and regional microbiota. For instance, some traditional cheonggukjang samples were enriched with *Lactobacillus* species, such as *Lactobacillus sakei* (*L. sakei*), while others were dominated by *Bacillus licheniformis* [35]. Although Firmicutes and Bacilli were the dominant phyla and classes across all samples, the relative abundance of taxa at lower taxonomic levels, including *Lactobacillaceae*, *Bacillaceae*, and *Enterococcus faecium*, varied depending on their origins (Table 1).

#### Meju-based fermented soybean products: Doenjang and Ganjang

Unlike the short-term fermentation of cheonggukjang, doenjang (paste) and ganjang (soy sauce) are produced via a long-term, two-stage fermentation involving a solid-state fermented soybean brick, meju. It is subsequently fermented in brine and then separated into

**Table 1** Changes in microbial composition and functional compounds during fermentation of Asian fermented plant foods

Food	Key microorganisms	Key functional/metabolic changes	Representative bioactive compounds	Reference
Cheonggukjang	Dominated by <i>Bacillus</i> spp. (e.g., <i>B. piscis</i> , <i>B. subtilis</i> , <i>B. thermomyovorans</i> ); Some regional variations show enrichment of LAB ( <i>L. sakei</i> )	Active proteolysis and amino acid biosynthesis; Conversion of tyrosine to tyramine and other BAs	Free amino acids: glycine, glutamic acid, histidine, tyrosine; BAs: tyramine (linked to <i>B. piscis</i> )	[33–35]
Doenjang, Ganjang (Meju-based)	Meju: <i>Bacillus</i> (high temperature) and LAB (low temperature, e.g., <i>Weissella</i> ); Brine: halophilic/halotolerant taxa dominate (e.g., <i>Leuconostoc</i> , <i>Tetragenococcus</i> , <i>Lactilactobacillus</i> , <i>Debaromyces</i> )	Proteolysis, saccharide fermentation, and secondary metabolism; Temperature and salt concentration drive LAB– <i>Bacillus</i> balance	Meju metabolites: lactate ( <i>Enterococcus</i> ), flavonoid aglycones (LAB), putrescine ( <i>Bacillus</i> ); Doenjang: isoflavones, soya saponins; Ganjang: BAs, phenylpropanoids	[36–43]
Gochujang	Firmicutes-dominated; <i>B. subtilis</i> , <i>B. licheniformis</i> , region-specific LAB ( <i>Weissella salipiscis</i> , <i>Enterococcus</i> spp.)	Long-term enzymatic degradation of proteins and starches; Generation of organic acids and flavor compounds	BAs (histamine, tyramine); Isoflavonoids; Phytosterols; Capsaicinoids	[44, 45, 103]
Natto	Starter: <i>B. subtilis</i> var. <i>natto</i> ; Co-fermentation with <i>Lactobacillus</i> , <i>Bifidobacterium</i> , <i>Mucor</i> enhances activity	Proteolysis, amino acid release; $\gamma$ -PGA and nattokinase production; Degradation of anti-nutritional factors (e.g., trypsin inhibitors)	Nattokinase; $\gamma$ -PGA; Free amino acids; Flavonoids; Alkaloids	[47–53]
Tempeh	Soaking: <i>Prevotella</i> , <i>Bacillus</i> , <i>Lactobacillus</i> spp.; Fermentation: fungal starter ( <i>Rhizopus</i> spp.); Over-fermentation: yeasts ( <i>Kluyveromyces</i> , <i>Candida</i> ) and LAB ( <i>L. agilis</i> )	Enzymatic hydrolysis of proteins, lipids, and glycosides; Increasing amino acids and isoflavone aglycones; Improved mineral bioavailability	Early: sugars/sugar alcohols (gentiobiose); Late: amino acids (glutamine), isoflavone aglycones (daidzein, genistein)	[54–63]
Kimchi	Early: <i>Leuconostoc gleidum</i> ; Mid/late: acid-tolerant <i>Lactobacillus</i> spp. ( <i>L. plantarum</i> ); Over-fermentation: <i>W. confusa</i>	LAB fermentation lowers pH, generates organic acids and SCFAs; Conversion of phytochemicals to more bioactive forms	Fermentation-derived: aspartic acid, putrescine, cadaverine (spring and summer) and glutamic acid, tryptamine, serine; Ingredient-derived: sulforaphane (cabbage), capsaicin (red pepper)	[67–75]

LAB, lactic acid bacteria; BA, biogenic amine;  $\gamma$ -PGA, poly- $\gamma$ -glutamic acid; SCFA, short-chain fatty acid

solid (doenjang) and liquid (ganjang) fractions for further aging [36, 37]. Microbial succession during meju fermentation is critically influenced by temperature. *Bacillus* dominates at high temperatures, whereas LAB such as *Weissella* and *Latilactobacillus* prevail at low temperatures [38]. In doenjang ferments, genera such as *Leuconostoc*, *Logilactobacillus*, and *Tetragenococcus* are predominant, regardless of the fermentation conditions. In the fungal community, *Mucor* was dominant in meju, whereas *Debaryomyces* was dominant in doenjang, with fungal succession largely unaffected by temperature.

In addition to temperature, variations in fermentation characteristics among different manufacturers lead to distinct the microbial and metabolic profiles. A comparative analysis of doenjang-meju revealed two distinct fermentation types—*Bacillus* dominated and LAB dominated—and fermentation was performed primarily by *Enterococcus* [39]. These microbial profiles were associated with distinct metabolic signatures, including differences in the concentrations of sugars, organic acids, BAs, and volatile compounds. The LAB-dominated samples contained fewer volatile compounds, and *Bacillus* and LAB exhibited a strong negative relationship. Bacterial species produce specific metabolites, including lactate (*Enterococcus*), flavonoid aglycones (LAB), and putrescine (*Bacillus*). Another comparative study identified doenjang was enriched with functional compounds, such as isoflavones, soyasaponins, and amino acids, as well as the bacterial genera *Debaryomyces* and *Staphylococcus* [40]. In contrast, ganjang contained elevated levels of BAs, phenylpropanoids, and the taxa *Meyerozyma* and *Tetragenococcus* [40].

In ganjang, the fermentation shifts the microbial community from meju-derived microbes to halophilic or halotolerant microbes from solar salts, such as *Debaryomyces*, *Tetragenococcus*, and *Staphylococcus* [41]. Salinity and meju proportion are key factors; *Tetragenococcus* was linked to lactate in low-salt batches, whereas *Staphylococcus* was enriched in high-salt batches. *Debaryomyces* remained abundant across all salt levels. Metabolite profiling revealed that carbohydrate and amino acid levels were largely influenced by the proportion of meju, while salt concentration played a lesser role. These findings suggest that amino acid production in ganjang is primarily driven by endogenous proteases present in meju rather than by microbial proteolytic activity during fermentation. While Bacilli were dominant at the class level, substantial variation exists at lower taxonomic levels (e.g., Lactobacillales vs. Bacillales) depending on fermentation conditions, influencing the final bioactive compounds [42, 43]. The above description is summarized in Table 1.

### Gochujang

Gochujang is a long-term ( $\geq 6$  months) fermented paste made from powdered meju, red pepper, a malted rice mixture, and salt [36, 37]. This process develops a diverse microbial community, dominated by the phylum Firmicutes [44]. *B. subtilis* and *Bacillus licheniformis* are the predominant species, and several region-specific bacterial species were identified, including *Bacillus sonorensis*, *Bacillus pumilus*, and *Weissella salipiscis* [44]. To support this regional variation, the analysis of 73 traditionally made gochujang samples from five provinces in South Korea identified significant geographic differences in bacterial composition and functional attributes [45]. Although *Bacillus* spp. remained the predominant genus across regions, samples from Kyungsang Province showed a marked reduction in the abundance of *Bacillus* species, along with an increase in the abundance of *Enterococcus* and *Staphylococcus* species [45]. Despite these microbial shifts, the levels of histamine and tyramine were not significantly different across regions [45] (Table 1).

### Natto

Natto is a traditional Japanese fermented soybean food produced by fermenting steamed soybeans with a starter culture of *B. subtilis* var. *natto* (commonly known as *Bacillus natto*) for 18–20 h at 40–45 °C [46, 47]. This bacterium contributes to the proteolysis and transformation of soy components, enhancing their digestibility and bioactivity. Among key functional products secreted during fermentation, nattokinase is a fibrinolytic enzyme with potential cardiovascular benefits [48, 49]. Fermentation leads to the degradation of anti-nutritional factors, such as trypsin inhibitors, and the formation of extracellular polymers composed of glutamic acid, amino acids, and fructans, which contribute to the slimy and sticky texture of natto [47]. In addition to these macroscopic changes, a recent untargeted metabolomics study found significant chemical differences between soybeans and natto, identifying 160 differentially abundant metabolites, including amino acids, flavonoids, alkaloids, and nucleotides [50]. Another metabolomic analysis of the production of poly- $\gamma$ -glutamic acid ( $\gamma$ -PGA), which is responsible for the slimy texture of natto, identified 257 key metabolites that were differentially abundant between high- and low- $\gamma$ -PGA-producing natto and soybean substrates [51]. Enrichment analysis revealed that the metabolites involved in the synthesis of purines, nucleotides, fructose/mannose, and isoflavonoids were significantly altered, providing a biochemical basis for optimizing natto fermentation and diversifying its characteristics.

Building on this metabolomic insight into the biochemical complexity of natto, recent advances in microbial

co-fermentation strategies aim to enhance its functionality. The co-fermentation strategies with *Lactobacillus*, *Bifidobacterium*, or *Mucor* strains can significantly increase nattokinase and protease activities, as well as free amino nitrogen content, compared to single-strain fermentation [52, 53]. This approach also reduced the levels of BAs, particularly tyramine and cadaverine, while improving sensory acceptance. The above description is summarized in Table 1.

### Tempeh

Tempeh is a traditional Indonesian food made from the solid-state fermentation of boiled soybeans inoculated with the fungus *Rhizopus* spp. The production process involves sequential steps such as soaking, dehulling, boiling, inoculation, and incubation [54], which create favorable conditions for microbial growth and enzymatic activity. Soaking initiates natural acidification, which suppresses the growth of pathogenic microorganisms. A metagenomic analysis of soaking water during tempeh production identified ten major bacterial genera, including *Prevotella*, *Bacillus*, *Paenibacillus*, *Staphylococcus*, and *Lactobacillus* [55]. The soaking process can be optimized by co-inoculation with *Lactiplantibacillus plantarum* [56]. A targeted metabolomic study revealed that soaking soybeans with *L. plantarum* or *Pichia burtonii* led to significant changes in the metabolite profile of tempeh [57]. This process increased the levels of amino acids and bioactive compounds and decreased the levels of sugars, indicating potential advantages for enhancing tempeh quality through microbial intervention.

After soaking and inoculation, the fermentation stage begins, during which fungal activity by *Rhizopus* mycelium becomes dominant and binds soybeans into a cohesive matrix [58]. Fermentation enhances the nutritional profile through the enzymatic hydrolysis of proteins, lipids, and isoflavone glycosides and improves the bioaccessibility of minerals, such as iron [59, 60]. Shotgun metagenomic analysis of tempeh samples revealed a high prevalence of genes related to iron acquisition, such as the iron complex outer membrane receptor protein [61]. The predominant bacterial phyla were Proteobacteria, Firmicutes, and Bacteroidetes, with representative species including *Lactobacillus fermentum*, *Enterococcus cecorum*, and *Klebsiella pneumoniae*. During over-fermentation, the community shifts toward yeasts belonging to the order Mucorales (*Kluyveromyces marxianus*, *Candida* spp., and *Trichosporon* spp.) and LAB (*Lactobacillus agilis* and *Lactococcus* spp.), accompanied by changes in metabolite composition [62]. Sugars and sugar alcohols such as gentiobiose and galactinol accumulated during early fermentation and declined over time. In contrast, amino acids such as glutamine and bioactive compounds

such as the isoflavones daidzein and genistein increased progressively up to 72 h [63] (Table 1).

### Fermented vegetable food: Kimchi

Kimchi is a traditional Korean dish, widely consumed as fermented cabbage in Northeast Asian countries. Recently, kimchi has drawn global attention for its symbiotic properties, as it contains non-digestible fibers, probiotics, and prebiotics [64]. Moreover, various health-promoting metabolites are produced during kimchi fermentation, which are not easily obtained from any single food source [64].

Kimchi is commonly fermented through lactic acid fermentation. Kimchi is made by salting various vegetables with condiments. There are more than two hundred varieties of kimchi depending on the major ingredients and preparation methods [65]. It can be produced with several vegetables (cabbage, radishes, cucumbers, mustard leaves, and green onions), spices (red pepper powder, garlic, and ginger), sugar, and fish sauce [66, 67]. Cabbage is the main ingredient [68] and is usually fermented with microorganisms that naturally exist in raw ingredients at temperatures below 10 °C [69].

The dominant microorganisms in kimchi are *Leuconostoc*, *Lactobacillus*, and *Weissella*; however, the microbial composition depends on the raw ingredients and environmental factors [67, 69]. During fermentation at temperatures from 4 to 10 °C, *Leuconostoc gelidum* is found at 4 °C, whereas *L. plantarum* and *L. spicheri* are detected in late fermentation at a temperature of 10 °C. *W. confusa* is found independently of temperature throughout the entire fermentation process [70]. Salinity also affects microbial composition. *L. sakei* is identified at a high salinity (1.6–2.1%) after 2 weeks of fermentation, while *Leuconostoc mesenteroides*, *Leuconostoc lactis*, and *Weissella soli* are present independently of salinity [71]. As essential ingredients, red pepper powder increases the proportion of *Weissella*, while allicin in garlic stimulates the growth of LAB [72, 73]. Different types of microbiomes were found depending on the varieties of jeotgal, a traditional salted fish consumed in South Korea. *L. sakei* and *Weissella koreensis* were predominant in salted anchovy and salted shrimp, respectively [74].

South Korea has four seasons, and kimchi is traditionally prepared in the fall and winter. However, modern refrigeration technologies allow for year-round production of kimchi. Seasonal harvesting affects microbial composition and demonstrates seasonal variations after 30 days of fermentation [75]. Microbial profiles differed between spring and fall. *Latilactobacillus* was dominant in fall-harvested kimchi, while *Weissella* prevailed in spring, summer, and winter. Hence, the metabolite profiles were similar in spring and summer. Aspartic acid,

putrescine, and cadaverine predominated in spring and summer, whereas glutamic acid, tryptamine, and serine persisted throughout the fermentation process.

Kimchi also contains bioactive compounds derived from its main ingredients: sulforaphane, 3,3'-diindolylmethane, indole-3-carbinol, benzyl isothiocyanate, phenyl isothiocyanate, and allyl isothiocyanate from cabbage; capsaicin from red pepper; organosulfur compounds from garlic; and shogaol and gingerol from ginger. These compounds have anti-obesity, anti-cardiovascular, anti-inflammatory, anti-cancer, and anti-COVID-19 effects [64]. The above description is summarized in Table 1.

### Clinical evidence: effects on human gut microbiota and health

#### Overall alterations in gut microbiota composition

Fermented soybean foods have beneficial effects on gut microbiota and host health. A large cross-sectional study involving 222 Korean adults revealed that the habitual intake of fermented foods such as doenjang and cheonggukjang was positively associated with gut microbial diversity and the relative abundance of Firmicutes genera, including *Lactobacillus*, *Ruminococcus*, and *Eubacterium* [76]. These associations were not observed in individuals who consumed non-fermented foods, suggesting that fermentation helps to modulate the gut microbiome. The consumption of fermented legumes, vegetables, nuts, and seeds was also associated with high alpha diversity of bacteria, particularly *Ruminococcus*. These findings underscore the potential of fermented soybean foods as key modulators of a healthy gut microbiome.

Cheonggukjang also influences gut microbiota and host metabolism. An interventional study involving 48 healthy Korean men investigated the gut microbiome and metabolomic responses to a 7-day intake of cheonggukjang [77]. The intake induced inter-individual shifts in B-type (*Bacteroides*), P-type (*Prevotella*), and R-type (*Ruminococcaceae*) enterotypes, reflecting the dynamic nature of the gut microbiome in response to the intake of fermented foods. Individuals with the R-type enterotype exhibited the most pronounced microbial shifts following cheonggukjang intake, including a significant decrease in the Firmicutes to Bacteroidetes (F/B) ratio, along with a decreased abundance of families *Ruminococcaceae*, *Lachnospiraceae*, and *Streptococcaceae*. At the genus level, the R-type group showed a decrease in the abundance of *Faecalibacterium*, *Gemmiger*, *Coprococcus*, and *Streptococcus*, while showing a significant increase in the abundance of *Prevotella*. Half of the R-type individuals transitioned to the P-type after the intervention, highlighting the responsiveness of this enterotype to dietary modulation. Individuals with

the P-type enterotype had higher levels of 5-hydroxy equol, an isoflavone metabolite produced by *Prevotella*. Metagenomic analysis identified clusters of reductase genes associated with equol biosynthesis in these individuals, suggesting that enterotype-specific microbial functions underlie individual differences in metabolite production.

In addition, natto can modulate the composition and metabolic activity of gut microbiota. In a clinical intervention study, eight healthy adults in Japan maintained their habitual free-choice diet for 7 days (run-in), then consumed miso soup containing natto once daily for 2 weeks, followed by 7 days of the habitual diet (wash-out) [78]. Fecal samples were collected at baseline (day 0), during the intervention (days 7 and 14), and after the intervention (day 21) to assess changes in fecal microbiota, short-chain fatty acids (SCFAs), and putrefactive metabolites. The intervention meal consisted of 50 g of commercially available natto—containing approximately  $9.0 \times 10^9$  CFU/g of *B. subtilis*—added to 200 mL of miso soup and boiled for 1 min. Despite heat treatment, the viability of *B. subtilis* spores was presumed to be retained because of thermal resistance. The intervention did not significantly affect the total bacterial count in the feces but significantly increased the fecal counts of *Bacillus* and *Bifidobacterium* and decreased the fecal count of *Enterobacteriaceae*. Additionally, the intervention tended to decrease the abundance of lecithinase-positive *Clostridium* species, including *C. perfringens*. These changes were accompanied by a significant increase in the concentration of SCFAs, particularly acetic and propionic acids, on day 14 of intake. In contrast, the intervention significantly decreased the fecal concentrations of putrefactive metabolites such as indole, *p*-cresol, ammonia, and sulfide. The intervention non-significantly decreased stool pH and non-significantly increased water content. The consumption of natto miso soup improved the intestinal environment by stimulating *Bifidobacterium* and the production of acetic and propionic acids, while suppressing *Enterobacteriaceae* and the production of putrefactive metabolites. These results align with previous findings from studies on raw natto and support the role of fermented soybean-based foods in modulating the gut microbiota [79]. These findings suggest that natto, even when consumed as part of a heat-treated preparation such as natto miso soup, can modulate the gut microbiota by increasing the abundance of beneficial taxa such as *Bifidobacterium* and *B. subtilis*, while suppressing the activity of harmful and putrefactive microorganisms, improving intestinal metabolic profiles in healthy adults [79].

## Obesity and metabolic health

### Fermented soybean foods

The anti-obesity effects of cheonggukjang in Korean adults with obesity were evaluated in a randomized, double-blind, placebo-controlled trial [80]. Fifty-nine overweight participants were randomly assigned to receive tablets made from traditional cheonggukjang with a high concentration of beneficial microorganisms (HTC), tablets made from traditional cheonggukjang with a low concentration of beneficial microorganisms (LTC), or pills made from commercially available cheonggukjang (CC) [80]. Cheonggukjang supplementation did not significantly improve obesity-related anthropometric or metabolic parameters, including serum inflammatory markers. In addition, although the F/B ratio across all groups and SCFA levels decreased in the HTC group, these changes were not statistically significant, suggesting the limited efficacy of supplementation at the tested dose and duration (Table 2).

Gochujang also has potential anti-obesity effects. A 6-week randomized, double-blind clinical trial assigned 54 South Korean adults with overweight or obesity to receive pills made from traditional gochujang with either a high (HTG) or low (LTG) concentration of beneficial microorganisms or pills made from commercial gochujang (CG) [81]. Participants consumed 25.3 g of gochujang pills daily, corresponding to 19 g of gochujang powder. This dosage was compared with the average daily gochujang intake among Koreans (10.75 g). The supplementation was divided into three doses administered after meals. Gochujang supplementation significantly reduced waist circumference, visceral fat area, and the serum concentrations of total cholesterol, low-density lipoprotein cholesterol (LDL-C), high-density lipoprotein cholesterol (HDL-C), triglycerides, and non-HDL-C levels in the HTG group [81]. Although between-group differences in the gut microbial composition were not statistically significant, there was a trend toward increased abundance of beneficial taxa, such as *Lactobacillus* spp., *Bifidobacterium* spp., *L. lactis*, *E. faecium*, and *Bacteroides* spp., across all groups, and decreased abundance of harmful taxa, such as *Clostridium perfringens*, *Bacteroides eggerthii*, *Sutterella stercoricanis*, *Ruminococcus torques*, and *Parabacteroides* spp. in the HTG and CG groups [81]. These results suggest that cheonggukjang and gochujang supplementation, particularly in its traditional formulation enriched with beneficial microbes, can modulate the gut microbiota or modestly improve metabolic parameters in adults with overweight or obesity (Table 2).

### Fermented vegetable food: Kimchi

Kimchi consumption exerts beneficial effects related to the prevention of obesity and associated metabolic parameters (Table 2). A 12-week randomized controlled trial allocated 83 Korean adults with obesity to receive (1) spontaneously fermented kimchi powder (S-K) dominated by *L. sakei*, (2) starter-fermented kimchi powder dominated by *L. mesenteroides* KCKM0828 (LMS-K), previously shown to have the strongest inhibitory effect on lipid accumulation among 50 strains, or (3) a placebo powder [82, 83]. The participants received 30 g of kimchi or placebo capsules to be taken three times a day with meals. The F/B ratio and the abundance of Proteobacteria decreased, whereas the abundance of *Akkermansia* spp., especially *A. muciniphila*, increased in both kimchi consumption groups compared to the placebo group. The abundance of *Escherichia*, *Enterobacter*, and *Citrobacter* was significantly lower in the S-K group, whereas the abundance of *Escherichia*, *Citrobacter*, *Streptococcus*, *Megamonas* and *Catenibacterium* decreased in the LMS-K group, compared to before the intervention. Body fat mass and body fat percentage decreased in both kimchi consumption groups. In turn, body weight, LDL-C, and HbA1c were significantly lower in the LMS-K group than in the placebo group. LMS-K increased fat-free mass and HDL-C compared to placebo and decreased body fat mass and body fat percentage compared to S-K.

The anti-obesity effects of kimchi and its underlying mechanisms were investigated by evaluating the association between the consumption of fresh and fermented kimchi, gut microbiota, and metabolic syndrome-related gene expression in 24 Korean women with obesity [84]. The participants were randomly assigned to receive fresh or fermented kimchi and were instructed to consume 60 g of kimchi three times per day for 8 weeks. Fermented kimchi had more beneficial effects on gut microbiome composition and metabolic disorders than fresh kimchi. Viable *Lactobacillus* counts were higher in fermented kimchi than in fresh kimchi. Fermented kimchi decreased the F/B ratio. In turn, both preparations increased the abundance of Proteobacteria and Actinobacteria. Actinobacteria were negatively associated with body fat percentage in participants who consumed fermented kimchi. Fermented kimchi increased the relative abundance of genera associated with low body fat percentage and a low-fat, high-fiber diet, such as *Bacteroides* and *Prevotella*, and decreased the abundance of *Blautia*. The abundance of *Bifidobacterium longum* was higher in the fermented kimchi group than in the fresh kimchi group and was negatively correlated with waist circumference. Fermented kimchi also improved cardiometabolic parameters by decreasing systolic blood pressure (SBP). Fermented kimchi increased the gene expression

**Table 2** Human intervention studies on the effects of fermented plant foods on gut microbiota and obesity

Food	Study design	Study period	Country, participants	Comparison	Microbiome change	Health outcome change	Ref
Cheonggukjang	RCT, parallel	8 weeks	South Korea, adults with obesity (BMI ≥ 25 kg/m <sup>2</sup> ) aged 19–70 years (n = 59)	Pre- vs. post-intake; HTC vs. LTC vs. CC tablets (3 g of tablets/day)	No significant change in the F/B ratio in all groups.	No significant changes in obesity and inflammatory markers	[80]
Gochujang	RCT, parallel	6 weeks	South Korea, adults with overweight or obesity (BMI ≥ 23 kg/m <sup>2</sup> ) aged 19–70 years (n = 54)	Pre- vs. post-intake; HITG vs. LTG vs. CG pills (19 g of gochujang powder/day)	No significant change in the HTG and CG groups	- WC decreased in the HTG and CG groups. - Visceral fat area, TC, LDL-C, HDL-C, TG, and non-HDL-C decreased in the HTG group	[81]
Kimchi	RCT, parallel	12 weeks	South Korea, adults with obesity (BMI 23–30 kg/m <sup>2</sup> ) aged 20–65 years (n = 83)	Pre- vs. post-intake; placebo vs. S-K vs. LMS-K (30 g of powder three times daily with meals)	- F/B ratio decreased in the placebo group. - <i>Akkermansia</i> spp. increased in the S-K and LMS-K (predominant species: <i>Akkermansia muciniphila</i> ) - Proteobacteria decreased in both the S-K and LMS-K groups, whereas <i>Escherichia</i> , <i>Enterobacter</i> , and <i>Citrobacter</i> decreased in only in the S-K group. - <i>Escherichia</i> , <i>Citrobacter</i> , <i>Streptococcus</i> , <i>Megamonas</i> , and <i>Catenibacterium</i> decreased in LMS-K	- Body fat mass and body fat percentage decreased in the S-K and LMS-K groups compared to placebo. - Body weight, LDL-C, and HbA1c decreased, while fat-free mass and HDL-C increased in the LMS-K group compared to the placebo group.	[82]
Kimchi	RCT, parallel	8 weeks	South Korea, women with obesity (BMI ≥ 25 kg/m <sup>2</sup> ) aged 30–60 years (n = 24)	Pre- vs. post-intake; fresh kimchi vs. fermented kimchi (60 g three times daily with meals)	kimchi - F/B ratio decreased in the fermented kimchi group compared to the control group. - Proteobacteria and Actinobacteria increased in both groups. - <i>Bacteroides</i> and <i>Prevotella</i> increased, whereas <i>Blautia</i> decreased in the fermented kimchi group. - <i>Bifidobacterium longum</i> increased in the fermented kimchi group compared to the fresh kimchi group.	- WC was negatively correlated with <i>Bifidobacterium longum</i> . - SBP decreased in the fermented kimchi group. - ACSL1 and VCAN expression increased in the fermented kimchi group, and both genes showed negative correlations with blood pressure.	[84]

ACSL1, Acyl-CoA synthetase long-chain family member 1; BMI, body mass index; CC, commercial cheonggukjang; CG, commercial gochujang; F/B, Firmicutes to Bacteroidetes ratio; HDL-C, high-density lipoprotein cholesterol; HTC, traditional cheonggukjang with a high concentration of beneficial microorganisms; HITG, traditional gochujang with a high concentration of beneficial microorganisms; LDL-C, low-density lipoprotein cholesterol; LMS-K, starter-fermented kimchi powder with *Lecanostoc mesenteroides* KCKM08285-K group; LTC, traditional cheonggukjang with a low concentration of beneficial microorganisms; LTG, traditional gochujang with a low concentration of beneficial microorganisms; RCT, randomized controlled trial; S-K, spontaneously fermented kimchi powder; SBP, systolic blood pressure; TC, total cholesterol; VCAN, versican; WC, waist circumference

of acyl-CoA synthetase long-chain family member 1 (ASCL1) and versican (VCAN), and these genes were negatively associated with SBP and diastolic blood pressure (DBP). These results suggest that kimchi consumption improves obesity-related metabolic parameters, including body fat, waist circumference, lipid profiles, and glycemic control at low and high levels of intake, possibly mediated by the modulation of the gut microbiota. Fermented kimchi had greater benefits than fresh kimchi, highlighting the importance of fermentation in enhancing the metabolic effects of kimchi.

### Gastrointestinal health

#### *Fermented soybean foods*

Consumption of fermented soybean foods showed beneficial effects on gastrointestinal function such as constipation and mucosal immunity (Table 3). A recent secondary analysis of a cheonggukjang clinical trial identified that subjective constipation is characterized by a *Lachnospiraceae*-dominant enterotype and an enrichment of mucin-degrading bacteria, which are associated with slow colonic transit [85]. While these bacteria were linked to increased levels of the mucin-derived metabolite N-acetyl-D-glucosamine (GlcNAc), network analysis revealed that fermented soybean consumption was inversely correlated with both GlcNAc levels and the abundance of these mucin-degrading taxa. These findings suggest that fermented soybean intake may help regulate colonic motility by inhibiting the overgrowth of specific mucin-degrading gut microbiota implicated in constipation.

In addition to improving bowel motility, fermented soybean foods such as tempeh have been shown to modulate the gut microbiota and enhance intestinal and systemic health. A human intervention study assessed the effects of tempeh on intestinal immune responses and gut microbiota in healthy young adults in Indonesia [86]. Participants consumed ultra-high temperature milk daily for the first 8 days, followed by 100 g of steamed tempeh (made in Empang) daily from days 9 to 24. The study included eight men and eight women, but the final analysis was conducted on ten participants. Tempeh supplementation tended to increase fecal immunoglobulin A concentrations, particularly among male participants, suggesting a potential enhancement of mucosal immune activity. Furthermore, the relative abundance of *Akkermansia muciniphila* significantly increased on day 9 in females and on day 25 in the overall cohort compared to day 0, suggesting that the intervention can modulate the gut microbiota. As ultra-high-temperature milk and tempeh differ markedly in their origin and protein composition—milk providing animal-derived proteins and tempeh providing plant-based proteins and

fermentation-derived peptides—distinct shifts in the gut microbiota were expected at each phase of the intervention. The bioactive effects were retained even after the steaming process, presumably through paraprobiotic mechanisms in which inactivated microbial cells stimulate host immune responses. These findings suggest that dietary patterns with fermented soybean foods are associated with lower abundance of mucin-degrading bacteria, and steamed tempeh can enhance mucosal immunity and modulate the gut microbiota by increasing *A. muciniphila*, even in the absence of live microorganisms.

#### *Fermented vegetable food: Kimchi*

A study assessed the effects of kimchi consumption on gastrointestinal health, specifically regarding the recurrence of colon adenoma, in 32 Korean adults [87]. Individuals with three types of colon adenoma status—normal colon, simple adenoma, and advanced adenoma—were recruited. Participants were administered 100 g of fermented kimchi for 10 weeks after a 4-week washout period. Kimchi was provided every 3 days to each individual's home in the same fermentation state. Fermented kimchi consumption inhibited colon adenoma formation and caused distinct changes in gut microbiota between patients and healthy individuals. Although species richness, species evenness, and bacterial community composition were not significantly different among the three groups at baseline, kimchi consumption increased the Chao1 richness index. Kimchi also increased the relative abundance of *Actinobacteria*, *Cyanobacteria*, *Clostridium sensu stricto 1*, *Turicibacter*, and *Gastranaerophilales* and decreased the abundance of *Roseburia*, *Akkermansia*, and *Bifidobacterium* spp. in the group with advanced colon adenoma, in line with previous studies [88, 89], supporting the notion that changes in gut microbiota may improve the diagnosis of early stages of colon carcinogenesis. Moreover, fermented kimchi decreased the serum levels of pro-inflammatory interleukin (IL)-1 $\beta$  in patients with advanced colon adenoma.

A double-blind randomized trial investigated the association between the consumption of kimchi and irritable bowel syndrome (IBS) in 87 Korean adults. The participants were assigned to receive standard kimchi (SK), functional kimchi (FK, developed by the authors) with anti-colorectal cancer activity, or kimchi supplemented with dead nano-sized *L. plantarum* nF1 (nLp) (nLpK) [90]. The participants were instructed to consume 210 g of kimchi per day for 12 weeks. All interventions increased fiber intake; nLpK and FK increased carbohydrate intake, and SK increased protein and fat intake. Kimchi consumption improved IBS symptoms, including abdominal pain or inconvenience, desperation, incomplete evacuation, and bloating, as well as the serum levels

**Table 3** Human intervention studies on the effects of fermented plant foods on gut microbiota and gastrointestinal health

Food	Study design	Study period	Country, participants	Comparison	Microbiome change	Health outcome change	Ref
Cheonggukjang	Secondary analysis: RCT, parallel	8 weeks	South Korea, adults with subjective constipation aged 19–40 (n = 94)	Secondary analysis: Normal-transit (< 36 h) vs. slow-transit (≥ 36 h) groups (Original RCT: CKJ vs. Placebo)	Mucin-degrading bacteria (e.g., <i>N. timonensis</i> , <i>I. massiliensis</i> ) increased in slow-transit group ( <i>Lachnospiraceae</i> enterotype).	Predicted GlcNAc* increased in slow-transit group.	[85]
Tempeh	Single-arm, open-label intervention study	24 days	Indonesia, healthy adults aged 20–23 years (n = 10)	Pre- vs. post-intake; 200 ml of UHT milk/day (days 0 to 8) → 100 g of steamed tempeh Empang/day (days 9 to 24)	<i>Akkermansia muciniphila</i> increased after tempeh supplementation.	No significant change in fecal immunoglobulin A in males.	[86]
Kimchi	RCT, parallel	10 weeks	South Korea, healthy adults and cancer patients (n = 32)	Pre- vs. post-intake; fermented kimchi (100 g/day) in individuals with normal colon, simple adenoma, and advanced colon adenoma	- Alpha diversity (Chao1 richness index) increased in each group compared to the baseline. - Actinobacteria, Cyanobacteria, Gastranaerophilales, <i>Clostridium sensu stricto</i> , <i>Turicibacter</i> , and <i>Haemophilus pittmaniae</i> HK B5 increased, whereas <i>Enterococcus</i> , <i>Roseburia</i> , <i>Coriobacteriaceae</i> , <i>Bifidobacterium</i> spp., and <i>Akkermansia</i> decreased in the advanced colon adenoma group.	- Serum level of IL-1β decreased in patients with advanced colon adenoma.	[87]
Kimchi	RCT, parallel	12 weeks	South Korea, adults with IBS symptoms aged 19–75 years (n = 87)	Pre- vs. post-intake; SK vs. nLpSK vs. FK (70 g three times daily with meals)	(Among 8 subjects) - Firmicutes increased, whereas Bacteroidetes, and Tenericutes decreased in all groups. - <i>Bifidobacterium adolescentis</i> -increased in the FK group.	- IBS symptoms attenuated in three groups. - TNF-α decreased in three groups, and IL-4, IL-10, and IL-12 decreased in the nLpSK and FK groups	[90]

\*Predicted GlcNAc levels were derived from metabolic models constructed using the AGORA2 framework and the COBRA toolbox. CKJ, cheonggukjang; FK, functional kimchi group; GlcNAc, N-acetyl-D-glucosamine; IBS, irritable bowel syndrome; IL, interleukin; nLpSK, dead nano-sized *Lactobacillus plantarum* nFq (nLp)-added standard kimchi group; RCT, randomized controlled trial; SK, standard kimchi; TNF, tumor necrosis factor; UHT, ultra-high temperature

of tumor necrosis factor (TNF)- $\alpha$ , in all groups. nLpSK and FK decreased the levels of several cytokines, including IL-4, IL-10, and IL-12. Kimchi consumption significantly changed the gut microbiota in nine participants. All three preparations increased the abundance of Firmicutes and decreased the abundance of Bacteroidetes and Tenericutes. Further, these interventions increased the abundance of probiotic genera and species, such as *Lactobacillus ruminis*, *Bifidobacterium*, and *Bifidobacterium adolescentis* and decreased the abundance of *Escherichia* and the *Escherichia coli* group, which contains six pathogenic species, in most participants. These results indicate that kimchi intake may help increase gut microbial diversity, regulate the abundance of microbiota associated with colon carcinogenesis and IBS, and alleviate inflammation. These study results are summarized in Table 3.

**Menopausal health**

Consumption of fermented plant foods, such as cheonggukjang and doenjang, can influence menopausal health (Table 4). An 8-week randomized double-blind study evaluated the effects of cheonggukjang supplementation in 62 postmenopausal women in South Korea experiencing menopausal symptoms. The participants were randomly assigned to receive tablets made from traditional cheonggukjang with HTC, LTC, or CC. Sixty participants completed the study [91]. Supplementation did not significantly improve obesity-related markers, such as body weight, body mass index (BMI), and lipid profiles, but

significantly reduced menopausal symptoms, particularly in the HTC group. This group showed improvements in specific symptoms, such as insomnia, hot flashes, and nervousness, along with an increase in the abundance of beneficial gut bacteria, including *Lactobacillus*, *Bifidobacterium*, *Lactococcus lactis*, *E. faecium*, and *Bacteroides* spp. Although changes in microbial community and the F/B ratio were not statistically significant in the HTC and CC groups, these findings suggest that cheonggukjang may modulate gut microbiota and alleviate menopausal symptoms in postmenopausal women.

Doenjang also can alleviate menopausal symptoms and modulate the gut microbiota in postmenopausal women in South Korea. An 8-week randomized clinical trial involving 56 postmenopausal women evaluated the effects of doenjang supplementation on menopausal symptoms and the modulation of the gut microbiota [92]. Participants were randomly allocated to receive doenjang tablets with a high dose of beneficial microorganisms (HDC), a low dose (LDC), or commercially available doenjang (CD), consuming 6 g twice daily for eight weeks [92]. Supplementation significantly improved menopausal symptoms, as evidenced by reductions in total Kupperman index scores, across all groups. Although the intervention did not significantly improve body weight or glucose metabolism, it reduced low-density lipoprotein cholesterol (LDL-C) levels in the HDC and LDC groups. Regarding the gut microbiome, doenjang supplementation increased the abundance of beneficial taxa such as

**Table 4** Human intervention studies on the effects of fermented plant foods on gut microbiota and menopausal health

Food	Study design	Study period	Country, participants	Comparison	Microbiome change	Health outcome change	Ref
Cheonggukjang	RCT, parallel	8 weeks	South Korea, postmenopausal women (BMI $\geq$ 23 kg/m <sup>2</sup> ) aged 19–70 years (n = 60)	Pre- vs. post-intake; HTC vs. LTC vs. CC tablets (3.3 g of tablets/day)	<i>Lactobacillus</i> spp., <i>Bifidobacterium</i> spp., <i>Lactococcus lactis</i> , <i>Enterococcus faecium</i> , and <i>Bacteroides</i> spp. increased in the HTC group.	- Kupperman index decreased in all groups. - Blood glucose decreased in the HTC group.	[91]
Doenjang	RCT, parallel	8 weeks	South Korea, postmenopausal women with overweight or obesity (BMI $\geq$ 23 kg/m <sup>2</sup> ) aged 45–70 years (n = 56)	Pre- vs. post-intake; HDC vs. LDC vs. CD tablets (6 g of tablets twice daily)	- Firmicutes decreased in the CD group. - Bacteroidetes increased in the HDC and CD groups. - <i>Lactobacillus</i> spp., <i>Bifidobacterium</i> spp., <i>Lactococcus lactis</i> , <i>Enterococcus faecium</i> , and <i>Bacteroides</i> spp. increased in all groups.	- Kupperman index decreased in all groups. - LDL-C decreased in the HDC and LDC groups.	[92]

BMI, body mass index; CC, commercial cheonggukjang; CD, commercial doenjang; F/B, Firmicutes to Bacteroidetes ratio; HDC, traditional doenjang with a high concentration of beneficial microorganisms; HTC, traditional cheonggukjang with a high concentration of beneficial microorganisms; LDC, traditional doenjang with a low concentration of beneficial microorganisms; LDL-C, low-density lipoprotein cholesterol; LTC, traditional cheonggukjang with a low concentration of beneficial microorganisms; ns, not significant; RCT, randomized controlled trial

*Lactobacillus*, *Bifidobacterium*, *L. lactis*, *E. faecium*, and *Bacteroides*. The most notable shifts in Firmicutes and Bacteroidetes were observed in the CD and HDC groups [92]. Fecal concentrations of SCFA, including acetate, propionate, and butyrate, increased non-significantly in the HDC group. These results indicate that doenjang supplementation helps alleviate menopausal symptoms and induces moderate changes in gut microbiota composition and microbial fermentation activity.

**Mechanistic insights from preclinical and animal studies**

Several preclinical and animal studies have investigated the underlying mechanisms linking fermented plant foods, gut microbiome, and host health and have demonstrated that the gut microbiota influences the levels of metabolic, inflammatory, and gut health markers (Fig. 1).

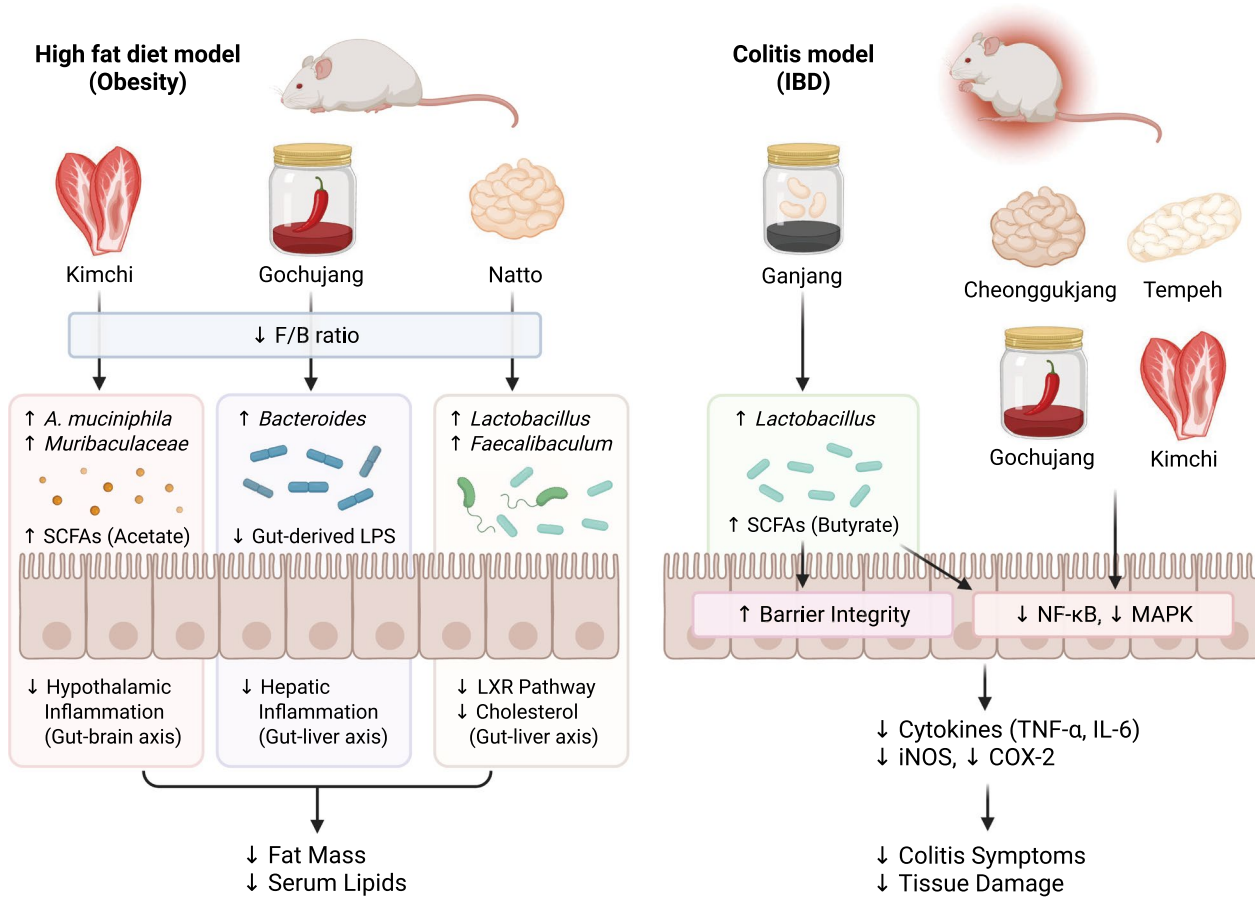
**Mechanisms related to obesity and metabolic regulation**

**Fermented soybean foods**

The anti-inflammatory properties of gochujang have been demonstrated in a mouse model of high-fat diet

(HFD)-induced inflammation. Gochujang significantly reduced body weight, visceral fat mass, liver weight, and serum lipid parameters, while elevating the concentrations of markers of hepatic injury and inflammation, compared to HFD and HFD with salt control, indicating its protective effects against metabolic inflammation [93]. Gochujang modulated gut microbiota composition by lowering the F/B ratio and decreasing the levels of gut-derived lipopolysaccharide, supporting its role in modulating the gut–liver axis. In mice, gochujang enriched *Bacteroides*, *Anaerotruncus*, and *Muribaculum* and decreased the relative abundance of inflammation-associated taxa such as *Lactobacillus*, *Clostridium*, and *Enterorhabdus* compared to HFD and HFD with salt control. These changes in microbial composition correlated with improvements in hepatic inflammation, suggesting that the anti-inflammatory effects of gochujang are mediated by the gut–liver axis.

The metabolic benefits of natto have been evaluated in animal studies of obesity and hyperlipidemia. A study found that the oral administration of natto powder for 8 weeks significantly reduced body weight and improved



**Fig. 1** Proposed mechanisms of fermented plant foods in modulating metabolism and inflammation via gut microbiota in animal models

cholesterol metabolism in rats with HFD-induced obesity [94]. These effects were associated with the suppression of the liver X receptor signaling pathway, including sterol regulatory element-binding protein and 3-hydroxy-3-methylglutaryl coenzyme A reductase, along with the elevated expression of cholesterol 7 $\alpha$ -hydroxylase. Natto also altered gut microbiota by decreasing the F/B ratio. A study investigated the systemic metabolic impact of natto in rats with HFD-induced hyperlipidemia. Natto significantly lowered the serum levels of total cholesterol, triglycerides, LDL-C, and fasting blood glucose, while increasing HDL-C [95]. Metabolomic profiling revealed that natto modulated the tricarboxylic acid cycle and amino acid metabolism by increasing amino acid-derived metabolites while reducing acylcarnitines and purine alkaloids. Natto significantly increased the abundance of *Lactobacillus*, *Faecalibaculum*, and *Oscillibacter*, while decreasing the levels of potentially pathogenic genera such as *Alistipes* and *Prevotellaceae-UCG-003*. These results demonstrate that natto improves host lipid metabolism and attenuates obesity-related parameters by regulating hepatic cholesterol homeostasis and reshaping the gut microbial ecology, supporting its potential as a functional fermented soybean food for metabolic health.

#### **Fermented vegetable food: Kimchi**

The effects of kimchi, particularly its microbial community (KMC), on obesity, gut microbiota composition, and serum metabolites were investigated in a mouse model of HFD-induced obesity [96]. KMC was obtained from kimchi fermented for 3 months and was administered to 6-week-old C57BL/6 male mice (KM) with HFD. Another group received a single strain of *L. plantarum* (LP). KMC and LP were supplied via oral gavage once daily. As a result, both KMC and LP supplementation led to significantly lower body weight gain compared to the HFD group, but only KMC reduced adipose tissue weight gain. Additionally, KMC supplementation modulated the gut microbial community. The F/B ratio in the KM group was lower than that in the HFD group. The abundance of *Muribaculaceae* is higher in the KM group, whereas the abundance of *Erysipelotrichaceae*, *Coriobacteriaceae*, and *Akkermansiaceae* was lower in the KM group than in the HFD group. Although the study could not establish a direct link between microbiota composition and blood metabolites, the results showed that the levels of arachidic acid, stearic acid, fumaric acid, and glucose, which are associated with energy metabolism, were lower in the kimchi group than in the HFD group.

Kimchi suppressed obesity-induced inflammation by modulating the central nervous system and gut microbiome profiles [97]. The oral administration of kimchi in combination with HFD for 10 weeks reduced the

activation of astrocyte and microglial cells involved in hypothalamic inflammation compared to HFD alone. HFD increased the levels of glial fibrillary acidic protein and ionized calcium-binding adapter molecule 1, markers for astrocytes and microglia, respectively, in the hypothalamus. However, kimchi reduced the number of reactive glial cells. Kimchi also decreased body weight and fat mass gain, serum free fatty acids, which induce oxidative stress, and pro-inflammatory cytokines such as monocyte chemoattractant protein-1, and TNF- $\alpha$ . Kimchi supplementation protected against neuroinflammation induced by blood-brain barrier dysfunction, evidenced by a decrease in immunoglobulin G permeability, which was otherwise elevated in the HFD group. Kimchi did not alter microbial species richness or diversity but increased the abundance of *Akkermansia muciniphila* in the intestinal tract and level of SCFAs, particularly acetate, compared to HFD alone.

These findings indicate that kimchi consumption can help prevent obesity and obesity-induced inflammation, possibly by modulating the gut-brain axis and improving gut microbial composition.

#### **Mechanisms related to gastrointestinal health and inflammation**

##### **Fermented soybean foods**

First, cheonggukjang has potential therapeutic effects in IBD. Traditional and commercial cheonggukjang mitigated the symptoms of colitis, including body weight loss, colon shortening, elevated disease activity scores, and histological damage in treated mice compared to mice with dextran sulfate sodium (DSS)-induced colitis [35]. Cheonggukjang attenuated the upregulation of pro-inflammatory cytokines, such as TNF- $\alpha$ , IL-6, and IL-1 $\beta$ , at the transcriptional and protein levels in colonic tissues and systemic circulation [35]. These anti-inflammatory effects were associated with the inhibition of the nuclear factor- $\kappa$ B (NF- $\kappa$ B) and mitogen-activated protein kinase (MAPK) signaling pathways, as evidenced by the reduced phosphorylation of NF- $\kappa$ B p65, p38, c-Jun N-terminal kinase (JNK), and extracellular signal-regulated kinase (ERK), along with the downregulation of inflammatory mediators such as cyclooxygenase-2 (COX-2) and inducible nitric oxide synthase (iNOS). Furthermore, cheonggukjang improved intestinal barrier integrity by preserving goblet cells and enhancing mucin expression.

Second, the potential anti-inflammatory effects of ganjang have been investigated in a mouse model of DSS-induced colitis. Regardless of food origin, the oral administration of ganjang alleviated the symptoms of colitis, and the effects were similar to those of the anti-inflammatory drug 5-aminosalicylic acid [42]. Ganjang significantly downregulated the mRNA and protein

expression of pro-inflammatory cytokines, including TNF- $\alpha$ , interferon- $\gamma$ , IL-1 $\beta$ , and IL-6, in colon tissues. These anti-inflammatory effects were associated with the downregulation of COX-2 and iNOS, which are regulated by the NF- $\kappa$ B and MAPK signaling pathways. The phosphorylation of NF- $\kappa$ B p65 and MAPK proteins, including p38, ERK, and JNK, was significantly lower in ganjang-treated mice than in DSS-treated controls, suggesting that the intervention inhibited these inflammatory signaling pathways. In addition, ganjang restored intestinal barrier integrity by elevating the expression of the tight junction proteins ZO-1 and occludin and significantly increased the fecal levels of SCFAs, particularly butyrate.

Ganjang can potentially reduce colitis-associated colorectal cancer (CAC). In a mouse model of CAC induced by azoxymethane (AOM) and DSS, the oral administration of ganjang attenuated disease symptoms and significantly decreased the number and size of colorectal tumors compared to the AOM/DSS control group [43]. Ganjang restored the expression of pro-apoptotic markers, such as *p53* and *Bax*, and decreased the expression of the anti-apoptotic genes *Bcl-2* and *Bcl-XL* in mice with CAC. Ganjang reduced the expression of the proliferation marker Ki-67, suggesting that this product can inhibit tumor growth. Ganjang suppressed systemic and local inflammation by downregulating TNF- $\alpha$ , IL-1 $\beta$ , and IL-6 levels in the serum and colon tissues and restored the expression of mucin MUC2 and mucin-associated trefoil factor family peptide 3. The analysis of gut microbial composition revealed that ganjang and 5-aminosalicylic acid significantly increased the relative abundance of beneficial *Lactobacillus* species, particularly *Lactobacillus murinus* and *Lactobacillus reuteri*, compared to the AOM-/DSS-treated group. These findings suggest that ganjang protects against colonic inflammation and CAC by modulating inflammatory signaling pathways, restoring epithelial barrier function, regulating apoptosis and cell proliferation, and reshaping gut microbial composition.

The anti-inflammatory effects of gochujang have been evaluated in a murine model of DSS-induced colitis. Gochujang did not significantly reduce body weight loss but effectively prevented DSS-induced colon shortening, suggesting a protective effect on intestinal morphology [98]. Gochujang significantly decreased the serum levels of pro-inflammatory cytokines, including IL-6 and TNF- $\alpha$ , compared to DSS. These effects were accompanied by the suppression of key inflammatory signaling pathways, evidenced by the decreased phosphorylation of NF- $\kappa$ B, p38 MAPK, and ERK proteins. Histological analysis confirmed that gochujang reduced mucosal damage and pathological scores in the colon tissue compared to DSS, supporting its role in maintaining epithelial integrity.

Tempeh supplementation protected against early colorectal carcinogenesis in a rat model of precancerous colorectal lesions induced by 1,2-dimethylhydrazine (DMH). The daily administration of tempeh powder for 12 weeks significantly attenuated the formation of aberrant crypt foci (ACF), a well-established biomarker of early colon neoplasia, in the DMH-induced group compared with the untreated DMH-induced group [99]. The high-dose tempeh group had 62.9% fewer large ACFs than the untreated group. The effects of low-dose tempeh and soybean were comparatively lower, indicating a dose-dependent effect. Additionally, although serum lipid profiles and antioxidant markers remained unchanged, the relative abundance of *C. perfringens*, a potentially carcinogenic gut pathogen, decreased significantly in tempeh-fed rats. These results suggest that tempeh reduces the formation of precancerous colorectal lesions by modulating microbial community composition and decreasing the levels of pro-carcinogenic bacterial species.

#### **Fermented vegetable food: Kimchi**

Fermented kimchi attenuates inflammation and has cytoprotective effects in mouse models of DSS-induced colitis and DSS-induced colon cancer, and the underlying molecular mechanisms have been elucidated in these models [100]. Mice were fed a pelleted diet supplemented with kimchi powder. Kimchi was freeze-dried, ground into powder, and extracted using methanol. The extracts were concentrated by heat evaporation. Fermented kimchi containing additional ingredients, including Chinese pepper, mustard leaf, mushrooms, pear, and sea tangle juice (instead of anchovy juice), suppressed the expression of inflammatory cytokine genes in both groups. The expression of iNOS decreased in both groups, whereas COX-2 expression decreased only in the colitis group. Cancer-preventive effects were also found in the colon cancer model, evidenced by the preserved expression of 15-PGDH, a prostaglandin-degrading enzyme with tumor-suppressive activity, as well as the transcriptional repression of NF- $\kappa$ B p65, a transcription factor involved in colitic cancer. Although the protective effects of kimchi consumption against colitis and colitis-associated cancer have been demonstrated, further studies are needed to clarify the role of the gut microbiome in mediating anti-inflammatory and anti-carcinogenic effects.

#### **Mechanisms related to glucose homeostasis and immune regulation**

Cheonggukjang and gochujang have demonstrated protective effects against glucose homeostasis and immune dysfunction. First, cheonggukjang has metabolic benefits in animal models of T2D. In partially pancreatectomized rats, which recapitulate the key features of Asian-type

T2D, supplementation with cheonggukjang fermented by *B. subtilis* or *Bacillus amyloliquefaciens* significantly improved glycemic control [101]. *B. amyloliquefaciens*-fermented cheonggukjang exerted stronger effects, enhancing pancreatic  $\beta$ -cell mass and reducing islet oxidative stress and pro-inflammatory cytokine expression. These improvements were accompanied by increased hepatic expression of peroxisome proliferator-activated receptor (PPAR)- $\alpha$  and PPAR- $\beta$ , increasing insulin sensitivity. Both fermentations shifted the gut microbial profile by enriching health-associated taxa, such as *A. muciniphila*, *Lactobacillales*, and *Bacillales*, while suppressing *Enterobacteriales*. The restoration of intestinal morphology, including villus structure and goblet cell numbers, supports the notion that the gut-mediated axis contributes to this systemic effect.

Furthermore, cheonggukjang enhances immune function under immunocompromised conditions. In a rat model of cyclophosphamide-induced immunosuppression, the oral administration of traditional or commercial cheonggukjang for 4 weeks significantly improved immune parameters, such as splenocyte proliferation, the activation of immune signaling pathways (MAPK and NF- $\kappa$ B) in splenic tissue, abnormal complete blood count, and elevated serum levels of immunoglobulin G and cytokines [102]. Cheonggukjang significantly decreased the fecal F/B ratio compared to pretreatment levels. These results highlight the therapeutic potential of cheonggukjang for gut integrity, systemic metabolism, and immune regulation by modulating gut microbiota and host signaling pathways.

Similarly, gochujang also exhibits beneficial metabolic effects. Recent studies have assessed its anti-diabetic potential using a mouse model of T2D induced by suppressing the parasympathetic nervous system with scopolamine. The administration of traditionally and commercially produced gochujang, particularly in the presence of high concentrations of capsaicin, improved fasting glucose, serum insulin, lipid profiles, and oral glucose tolerance in parasympathetic nervous system-suppressed rats [103]. These improvements were associated with increased glucagon-like peptide-1 (GLP-1) levels and reduced insulin resistance. Network pharmacology analysis revealed that bioactive compounds in gochujang, such as isoflavonoids, phytosterols, and capsaicinoids, targeted genes linked to insulin signaling and neuronal function (*AKT1*, *BCL2*, and *CASP3*), the JNK/I $\kappa$ B/NF- $\kappa$ B pathway, and calcium signaling pathways. Gochujang attenuated liver damage and systemic inflammation while reshaping the gut microbiota composition by increasing  $\alpha$ -diversity and regulating the abundance of *Akkermansia*, *Oscillospiraceae*, and *Clostridiaceae*. In conclusion, the effects of cheonggukjang and gochujang are

mediated by the suppression of pro-inflammatory signaling pathways, the improvement in glucose and lipid homeostasis, and the modulation of gut microbiota composition and function, underscoring its potential as a dietary intervention for treating chronic inflammatory and metabolic disorders.

#### **Future perspectives and potential applications for personalized nutrition**

This review highlights the microbial diversity present in Asian fermented plant-based foods and their potential effects on obesity, gastrointestinal health, and inflammation. The microbial diversity of these foods is influenced by multiple factors, including raw ingredients, geographical origin, seasonality, temperature, salinity, and fermentation duration. Moreover, variations in gut microbial composition have been observed depending on the types of fermented foods consumed. Fermented food consumption can alter gut microbial communities, change the abundance of specific microbes, and interact with disease-related mechanisms in conditions such as obesity, IBD, and colon cancer. These factors collectively impact various aspects of host health. Thus, factors influencing the gut microbial community in Asian fermented plant-based foods should be carefully considered in personalized nutrition strategies, and disease-specific dietary guidelines may be necessary. Furthermore, the methods for standardizing fermented food products with proven health benefits require further methodological improvement.

While standardizing fermented foods is a valid goal for commercial production, the future of this research lies in embracing and understanding the variability of both the food and host. However, existing studies do not fully elucidate the relationship between the intake of fermented plant foods, the gut microbiome, and host health. Most clinical trials analyzed in this review used single or parallel designs, had small sample sizes, and included participants exclusively from Asian populations. Moreover, despite the wide diversity of fermented plant foods, items such as Chinese suan cai and Japanese tsukemono have been scarcely investigated with respect to their associations with gut microbiome composition and health outcomes.

A key future direction is the use of multi-omics approaches to move beyond simple correlations and elucidate the specific mechanisms that drive individualized health responses. Recent studies on personalized nutrition increasingly focus on inter-individual variation in dietary response and their relationships with multi-omics factors such as gut microbiome, genetics, and metabolites. For example, a clinical study on cheonggukjang demonstrated that the baseline gut microbiome structure

dictates the magnitude and direction of microbial shifts and metabolite production (e.g., 5-hydroxy equol) upon consumption [77]. This finding is critical because the health benefits of fermented foods may be contingent upon the consumer possessing the necessary microbial functional genes (e.g., reductase genes for equol biosynthesis). Therefore, future interventions should integrate metagenomics, metabolomics, and transcriptomics to understand host–microbe–metabolite interplay and develop personalized dietary guidelines. In addition, the studies reviewed here have potential translational values for industrial applications. For example, these findings may serve as important scientific evidence supporting the role of fermented plant-based food intake as a key determinant in the development of microbiome-based dietary response prediction models.

Fermented foods from Asia have become popular and are consumed worldwide. Thus, well-designed, large-scale clinical or prospective studies integrating multi-omics approaches across diverse ethnic groups are warranted to translate these traditional foods into evidence-based, personalized microbiome-targeted health interventions.

## Conclusion

Previous studies have demonstrated the beneficial effects of the consuming fermented plant foods, such as fermented soybean foods and fermented vegetable, on host gut microbial diversity and composition. These fermented plant foods have been shown to improve obesity-related parameters and gastrointestinal health over short- to long-term intervention periods ranging from 1 to 12 weeks. Although effective intake levels varied across studies, most interventions reported beneficial or preventive effects at doses between 50 g and 100 g per day. Large-scale prospective clinical studies incorporating diverse types of fermented plant foods and dose-dependent intervention designs across multiple ethnic groups are warranted to inform dietary guidelines and to identify the factors influencing microbial communities during the fermentation, as well as their potential to improve clinical parameters and prevent diseases.

## Abbreviations

ACF	Aberrant crypt foci
ASCL1	Acyl-CoA synthetase long-chain family member 1
AOM	Azoxymethane
BMI	Body mass index
BA	Biogenic amine
CAC	Colitis-associated colorectal cancer
COX-2	Cyclooxygenase-2
DBP	Diastolic blood pressure
DMH	1,2-Dimethylhydrazine
DSS	Dextran sulfate sodium
ERK	Extracellular signal-regulated kinase
F/B	Firmicutes to Bacteroidetes
γ-PGA	Poly-γ-glutamic acid

GlcNAc	N-acetyl-D-glucosamine
GLP-1	Glucagon-like peptide-1
HDL-C	High-density lipoprotein cholesterol
HFD	High-fat diet
IBD	Inflammatory bowel disease
IBS	Irritable bowel syndrome
IL	Interleukin
iNOS	Nitric oxide synthase
JNK	C-Jun N-terminal kinase
LAB	Lactic acid bacteria
LDL-C	Low-density lipoprotein cholesterol
MAPK	Mitogen-activated protein kinase
NF-κB	Nuclear factor-κB
PPAR	Proliferator-activated receptor
SBP	Systolic blood pressure
SCFA	Short-chain fatty acid
T2D	Type 2 diabetes
TNF	Tumor necrosis factor
VCAN	Versican

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Not applicable.

## Author contributions

Both authors conceptualized this study. BS contributed to the literature search. Both authors interpreted the evidence and drafted the initial manuscript. Both authors revised the manuscript, and SC supervised the review. Both authors approved the final version of the manuscript and agree to be accountable for all aspects of the work.

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## Data availability

This is a narrative review based on previously published studies; all data supporting the findings are available in the cited articles

## Declarations

### Ethics approval and consent to participate

Not applicable.

### Consent for publication

Not applicable.

### Competing interests

The authors declare that they have no competing interests.

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