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Examining the potential prebiotic effect of almonds

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Abstract

Almonds, a nutrient-dense food rich in dietary fiber, polyphenols, and unsaturated fatty acids, exhibit significant potential as a functional food with prebiotic effects. Prebiotics selectively stimulate the growth and activity of beneficial gut microbiota, leading to improved gut and systemic health. This review synthesizes evidence from *in vitro* studies, clinical trials, and systematic reviews to elucidate the prebiotic effects of almond consumption. Almonds enhance gut microbiota diversity and composition, particularly increasing beneficial bacteria such as Bifidobacterium and Roseburia, while promoting the production of short-chain fatty acids (SCFAs), such as butyrate, which are critical for gut barrier integrity and inflammation modulation. The presence of polyphenols, such as proanthocyanidins, contributes to their antioxidative and antimicrobial properties, further supporting microbiome health. Despite variability in study outcomes, likely due to differences in population health status, study design, and almond preparation methods, the cumulative findings underscore almonds' role as a potential prebiotic food with the potential to improve cardiovascular health. Continued research focusing on individualized responses and standardized methodologies is essential to fully harness the health benefits of almond consumption.

Impact Statement

This review covers prebiotic potential of almonds, demonstrating their ability to enhance gut microbiota diversity, promote beneficial bacterial growth, and stimulate short-chain fatty acid production, contributing to improved gastrointestinal and systemic health.

Keywords: almonds; prebiotics; gut microbiome; short-chain fatty acids; dietary fiber; polyphenols; metabolomics; functional foods; gastrointestinal health; cardiometabolic benefits

Introduction

The prebiotic effect is a well-defined and accepted concept. Prebiotics are usually defined as non-digestible food ingredients that selectively stimulate the growth and/or activity of beneficial bacteria in the colon, thereby imparting a benefit to a host's health (Gibson et al. 2004, Akram et al. 2019, Abdi and Joye 2021). The International Scientific Association for Probiotics and Prebiotics (ISAPP) has updated the definition of prebiotics as "a substrate that is selectively utilized by host microorganisms conferring a health benefit" (Gibson et al. 2017, Delzenne et al. 2020, Beaumont et al. 2022). This definition emphasizes the selective fermentation of prebiotics by the gut microbiota, resulting in specific changes in microbial composition and/or metabolic activity, which ultimately confers health benefits upon the host. Prebiotics are primarily carbohydrate compounds, such as polysaccharides and oligosaccharides, which includes indigestible fiber that can be fermented by gut bacteria resulting in the production of a wide variety of compounds, including short-chain fatty acids (SCFAs) (Slavin 2013, Alexander et al. 2018, Dixon et al. 2023). Therefore, the beneficial effects of prebiotics are derived from their ability to stimulate beneficial microorganisms whose metabolism can modulate immune, endocrine, neurological and even metabolic health through myriad mechanisms; ultimately prebiotics can exert long-lasting effects beyond their active administration (Alexander et al. 2018, Miqdady et al. 2020).

While traditionally the definition of prebiotics was limited to only non-digestible carbohydrates, recent changes suggest that other compounds could also have a prebiotic effect. For example, based on the International Scientific Association for Probiotics and Prebiotics (ISAPP) consensus, polyphenols that modulate the gut microbiota may now be considered as prebiotics. The ISAPP updated the definition of prebiotics in 2017 to "a substrate that is selectively utilized by host microorganisms conferring a health benefit" (Gibson et al. 2017). Polyphenols have been known to exhibit antimicrobial effects by inhibiting pathogenic bacteria and antioxidant effects by neutralizing free radicals in the gut, thus supporting a balanced microbiome and protecting gut cells from oxidative damage (Makarewicz et al. 2021). However, several studies support the notion that polyphenols can exert prebiotic-like effects by modulating the gut microbiota. For example, Molinari and colleagues highlighted that dietary polyphenol can modulate pre-existing dysbiosis by stimulating the growth of beneficial bacteria and inhibiting pathogenic bacteria in both animal models and humans (Molinari et al. 2022). Similarly, Rodríguez-Daza and colleagues discussed how polyphenols modulate the microbiome, conferring health benefits to the host (Rodríguez-Daza et al. 2021). Furthermore, a study that

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tested a blended prebiotic containing polyphenols on mice, showing anti-inflammatory effects and modulation of the microbiota with improvement in inflammatory bowel syndrome like symptoms (Chen et al. 2017). In addition, recent research has shown that polyphenols can reach the colon, and be metabolized by bacteria, significantly increasing their bioavailability and result in further secondary metabolite production, such as phenolic acids, flavonoid metabolites, or specific compounds like urolithins, and can even stimulate bacteria to produce SCFAs (Plamada and Vodnar 2021, Zheng et al. 2021, Zhang et al. 2022). Therefore, though not traditional prebiotics, polyphenols exhibit prebiotic-like effects by selectively promoting the growth of beneficial gut bacteria and modulating the microbiome through their antioxidant activity and antimicrobial activity. Further microbial metabolism of polyphenols produces bioactive compounds, such as phenolic acids and SCFAs, which enhance gut health, strengthen the intestinal barrier, and provide systemic health benefits.

Nuts, particularly almonds, possess significant prebiotic potential due to their nutrient-dense composition and rich content of dietary fiber, polymerized polyphenols, and non-digestible components that selectively promote beneficial gut microbiota (Lamuel-Raventos and Onge 2017). Almonds are a source of macronutrients like monounsaturated fatty acids, carbohydrates, and proteins, as well as micronutrients including vitamin E, magnesium, and calcium. Their high levels of insoluble fiber, non-digestible oligosaccharides, and polyphenols, such as proanthocyanidins, play a central role in their prebiotic effects. These compounds resist digestion in the upper gastrointestinal tract and reach the colon intact, where they are metabolized by gut microbiota to produce bioactive compounds like SCFAs and metabolites such as valerolactones and urolithins. These microbial-derived products enhance gut barrier integrity, modulate inflammation, and support metabolic health, with proanthocyanidins specifically linked to a reduced risk of type 2 diabetes (Zamora-Ros et al. 2014). The physical structure of almonds, including their fibrous cell walls, further supports their prebiotic function by encapsulating lipids and bioactives, ensuring availability for fermentation. Additionally, these processes suppress pathogenic bacteria such as *Clostridium perfringens* while promoting beneficial genera like *Bifidobacterium* and *Lactobacillus*. Together, these components underscore almonds' potential as functional foods that modulate the gut microbiome, confer health benefits, and warrant further exploration in preclinical and clinical studies. Here we review the evidence supporting these claims, with both *in vitro* studies and clinical trials.

Chemical analysis of almonds and *in vitro* evidence of prebiotic effects

Almonds (*Amygdalus communis* L. *var. dulcis* .) are composed of a diverse array of bioactive compounds, including polyphenols, dietary fibers, lipids, and proteins, each contributing to their nutritional and functional properties. Almond skins, which constitute 4%–8% of the total weight of shelled almonds, are particularly rich in these components and vary in their composition based on processing methods such as blanching or natural drying (Giuseppina Mandalari et al. 2010). Almond skins are a significant source of polyphenolic compounds, including flavonoids and phenolic acids. Flavan-3-ols (catechin and epicatechin), flavonols (quercetin and isorhamnetin), and phenolic acids (protocatechuic acid, chlorogenic acid) are abundant, especially in natural almond skins. These compounds exhibit antioxidant activity and are integral to the health-promoting effects of almonds. The total phenolic content is significantly reduced by blanching, yet blanched skins retain high antioxidant activity due to heat-generated bioactive compounds. Almonds contain a high level of dietary fiber, primarily insoluble fibers, which include pectic polysaccharides and cellulose. The cell walls of almond skins are rich in pectin and hemicelluloses, with glucose and galacturonic acid being dominant sugar components. The lipid content of almond skins ranges from 22%–24% by dry weight, dominated by monounsaturated fatty acids such as oleic acid and polyunsaturated fatty acids like linoleic acid. Vitamin E, primarily as α-tocopherol, is also present in significant amounts, adding to the antioxidant properties of almond skins. Meanwhile, proteins account for approximately 10%–13% of almond skin dry weight, with soluble proteins also found in blanch water. Additionally, almond skins contain ash, Klason lignin, and trace minerals, further contributing to their functional properties and potential applications in food and pharmaceutical industries (Giuseppina Mandalari et al. 2010).

The potential of almond products as prebiotics has been supported by *in vitro* fermentation analysis. Using a gastrointestinal simulation model followed by batch culture fermentation, finely ground almonds were shown to significantly enhance the populations of beneficial gut bacteria, including *Bifidobacterium* and *Eubacterium rectale* (Mandalari et al. 2008). Notably, the prebiotic index for finely ground almonds exceeded that of traditional prebiotics such as fructooligosaccharides (FOS) after 24 hours, indicating its ability to sustain fermentation and modulate the gut microbiota over time. Additionally, finely ground almonds stimulated the production SCFAs *in vitro*, specifically butyrate (Giuseppina Mandalari et al. 2008). This butyrate production was positively correlated with the relative proportion of *E. rectale*, which is a known butyrate-producer (Lu et al. 2022). In contrast, defatted finely ground almonds had no significant impact on microbial composition or SCFA production, suggesting a critical role for almond lipids in mediating these prebiotic effects (Giuseppina Mandalari et al. 2008).

Evidence of the prebiotic effect of almonds from clinical trials

The potential for almonds to act as prebiotics has been explored extensively in preclinical and observational studies, and more recently, in clinical trials (Table 1). Clinical trials have started to elucidate how almond consumption impacts gut health by promoting beneficial bacterial populations and increasing the production of SCFAs, particularly butyrate, a key metabolite linked to anti-inflammatory and gut-barrier-enhancing effects (Singar et al. 2024). Emerging evidence suggests that regular almond consumption fosters microbial diversity and shifts microbiota composition toward a healthier profile (Choo et al. 2021). For example, trials have demonstrated increases in beneficial genera such as *Bifidobacterium* and *Roseburia*, which are associated with improved gut function and metabolic health (Liu et al. 2014, Holscher et al. 2018). This section will review the current clinical evidence supporting almonds' prebiotic potential, focusing on how clinical trials have leveraged advanced microbiome and

Table 1. Characteristics of included trials examining the effect of nut consumption on the gut microbiota; NS—not significant; NR—not reported.

REF	Country	Sample size (*n*), mean age (years), (% female) Population; BMI (kg/m^2)	Study design and NHMRC level of evidence, Study duration and washout	Nut type and format; dose (g/d)	Diet of participants; fiber intake	Control group	Results		
							Alpha diversity	Beta diversity	Taxonomic changes
Holscher et al. (2018)	USA	*n* 18, 56.7 (SD 10.2) years (44%), Healthy adults, BMI 29.7 (SD 4.4)	RCT-C Feeding trial Level II, Run-in period: 9 d Intervention period: 3 weeks Washout period: 1 week	Whole raw, whole dry roasted, chopped dry roasted and dry roasted almond butter) 42 g/d	Isoenergetic standard American diet (15% PRO, 32% fat, 53% CHO) Almonds substituted for base diet foods Dietary fibre intake: NR	No nuts	NS	NS	Almond consumption increased *Lachnospira*, *Roseburia*, and *Dialister* ($P \leq 0.05$). Chopped almonds increased *Lachnospira*, *Roseburia*, and *Oscillospira* compared to control ($P < 0.05$), while whole almonds increased *Dialister* compared to control ($P = 0.007$).
Burns et al. (2016)	USA	*n* 29 child–parent pairs. Adults: 35 (SE 0.6) years (83%), children: 4 (SE 0·2) years (48%), Healthy adults (BMI < 18.5 to > 30) and children	RCT-C Free-living trial Level II, Run-in period: 1 week Intervention period: 3 weeks Washout period: 6 weeks	Almonds (whole raw or almond butter equivalent) Adults: 43 g/d (1.5 oz) Children: 14 g/d (0.5 oz)	Diet recommendations NR Dietary fibre intake: mean 2.6 g/1000 kJ (children), 2.5 g/1000 kJ (adults). NS change during treatment periods	No nuts	NS	NR	Almond consumption increases *Turicibacter, Enterococcus* and *Bacteroides* in Adults, and *Lachnospira* and *Blautia* in Children.
Dhillon et al. (2019)	USA	*n* 73, aged 18–19 years (56%), Healthy adults, BMI 25.3 (almond group), 25.6 (cracker group)	Parallel design RCT Free-living trial Level II, Intervention period: 6 weeks	Almonds, whole, dry roasted 57 g/d	Diet recommendations not provided; however, both groups advised to avoid consumption of other nuts or seeds during the intervention period Dietary fibre intake: Almond group: mean 12.5 g/d at baseline, NS change during study Cracker group: mean 13.6 g/d at baseline, NS change during study	Graham crackers (77.5 g/d)	Significant increase (Shannon; Chao1; ($P < 0.05$). Significant decrease in Simpsons.	Significant differences between groups (PERMANOVA using unweighted UniFrac and Bray-Curtis; $P < 0{\cdot}05$)	Significant decrease in *Bacteroides fragilis*, *Alistipes*, Butyricimonas, and Odoribacter. A significant increase in Lachnospira.

Table 1. Continued

REF	Country	Sample size (*n*), mean age (years), (% female) Population; BMI (kg/m^2)	Study design and NHMRC level of evidence, Study duration and washout	Nut type and format; dose (g/d)	Diet of participants; fiber intake	Control group	Results		
							Alpha diversity	Beta diversity	Taxonomic changes
Ukhanova et al. (2014)	USA	*n* 18 almond study; age 56.0 (SEM 8.6) years (44%); *n* 16 pistachio study; age 50 (range 29–64) years (50%), Healthy non-smokers, BMI Almond group: 27.4 (SEM 4·2); pistachio group: 27.9 (range 20.8–34.5)	RCT-C Feeding trial Level II, Intervention period: 18 d Washout period: minimum 2 weeks	Almonds (whole, raw) or pistachios (whole, raw) 43 g or 85 g/d (equal to 1.5 or 3 servings/d)	Isoenergetic standard American diet fat: fibre ratio matched between diets. Macronutrient distribution NR Almonds/pistachios substituted for base diet foods Dietary fibre intake: Pistachio group: 32.7 g (0 g pistachios/daily), 35.2 g (1.5 oz pistachios/daily) and 37.6 g (3 oz pistachios/daily) Almond group: 8.5 g/100 g food (0 g almonds/daily), 10.2 g/100 g food (almond treatment group)	No nuts	NS	NS	*Bifidobacteria* unchanged by Almond. *Clostridium* was significantly decreased in abundance.
Liu et al. (2014)	China	*n* 48, aged 18–22 (50%) FOS group (control) (*n* 15) 21.22 ± 2.13, Almond skin group(n 16) 20.83 ± 1.74, Almond group(n 15) 20.53 ± 2.06	Run-in period: 2 weeks, Intervention period: 6 weeks Washout period: 2 weeks	Almonds 56 g, Almond Skin 10g	The average energy content of the basic diet was controlled as 10 MJ/d for male and 8 MJ/d for female subjects. Subjects received daily commercial fructooligosaccharides (FOS), 8 g/d (4 g/serving for lunch and supper, almond skin powder, 10 g/d (5 g/serving for lunch and supper, which was consumed after mix into the basic diet); or roasted, unsalted whole almonds, 56 g/d (28 g/serving for lunch and supper, consumed directly), respectively.	8 g fructooligosaccharides as positive control	NR	NR	Stimulated the growth of beneficial bacteria such as *Bifidobacterium* spp. and *Lactobacillus* spp. Decrease in *Clostridium perfringens*. Increase in b-galactosidase activity and a decrease in b-glucuronidase, nitroreductase, and azoreductase activities.

Table 1. Continued

REF	Country	Sample size (*n*), mean age (years), (% female) Population; BMI (kg/m^2)	Study design and NHMRC level of evidence, Study duration and washout	Nut type and format; dose (g/d)	Diet of participants; fiber intake	Control group	Results		
							Alpha diversity	Beta diversity	Taxonomic changes
Ren et al. (2020)	China	*n* 22 Almond low Carbohydrate diet 73.55 ± 4.99, (60%) 23.53 ± 2.33, *n* 23 low fat diet 70.48 ± 5.91 (52%) 23.69 ± 2.83 with type 2 diabetes	Parallel RCT, Intervention period: 12 weeks	a-LCD group consumed 56 g/day almond which replaced 150 g/d staple food	A low-fat diet includes one serving of vegetables per day, 300 g of staple food (divided into two servings per meal), and a limit of three tablespoons of oil daily. Fruit consumption is allowed only under specific conditions: stable glycemia, low glycemic index, between meals, and accounted for in total calorie intake. Protein intake should consist of five sources daily: 220 ml of milk, one egg, fish or shrimp, a soy product, and meat. Salt intake is restricted to 6 g per day.	Low fat diet	Significantly increased Chao and PD index.	NS.	Almond-based low-carbohydrate diet increased the presence of *Roseburia, Ruminococcus*, and *Eubacteriu*m, and decreased the abundance of *Bacteroides*.
Choo et al. (2021)	Australia	*n* 69 age: 60.8 ± 7.4, BMI ≥ 27 kg/m2, Fasting plasma glucose ≥ 5.6 to < 7.0 mmol/l)	Parallel design RCT Free-living trial, Intervention period:: 8 weeks	56 g of raw almonds/day as 28 g morning and afternoon snacks	Not described	72 g (energy matched) of a commercially available, sweet, nut and seed-free biscuits/day, as 36 g morning and afternoon snacks	Significant increase in observed species, evenness [Simpson's index (1 − D)] and Faith's phylogenetic diversity ($P = 0.011$).	Significant change in Weighted Unifrac distance.	Significant increase in Ruminiclostridium (P = .042, Wilcoxon test with FDR correction), Ruminococcaceae NK4A214 ($P = 0.0004$) and Ruminococcaceae UCG-003 ($P = 0.0002$).
Creedon et al. (2022)	UK	*n* 87, healthy adults (86%), BMI 22.9 ± 2.8	3-arm RCT, Intervention period 4 weeks	whole and ground almonds (56 g/d)	Not described	Isocaloric control muffin in place of habitual snacks	NS	NS	Significant increase in Lachnospiraceae_UCG_001, Phascolarctobacterium, Tuzzerella, Tyzzerella; all $P < 0.05$–but these were NS after FDR correction.

metabolomic analyses to uncover the mechanisms underlying these effects.

In a randomized, controlled, crossover trial, Holscher and colleagues investigated the impact of almond consumption and processing on the gastrointestinal microbiota of healthy adults (Holscher et al. 2018). The study included 18 participants who consumed five distinct diets for 3-week periods: a control diet and diets supplemented with 42 g/day of either whole natural almonds, whole roasted almonds, roasted chopped almonds, or almond butter. Using high-throughput sequencing of fecal samples, the researchers demonstrated that almond consumption altered the gut microbial composition, with processing methods influencing the extent of these changes. Almond consumption was associated with increases in the relative abundance of beneficial bacterial genera, including *Roseburia*, *Lachnospira*, and *Dialister*. Notably, roasted chopped almonds showed the most significant impact, increasing the abundance of *Roseburia*, *Lachnospira*, and *Oscillospira* compared to the control diet. Whole almonds, whether raw or roasted, also promoted *Lachnospira* and *Dialister* but to a lesser extent. In contrast, almond butter had minimal effects on the microbiota, potentially due to increased nutrient bioavailability reducing the substrate reaching the colon. Whole almonds and roasted chopped almonds retain their structural matrix, leading to incomplete digestion in the small intestine, which potentially allows more nutrients to reach the colon, where they can be metabolized by gut microbes. While many of the microbes that were shown to be stimulated by almond consumption are likely fermenting the dietary fiber, genera like *Roseburia*, are known to contain species that can metabolize fatty acids and polyphenols (Molinari et al. 2022).

Another study explored the impact of almond and pistachio consumption on gut microbiota composition using two separate randomized, controlled, cross-over trials involving healthy adults (Ukhanova et al. 2014). Participants consumed a typical low-fiber "American" diet supplemented with either almonds or pistachios at varying daily doses (0, 1.5, or 3 servings) over three 18-day feeding periods, with two-week washout intervals between treatments. Fecal samples were collected at the start and end of each feeding period for microbiota analysis using 16S rRNA amplicon sequencing and qPCR. The results indicated that nut consumption led to subtle changes in gut microbiota composition, with pistachios exerting a stronger effect than almonds. Interestingly, neither nut type significantly increased the abundance of *Bifidobacteria* or *Lactobacillus*, which are often targeted by traditional prebiotics. Instead, the shifts observed suggested that almond consumption selectively modulates microbial populations to enhance functional capabilities, such as butyrate production. Conversely a trial conducted in healthy adults to determine how the consumption of almonds and almond skins altered the fecal microbiome found that almond skins and almonds stimulated the growth of *Bifidobacterium* and *Lactobacillus* (Liu et al. 2014). Forty-eight healthy college students participated in a trial with a 2-week run-in period, a 6-week treatment period, and a 2-week wash-out period. The subjects were then divided into three groups: a fructooligosaccharides control group, an almond skin group, and an almond group. Interestingly, the effects of almond skin intake were more immediate compared to almond intake, but both eventually resulted in similar increases in *Bifidobacterium* and *Lactobacillus*. Additionally, both almond skin and almond intake led to a decrease in the population of *C. perfringens*, a bacteria associated with gastrointestinal diseases. The study also observed changes in fecal bacterial enzyme activity, with an increase in bifidobacterial and lactobacilli associated b-galactosidase activity, which drives lactose metabolism. and a decrease in beta-glucuronidase, nitroreductase, and azoreductase activities. The activity of these enzymes can lead to the reactivation of potentially harmful compounds like toxins or certain medications, and has been associated with colon cancer, inflammatory bowel disease, and estrogen-related disorders due to the potential for excessive hormone reactivation (Wilson and Nicholson 2017, Gao et al. 2022, Braccia et al. 2023).

Burns and colleagues investigated whether incorporating almonds into the daily diet affected diet quality (Burns et al. 2016). This randomized, crossover study revealed that the inclusion of almonds in the daily diet led to improvements in diet quality for both parents and children, however, as with most studies the effects on the microbiome were subtle. Interestingly, the microbiome was much more affected in children than parents, showing pronounced increases in *Bifidobacteria*. Another study investigated the effects of consuming almonds as a snack for 8 weeks on the diversity and abundance of gut microbiota in college freshmen compared to an isocaloric snack (Dhillon et al. 2019). The study results showed that almond snacking resulted in a 3% increase in quantitative alpha-diversity (Shannon index) and an 8% increase in qualitative alpha-diversity (Chao1 index). Furthermore, the proportion of the potentially pathogenic bacterium *Bacteroides fragilis* decreased by 48% compared to the control, suggesting significant improvements in gut health. Almond consumption and changes in the gut microbiome were associated with an increase in unsaturated triglycerides, unsaturated phosphatidylcholines, saturated and unsaturated lysophosphatidylcholines, tricarboxylic acids, and tocopherol clusters in serum, whose enrichment is generally associated with health. Microbial amino acid biosynthesis, and amino sugar and nucleotide sugar metabolism pathways were also enriched, which may point to potential mechanism of action.

A parallel randomized controlled trial allocated 45 subjects with type 2 diabetes to either an almond-based low-carbohydrate diet or a control low-fat diet for 12 weeks (Ren et al. 2020). The almond-based diet involved substituting 56 grams of almonds for 150 grams of carbohydrate foods. Both diets led to a significant increase in the diversity of the colonic microbiota compared to baseline. Interestingly, those consuming almonds also experienced significant improvements in both glycemic control (HbA1c reduction) and depression scores, compared to the low-fat diet only group. The almond-based diet also increased the proportion of SCFA-producing bacteria such as *Roseburia, Ruminococcus,* and *Eubacterium*. SCFAs interact with G-protein coupled receptors (e.g. GPR43), enhancing the secretion of glucagon-like peptide-1 (GLP-1), a key modulator of glucose metabolism and mood regulation. This suggests another potential prebiotic mechanism of action by which almond consumption may influence health.

Creedon and colleagues explored the impact of almond consumption and processing (whole vs. ground almonds) on gut microbiota composition, microbial metabolites, gut physiology, and gastrointestinal symptoms in a randomized controlled trial (Creedon et al. 2022). Over four weeks, healthy adult participants consumed 56 g/day of whole almonds, ground almonds, or an isocaloric control snack (muffins). Al-

mond consumption was associated with increased butyrate production, but had no significant effect on fecal bifidobacteria abundance, microbial diversity, or gut transit time. Interestingly, the form of almond (whole or ground) did not influence study outcomes significantly, though ground almonds showed greater lipid bioaccessibility due to reduced particle size after mastication. Meanwhile, Choo et al. investigated the impact of daily almond consumption over 8 weeks on fecal microbiota composition in overweight or obese individuals with elevated fasting blood glucose (Choo et al. 2021). Almond consumption led to an increased proportion of the Ruminococcaceae family, including, as with other studies, the genera *Oscillospira* and *Butyricicoccus*. Additionally, almond consumption significantly lowered fecal pH compared to the biscuit snack, which is generally indicative of a healthier colonic microbiota. However, in contrast to other studies, and despite these microbiota shifts, there were no notable changes in SCFA levels or intestinal permeability, indicating limited effects on microbial metabolic outputs such as butyrate synthesis.

Metanalyses and systematic reviews

The similarities and differences among these studies reveal the complex and context-dependent nature of almond consumption on gut microbiota and SCFA production. Across studies, a shared finding is the ability of almonds to influence microbial composition and functionality, often through promoting the abundance of beneficial taxa or metabolites. For example, Creedon et al. (2022) and Ren et al. (2020) both observed increased butyrate production, suggesting enhanced microbial functionality linked to SCFA synthesis. Choo et al. (2021), while noting shifts in the microbiota composition—such as increased Ruminococcaceae—did not detect corresponding changes in SCFA levels, emphasizing that compositional changes do not always translate to metabolic outcomes. A notable contrast lies in the populations studied; Ren et al. and Choo et al. involved metabolically challenged individuals, where almonds' prebiotic effects appeared to exert more profound or specific health impacts, such as improved glycemic control (Ren et al. 2020) and lowered stool pH (Choo et al. 2021). In contrast, Creedon et al., focusing on healthy adults, highlighted almonds' role in enhancing microbial metabolites without significant alterations to diversity or gut transit time. These studies also differ in their exploration of almond processing. Creedon et al. uniquely investigated the effects of whole versus ground almonds and found no significant differences in outcomes, suggesting that the structural form of almonds does not alter their prebiotic potential under the tested conditions. Choo et al., by contrast, did not explore processing but identified important fecal characteristic changes, potentially reflecting the interaction of almonds with a more compromised gut environment. Together, these findings underscore almonds' broad potential as a prebiotic food, while also highlighting how health status, study duration, and methodological focus can influence observed effects. Further research is necessary to elucidate how these factors shape the nuanced interplay between almonds, gut microbiota, and SCFA production.

Three recent systematic reviews and meta-analyses confirm this variable response (Creedon et al. 2020, Fitzgerald et al. 2021, Ojo et al. 2021), acknowledging the modest and inconsistent effects of almonds on microbial composition and functionality. Ojo et al. provided additional insights into the clinical implications for glycemic control and inflammatory markers. The observed variability is likely influenced by differences in population health status, study design, and intervention specifics. These systematic reviews collectively highlight the potential of nut consumption, particularly almonds, to modulate gut microbiota, but they reveal varying degrees of impact and notable inconsistencies. Creedon et al. emphasized the variability in almonds' effects on microbial composition and diversity, with conflicting findings for taxa like *Bifidobacterium* and limited changes in α- and β-diversity. Similarly, Fitzgerald et al. found modest and inconsistent impacts across studies, with some showing increases in SCFA-producing bacteria like *Roseburia* and *Clostridium*, but these findings were not uniform. Both reviews attributed this variability to heterogeneity in study designs, including differences in almond dosage, duration, and populations studied. In contrast, Ojo et al. (2021) provided a more focused examination of almond-based diets in patients with type 2 diabetes, revealing significant increases in SCFA-producing bacteria (*Roseburia*, *Ruminococcus*, and *Eubacterium*) and clinically meaningful reductions in HbA1c and BMI. Unlike the broader focus of Creedon and Fitzgerald, Ojo's analysis centered on almonds' metabolic and inflammatory effects, highlighting their potential benefits in glycemic control and weight management. Notably, while Creedon and Fitzgerald observed modest microbiota impacts, Ojo identified more pronounced changes in clinical and microbiota outcomes, albeit within a specific patient population. Together, these reviews illustrate how population health status, dietary context, and study design can influence findings, underscoring the need for standardized methodologies to better understand almonds' prebiotic and metabolic roles.

This variability observed in host and microbiome responses to almond and nut consumption reflects the broader diversity of human microbiomes and their influence on health and disease. This interindividual variability in microbiome composition and function plays a critical role in shaping how people respond to dietary interventions, as well as to other external factors such as medication (Zeevi et al. 2015, Gilbert et al. 2018, Bermingham et al. 2024). For example, specific microbial taxa may mediate the production of beneficial metabolites like SCFAs in some individuals but not others, leading to divergent health outcomes. Similarly, gut microbiota differences can modulate the efficacy of medications or the impact of diet on metabolic and inflammatory pathways, resulting in distinct physiological and clinical responses. These findings underscore the importance of personalized approaches to dietary recommendations and clinical treatments, accounting for the unique microbiome landscape of each individual to optimize outcomes and bridge the gap between microbiome research and practical applications.

Potential human physiological responses to prebiotic effect

Recent results from a global consensus paper developed through a roundtable of experts highlight the significant cardiometabolic benefits of almond consumption (Trumbo et al. 2024). Almonds, rich in monounsaturated fats, polyunsaturated fats, dietary fiber, and protein, have been shown to support weight management, cardiovascular health, and diabetes risk reduction. The consensus confirms that almond consumption, even at doses ranging from 10–100 g/day for periods up

to 18 months, does not lead to weight gain and may contribute to slight weight loss. This effect is attributed to almonds' lower metabolizable energy, incomplete fat absorption, and their role in promoting satiety, which may reduce overall calorie intake. The expert panel also concluded that almond consumption contributes to modest but significant reductions in LDL cholesterol levels, averaging 5 mg/dl, and small decreases in diastolic blood pressure (0.17–1.3 mm Hg). These benefits, while individually modest, are clinically meaningful when almonds are included as part of dietary patterns such as the Portfolio or DASH diets. Regarding glycemic control, the roundtable identified mixed findings overall, but specific studies in Asian Indians with prediabetes demonstrated significant reductions in fasting blood glucose and HbA1c, underscoring the potential for population-specific benefits. The experts emphasized the need for further research to clarify the mechanisms behind weight stability, and to evaluate almonds' role in health-promoting dietary patterns. It is reasonable to hypothesize that the microbiome is mediating some of consistently observed cardio metabolic effects of Almonds. This consensus positions almonds as a valuable component of evidence-based dietary strategies for improving cardiometabolic health.

Recommendations for future research

While the evidence supporting the prebiotic potential of almonds is growing, variability in findings across studies highlights the need for more standardized methodologies to enhance reproducibility and comparability. Based on existing research, we propose the following considerations for future studies. (i) Dosage. Studies examining almond consumption have utilized a wide range of dosages, typically between 10–100 g/day. Future trials should establish an optimal dosage that balances effectiveness with practicality in dietary interventions. A range of 42–56 g/day (approximately one to two servings) has demonstrated significant microbiome-modulating effects and could serve as a useful benchmark. (ii) Intervention Period. The duration of almond supplementation has varied from short-term (2–4 weeks) to long-term (up to 18 months), with most studies spanning 4–12 weeks. Longer intervention periods may be necessary to observe stable shifts in microbiome composition and metabolic effects. Future studies should incorporate follow-up assessments to evaluate the persistence of microbial and health benefits after almond consumption ceases. (iii) Study Population and Health Status. The impact of almonds on the microbiome appears to be modulated by the baseline health status of participants. Studies have shown more pronounced effects in individuals with metabolic disorders or dysbiosis compared to healthy controls. Future research should stratify participants based on metabolic health, diet, and microbiome composition at baseline to better understand individualized responses. (iv) Almond Preparation and Bioavailability. Almond processing (whole, ground, roasted, blanched, defatted) influences microbial fermentation patterns. Whole and chopped almonds retain their structural matrix, allowing for gradual fermentation in the colon, whereas almond butter and finely ground almonds may alter bioavailability. Standardizing preparation methods or investigating their differential effects systematically would improve cross-study comparisons. (v) Microbiome and Metabolome Assessments. Future research should also incorporate multi-omics approaches to elucidate mechanistic pathways linking almond consumption to gut microbial changes. (vi) Dietary Control and Confounding Factors. A lack of control for background diet may have confounded microbiome responses in previous trials. Future trials should implement controlled feeding designs or rigorous dietary tracking to isolate the specific effects of almond consumption. (vii) Geographic and Ethnic Variability. Gut microbiota composition varies across geographic regions and ethnic backgrounds due to differences in diet, lifestyle, and genetics. Individuals with a predominantly "Western" microbiome, characterized by lower microbial diversity and higher *Bacteroides* abundance (Hjorth et al. 2019, Adolph and Tilg 2024), may respond differently to prebiotics like almonds compared to those from African or Asian populations, where fiber-degrading taxa are more prevalent (Ecklu-Mensah et al. 2023). Ethnicity can also modulate microbiome function within regions (Shanahan et al. 2021). To improve study comparability, future research should report participants' geographic location and ethnicity and explore their influence on microbiome responses to almonds. By integrating these methodological improvements, it should be possible to generate more consistent and generalizable findings on the prebiotic effects of almonds, ultimately strengthening their potential role in dietary recommendations for gut and metabolic health.

Conclusion

Based on the available evidence from *in vitro* studies, clinical trials, and systematic reviews, almonds demonstrate significant potential to modulate the gut microbiota and confer health benefits, fulfilling the criteria of a prebiotic. Almond consumption has been shown to alter the composition and diversity of gut microbiota, often increasing the relative abundance of beneficial bacteria such as *Bifidobacterium*, *Lactobacillus*, and SCFA-producing genera like *Roseburia*, *Lachnospira*, and *Dialister*. These changes are accompanied by increased production of SCFAs, which play essential roles in enhancing gut barrier function, modulating inflammation, and supporting metabolic health. Furthermore, almonds' high content of dietary fiber and polyphenols contributes to their selective fermentation in the colon, promoting microbial populations associated with health benefits. Despite some variability in findings across studies due to differences in populations, study designs, and methodologies, there is converging evidence supporting the prebiotic potential of almonds. These findings underscore almonds' role in promoting gut and systemic health, highlighting their importance as part of a healthy diet and their potential in clinical applications for managing metabolic and gastrointestinal health. Future research should focus on standardizing methodologies and exploring individualized responses to optimize the health benefits of almonds.

Author contributions

Maha Tahiri (Conceptualization, Formal analysis, Writing – review & editing), and Jack A. Gilbert (Conceptualization, Formal analysis, Project administration, Supervision, Writing – original draft, Writing – review & editing).

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Data availability

No new data were generated or analysed in support of this research.

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