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Beyond probiotics: Postbiotic compounds, intestinal health, and food technology perspectives in traditional Asian fermented soybean foods

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ABSTRACT

As the world grapples with rising cases of metabolic disorders, inflammatory bowel diseases, and immune-related disorders, gut health has become a pressing health and food technology issue. In this context, traditional fermented soybean products such as doenjang, natto, cheonggukjang, and tempeh in Asia are being reevaluated not only as sources of probiotics but also as providers of postbiotics, the non-viable microbial products and metabolites implicated in gut health. This PRISMA-guided narrative review examines the role of postbiotics produced in fermented soybean foods in maintaining gut microbiota balance, gut barrier function, and inflammation regulation, and explores their technological potential in functional food development. The study followed PRISMA 2020 guidelines, and the literature was searched through Scopus, PubMed, and Google Scholar from 2010 to 2025. Selected studies emphasized metabolic byproducts of Bacillus and Rhizopus species, their mucosal protective mechanisms, anti-inflammatory effects, and processing compatibility. Findings indicate that γ-PGA and SCFA exhibit barrier-regulating and immunomodulatory functions, while enzymes such as nattokinase and bacteriocins play roles in inhibiting pathogenic microorganisms and supporting microbial ecosystem balance. Due to their stability under refrigerated, acidic, and heat conditions, postbiotics are suitable for incorporation into functional foods and supplements. However, human clinical evidence remains limited, and future work should address dosage, standardization, and fermentation parameters. This review positions traditional fermented soybean foods as a promising platform for next-generation gut health functional foods, with relevant implications for food formulation and processing.

Contribution/Originality: This study contributes to the existing literature by synthesizing postbiotic compounds from traditional fermented soybean foods and their mechanistic roles in gut health. This study is one of the very few studies that have investigated postbiotics from a food technology perspective. The paper's primary contribution is finding that postbiotics offer stability advantages for functional food applications.

1. INTRODUCTION

The increasing prevalence of gastrointestinal disorders, metabolic diseases, and immune-related diseases has prompted global interest in dietary interventions that can modulate intestinal health through microbiome targeting strategies (Aggarwal et al., 2022; Mafe et al., 2025). Functional foods containing probiotics and prebiotics have been widely studied and commercialized due to their ability to influence intestinal homeostasis (Peng et al., 2020).

However, in recent years, scientific discourse has shifted to postbiotics, which are nonviable microbial cells, metabolites, and cellular components that provide health benefits to their hosts (Aguilar-Toalá et al., 2018; Salminen et al., 2021). Postbiotics have emerged as a safe and stable alternative to probiotics, especially in the context of food processing and product development, where the viability of living microorganisms raises logistical and regulatory challenges (Ramazanidoroh, Hosseininezhad, Shahrampour, & Wu, 2024). At the same time, traditional fermented foods are receiving new attention as a source of naturally occurring microbial metabolites (Feng, Chen, & Chen, 2018; Nagarajan, Rajasekaran, & Venkatachalam, 2022). Having been consumed by various Asian cultures for centuries, these foods are increasingly recognized for their sensory and nutritional value, as well as their potential as vehicles for delivering postbiotic compounds (Hashimoto, Hamaguchi, & Fukui, 2023). Among them, fermented soybean products such as soybean paste, natto, tempeh, and cheonggukjang stand out due to their abundant microbial diversity and unique fermentation processes (Jang, Oh, Lim, Kim, & Kim, 2021). These products are produced using bacterial or fungal cultures, especially short-chain fatty acids (SCFAs), poly γ-glutamic acid, nattokinase, and bacteriocin, which produce a variety of health-promoting compounds such as Bacillus subtilis, Rhizopus oligosporus, and naturally occurring fungi (Markowiak-Kopeć & Śliżewska, 2020). Derived from fermented soybean products, postbiotics provide a number of mechanisms that promote intestinal health (Lee, Im, Lee, & Choi, 2024). SCFAs such as butyrate, acetate, and propionate have been shown to improve epithelial barrier function, regulate immune response, and inhibit intestinal inflammation (Corrêa-Oliveira, Fachi, Vieira, Sato, & Vinolo, 2016). Polyglutamic acid and physiologically active peptides, which are frequently observed in natto and cheonggukjang, have demonstrated immune-regulating and antioxidant effects (Dahiya & Nigam, 2022). In addition, the bacteriocins produced in Bacillus species have shown potential in suppressing enteric pathogens and promoting beneficial microbial communities (Zhu et al., 2023). Despite a growing body of literature on postbiotics, most existing reviews address postbiotics in general or focus on probiotic interventions, with limited attention to postbiotic compounds specifically derived from traditional Asian fermented soybean foods. Moreover, current reviews rarely integrate compound profiles with gut-related mechanisms and potential applications in functional food development. This gap is noteworthy given the expanding interest in the intersection of traditional food practices, microbiome science, and food technology innovation.

To address this gap, this review (i) compiles major postbiotic compounds characteristic of fermented soybean foods, (ii) synthesizes mechanistic pathways relevant to gut microbiota, epithelial barrier function, and inflammation, and (iii) considers their technological advantages in functional food formulation. Accordingly, the review is guided by the following research questions.

RQ1: Which postbiotic compounds arise from the fermentation of traditional Asian soybean foods?

RQ2: Through what mechanisms do these compounds influence gut health?

RQ3: What implications do these findings have for developing functional foods?

The purpose of this review is to examine postbiotic compounds found in traditional Asian fermented soybean foods, clarify their mechanisms related to gut physiology, and evaluate their advantages relative to probiotics in functional food development. The review proceeds by outlining the methodological approach, synthesizing key findings, and concluding with implications and avenues for future research.

2. METHODS

This review was conducted using a structured narrative review approach informed by the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 guidelines, with the aim of enhancing transparency and methodological clarity in the literature search and selection process (Page et al., 2021). While this study does not constitute a full systematic review or meta-analysis, PRISMA principles were applied to guide the identification, screening, and qualitative synthesis of relevant studies. The following subsections describe the research framework, data sources, search strategy, selection criteria, data extraction and synthesis, and quality considerations used to address the research question.

2.1. Research Question and Framework

This review aims to examine the types of postbiotic compounds derived from traditional Asian fermented soybean foods and to evaluate their contributions to gut-related functional properties relevant to food technology and functional food development. The analytical framework of this study integrates traditional fermentation processes of Asian soybean-based foods, the generation and characterization of postbiotic compounds, and their functional relevance to intestinal health and food system applications. A structured narrative review approach was adopted to synthesize existing evidence, with an emphasis on technological mechanisms and food-oriented implications rather than clinical or therapeutic outcomes, as illustrated in Figure 1. Unlike most existing reviews that focus broadly on probiotics or generalized postbiotic concepts, the present review places specific emphasis on postbiotic compounds originating from fermented soybean foods and evaluates their mechanistic and technological relevance within food science and functional food contexts. This distinguishes the methodological focus of this review from clinically oriented or microbiology-centered analyses.

2.2. Data Sources

A comprehensive literature search was conducted using major scientific databases, including Scopus, PubMed, and Google Scholar, to ensure broad coverage of food science, microbiology, and functional food research. Additionally, reference lists of relevant review articles and key original studies were manually screened to identify publications not captured through the database search.

2.3. Search Strategy

The literature search employed combinations of keywords related to fermented soybean foods, postbiotics, and gut-related functionality. Core search terms included “postbiotics,” “fermented soybean,” “doenjang,” “natto,” “tempeh,” “bioactive metabolites,” “intestinal health,” and “functional food.” Boolean operators (AND, OR) were used to refine search results. Only articles published in English were considered. The search primarily focused on studies published between 2010 and 2025, reflecting the rapid growth of research on postbiotics and non-viable microbial components in food systems.

2.4. Selection Criteria

Studies were included if they focused on traditional Asian fermented soybean foods or their derived components, examined postbiotic compounds such as microbial metabolites or non-viable microbial structures, and addressed functional, biochemical, or mechanistic aspects relevant to gut health or food applications. Studies were excluded if they were purely clinical trials unrelated to food matrices, focused exclusively on live probiotics without consideration of postbiotic components, or lacked sufficient methodological detail to support qualitative synthesis.

2.5. Data Extraction and Synthesis

Relevant information was extracted from eligible studies, including fermentation substrates, microbial strains, identified postbiotic compounds, and reported functional properties. Extracted data were qualitatively synthesized and organized according to compound type and functional relevance. Instead of conducting a quantitative meta-analysis, a thematic synthesis approach was applied to identify recurring patterns, technological implications, and research gaps within the existing literature.

2.6. Quality Considerations and Ethical Issues

The quality of included studies was assessed based on the clarity of experimental design, transparency of analytical methods, and relevance to food science and technology. As this review was based exclusively on previously published literature, ethical approval was not required. Throughout the review process, careful attention was given to data integrity and appropriate citation practices.

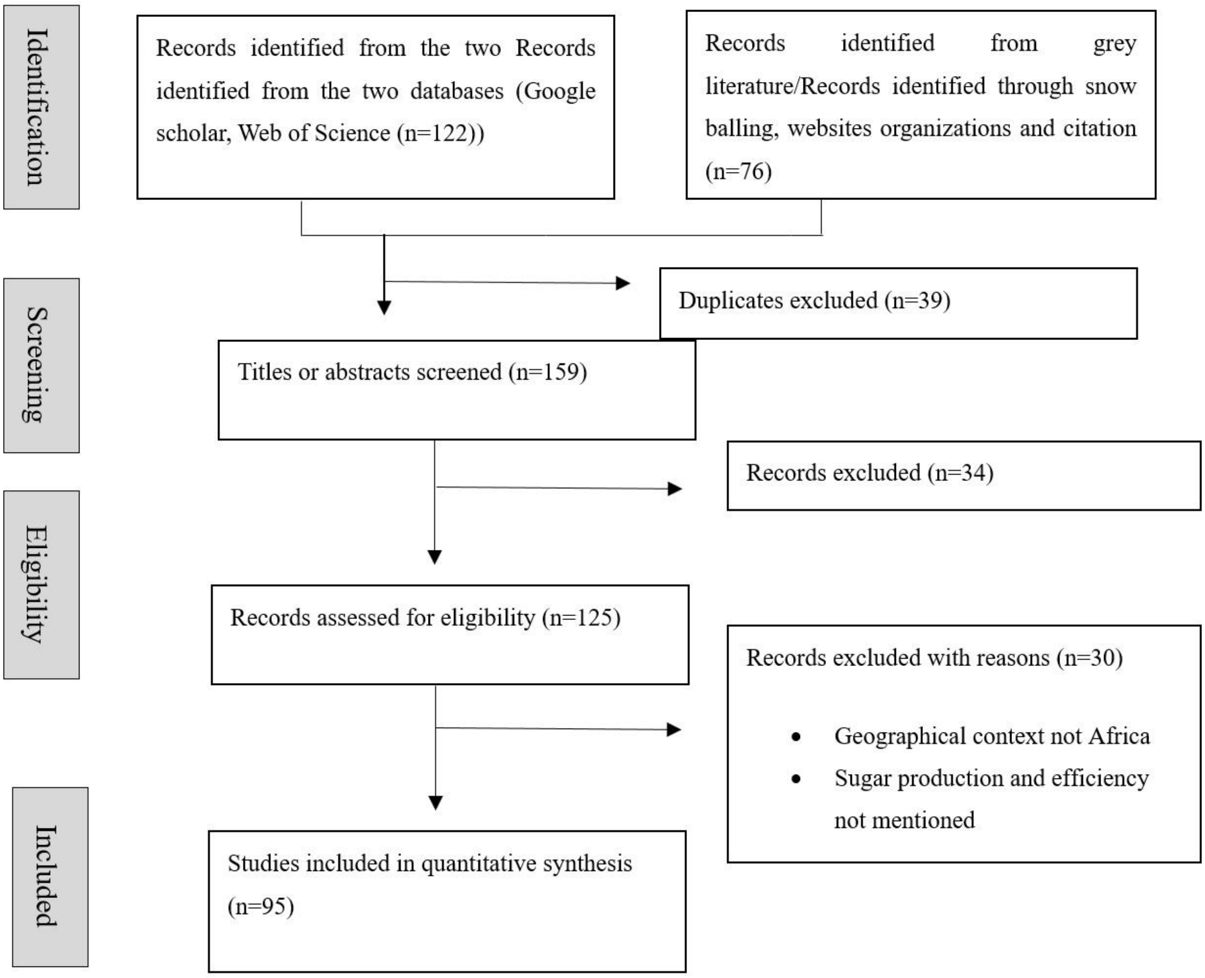

Figure 1. Records retrieval process using the PRISMA flow diagram.

3. RESULTS

3.1. Concept and Classification of Postbiotics

The term postbiotics refers to non-viable microbial cells, cell fragments, and metabolites that provide physiological benefits to the host. Unlike probiotics that must remain viable for them to be effective, postbiotics perform their functions without living microorganisms (Vinderola, Sanders, & Salminen, 2022). This distinction offers practical benefits in food applications, with higher stability during storage and processing and a reduced risk of infection, especially in vulnerable populations (Żółkiewicz, Marzec, Ruszczyński, & Feleszko, 2020). Postbiotics include a variety of biologically active compounds that are produced during microbial fermentation (Rad, Hosseini, & Pourjafar, 2022). These include short-chain fatty acids (SCFAs), such as acetate, propionate, and butyrate, which are known to support the integrity of the intestinal barrier and reduce intestinal inflammation (Parada Venegas et al., 2019). Other important compounds include physiologically active peptides, which are produced during microbial protein degradation of soybean proteins and can exert antibacterial, antihypertensive, or immunomodulatory effects (Chatterjee, Gleddie, & Xiao, 2018). In addition, exopolysaccharides, enzymes, polyglutamic acid, and bacteriocins are frequently observed in fermented foods and contribute to various aspects of intestinal health (Dimidi, Cox, Rossi,

& Whelan, 2019). In the context of fermented soybean foods, nattokinase and poly-glutamic acid have been shown to be promising for regulating intestinal function and reducing systemic inflammation (Johnson, Akinmola, & Scholz, 2022). In addition, cell wall components of inactive bacteria, such as lipoteichoic acid and peptidoglycan, can stimulate the host's immune response through interaction with pattern recognition receptors (Sukhithasri, Nisha, Biswas, Kumar, & Biswas, 2013). Given this chemical and functional diversity, postbiotics can be largely classified according to their biological role and origin (Nataraj, Ali, Behare, & Yadav, 2020). Metabolic by-products, structural fragments, or secreted proteins. This classification framework is essential for identifying postbiotics-rich foods and specifically targeting intestinal health (Prajapati et al., 2023).

3.2. Fermented Soy Foods as Postbiotic Sources

Traditional fermented soybean foods are a source of a variety of postbiotic compounds that are formed by local fermentation practices, microbial communities, and substrate composition (Liu et al., 2022). Among them, soybean paste (Korea), natto (Japan), cheonggukjang (Korea), and tempeh (Indonesia) have been widely studied as functional health characteristics, especially about intestinal health (Park, Kim, Ryu, Jeong, & Yang, 2024; Qiao et al., 2022). Soybean paste, a Korean fermented soybean paste, is produced by aging naturally occurring mold, yeast, and Bacillus species. During fermentation, various bioactive metabolites are produced, including short-chain fatty acids, polyglutamic acid, and isoflavone aggregates (Jung & Shin, 2024). These compounds have been reported to be associated with improved antioxidant capacity in vitro and in animal studies as well as intestinal microbiological control and anti-inflammatory effects (do Prado, Pagnoncelli, de Melo Pereira, Karp, & Soccol, 2022). A Japanese fermented soybean product, natto, is characterized by the activity of Bacillus subtilis natto, which synthesizes high levels of polyγ-glutamic acid (γ-PGA) and the well-known enzyme nattokinase (Gopikrishna, Suresh Kumar, Perumal, & Elangovan, 2021). These ingredients not only contribute to the sticky texture and unique flavor of natto but also exhibit physiological effects such as improved blood flow, immune regulation, and intestinal barrier protection (Dwivedi et al., 2024). Specifically, γ-PGA exhibits similar properties to prebiotic properties, promoting the growth of beneficial intestinal bacteria (Jin, Choi, Lim, & Sung, 2017). Another traditional Korean fermented bean food, cheonggukjang, shares similarities with natto in terms of microbial composition, but is characterized by its short fermentation period and high water content (Kim, Hwang, Yang, & Kim, 2021). Cheonggukjang has been reported to contain bacteriocins, physiologically active peptides, and SCFAs associated with intestinal health (Shin, Kim, Park, & Kim, 2016). Studies have shown that it has the potential to suppress harmful pathogens, reduce intestinal inflammation, and increase the abundance of beneficial microorganisms such as lactic acid bacteria and bifidobacterium (Saez-Lara, Gomez-Llorente, Plaza-Diaz, & Gil, 2015).

Tempe, which is derived from Indonesia, is produced by fermenting soybeans with the rhizopus species (Sjamsuridzal et al., 2021). Unlike bacterial fermentations seen in East Asian soy products, Tempe relies on fungal activity that degrades complex soy components and releases bioactive peptides, isoflavone aglycone, and antioxidant metabolites (Mani & Ming, 2017). Tempe has been shown to support intestinal health by improving microbial diversity, increasing intestinal integrity, and relieving oxidative stress in the large intestine (Surya et al., 2024).

Taken together, these fermented soy products provide a variety of postbiotic compounds depending on microbial species, fermentation time, and processing conditions (An et al., 2023). Their contribution to intestinal health has been supported by several in vitro, in vivo, and clinical studies, suggesting their potential role as an effective functional food ingredient in dietary interventions that target intestinal health (Cencic & Chingwaru, 2010). The major postbiotic compounds identified in traditional fermented soy foods and their gut health-related functions are summarized in Table 1.

Table 1. Major postbiotic components and gut health-related functions of traditional Asian fermented soy foods.

Fermented Soy Food	Main Microorganisms	Key Postbiotic Components	Gut Health Functions
Doenjang (Korea)	Bacillus spp., lactic acid bacteria	SCFAs, polyglutamic acid, bioactive peptides, isoflavone aglycones	Microbiota modulation, antioxidant effects, and anti-inflammatory
Natto (Japan)	Bacillus subtilis natto	γ-PGA, nattokinase, SCFAs, cell wall fragments	Barrier integrity, immune modulation, microbiota balance
Cheonggukjang (Korea)	Bacillus spp.	Bacteriocins, SCFAs, peptides, EPS	Antimicrobial, anti-inflammatory, and microbiota diversity
Tempeh (Indonesia)	Rhizopus spp.	Isoflavone aglycones, peptides, antioxidants	Antioxidant effects, microbiota enrichment, epithelial repair

3.3. Mechanisms of Gut Health Promotion by Postbiotics

Postbiotics derived from fermented soybean foods can positively affect intestinal health through a variety of biological mechanisms. These mechanisms are mediated by structurally and functionally diverse compounds, such as short-chain fatty acids (SCFAs), physiologically active peptides, polyglutamic acid, enzymes, and bacteriocins, each contributing to intestinal homeostasis in a unique way (Jastrząb, Graczyk, & Siedlecki, 2021; Liu et al., 2023). One of the major actions of postbiotics is the regulation of intestinal microbial composition. Certain postbiotic compounds, such as γ-polyglutamic acid and SCFA, provide selective substrates or signals that promote the growth of beneficial microorganisms while inhibiting potential pathogens (Thapa et al., 2024). This balance of intestinal ecosystems has been associated with improvements in digestion, immune regulation, and overall intestinal function (Liu, Wang, & Wu, 2022). Postbiotics also play an important role in strengthening intestinal barriers essential for preventing the movement of harmful microorganisms and toxins (Gao et al., 2019; Moradi et al., 2020). SCFAs, especially butyrate, act as energy sources for colonic epithelial cells and upregulate the expression of tight-junction proteins, thereby enhancing mucosal integrity (Salvi & Cowles, 2021). Polyglutamic acid and bacterial cell wall fragments can also activate signaling pathways that enhance the epithelial barrier and maintain permeability balance (Wang et al., 2015). In addition, many postbiotic compounds exhibit anti-inflammatory properties by downregulating the expression of inflammatory cytokines such as TNF-α, IL-6, and IL-1β (Bourebaba, Marycz, Mularczyk, & Bourebaba, 2022). This is especially important for alleviating chronic low-grade inflammation, a common feature of intestinal-related diseases, including inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) (Abouelela & Helmy, 2024; Zhang, Zhang, & Li, 2023). For example, peptides produced during soybean fermentation have been shown to inhibit the nuclear factor-kappa B (NF-κB) signaling pathway, which is a major mediator of inflammation (Patel & Mani, 2024). In vitro studies using RAW264.7 macrophages stimulated with LPS have shown that soybean-derived peptides inhibit the nuclear translocation of the NF-κB p65 subunit and reduce the production of inflammatory cytokines such as TNF-α and IL-6 (Kusumah & de Mejia, 2022). Some postbiotics exhibit antioxidant activity, further contributing to intestinal health by neutralizing reactive oxygen species and reducing oxidative damage to intestinal tissues (Izuddin, Humam, Loh, Foo, & Samsudin, 2020). This antioxidant function has been demonstrated in vitro for isoflavone aglycone-rich fermented soy extracts and microbial metabolites such as glutathione and catalase (Blazheva et al., 2022; Sadeghi, Ebrahimi, Shahryari, Kharazmi, & Jafari, 2022). In addition, certain enzymatic postbiotics, such as nattokinase, can indirectly support intestinal function by improving blood flow and reducing fibrin accumulation, which have systemic effects that also affect gastrointestinal health (Flori, Benedetti, Martelli, & Calderone, 2024). These various mechanisms demonstrate that postbiotics in traditional fermented soy foods provide multifaceted benefits for intestinal physiology, supporting not only microbial balance but also intestinal structural and immune defense (Zhou, Chen, Patil, & Dong, 2024). To synthesize these mechanistic observations, Table 2 provides a comparative overview of major postbiotic compounds, their microbial origins, gut-related mechanisms, evidence levels, and limitations based on current literature.

In addition, the overall interactions between fermented soybean foods, postbiotic compound classes, and their downstream physiological effects are summarized schematically in Figure 2, illustrating how postbiotic-rich foods contribute to improved gut health outcomes (Asefa, Belay, Welelaw, & Haile, 2025). Collectively, current evidence indicates that fermented soybean-derived postbiotics exert complementary effects on gut health by shaping microbial communities, reinforcing epithelial integrity, and modulating inflammatory pathways.

However, most evidence is derived from in vitro or animal models, and few studies directly compare fermentation parameters, standardized dosages, or food matrices.

These limitations underscore the need for human studies and standardized analytical approaches to advance translational applications in functional food development.

Table 2. Comparative overview of key postbiotic compounds from traditional fermented soybean foods.

Compound	Source (Food)	Microbial Producer	Proposed Mechanism	Gut Health Relevance	Evidence Type	Limitations
SCFAs (butyrate, acetate, propionate)	Cheonggukjang, soybean paste	Bacillus spp., mixed anaerobes	Increases tight junction expression, regulates Treg cells, and reduces NF-κB signaling	Improved barrier integrity, reduced inflammation, and microbiota modulation	In vitro, animal, limited human	Dose variability is influenced by diet & microbiota composition
γ-PGA	Natto, cheonggukjang	Bacillus subtilis	Enhances mucosal hydration, modulates immune signaling, and has antioxidant activity	Reduced oxidative stress, improved immune modulation	In vitro, animal	Limited translational data; lack of standardized dosing
Nattokinase	Natto	Bacillus natto	Fibrinolytic activity, potential anti-inflammatory signaling	Indirect gut benefit via circulation; potential microbial ecosystem support	Animal, limited human	Mechanisms in gut unclear; not gut-specific
Bacteriocins	Cheonggukjang, soybean paste	Bacillus spp., lactic acid bacteria	Inhibits pathogens, promotes beneficial microbial colonization	Reduced pathogen load, improved microbial balance	In vitro, animal	Spectrum varies by strain; stability in food matrices varies

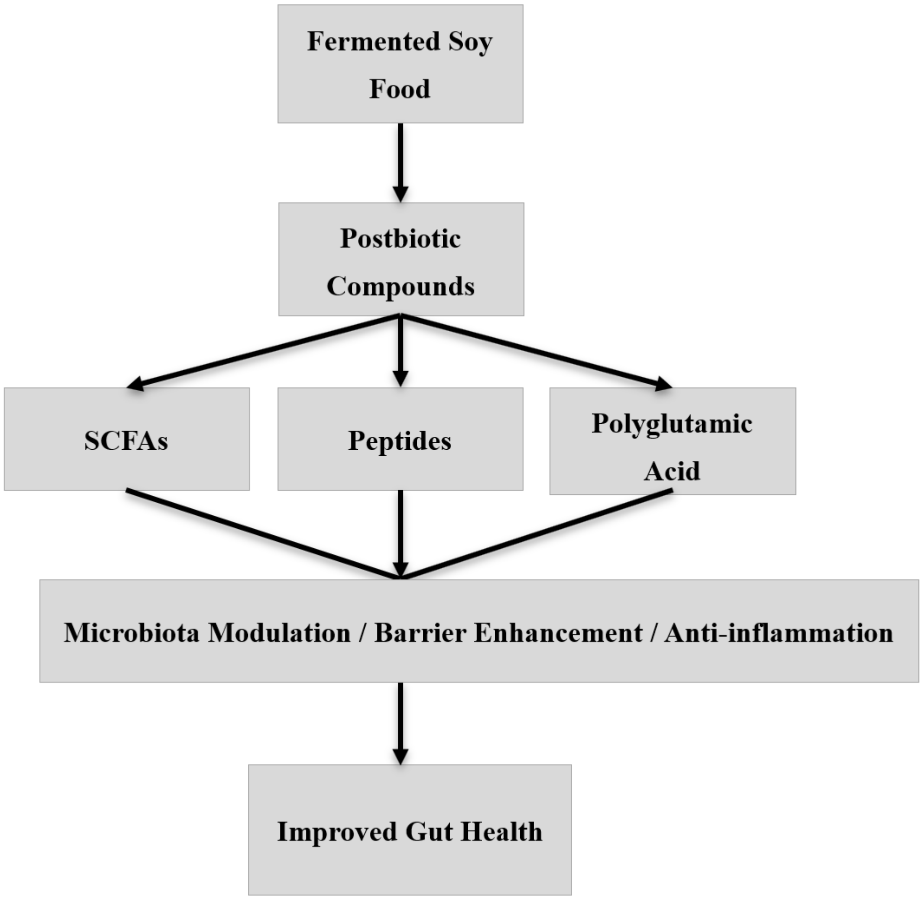

Figure 2. Proposed mechanisms by which postbiotic compounds derived from traditional fermented soy foods promote gut health. SCFAs, bioactive peptides, and polyglutamic acid contribute to microbiota modulation, barrier integrity, and anti-inflammatory effects.

3.4. Comparative Advantages of Postbiotics over Probiotics

Although probiotics have long been the focus of research and product development of intestinal functional foods, there is a growing interest in postbiotics in terms of safety, stability, and applicability in the food industry (Balthazar et al., 2022). One of the most important advantages of postbiotics is their improved stability (Yeşilyurt, Yılmaz, Ağagündüz, & Capasso, 2021). Unlike probiotics, which require careful handling to maintain viability during manufacturing, distribution, and storage, postbiotics remain functionally active even after exposure to heat, oxygen, or acidic environments (Pimentel et al., 2023). Therefore, postbiotics are highly suitable for integration into various food matrices, such as processing, shelf stability, and heat-treated products (Zhong et al., 2024). In terms of safety, postbiotics eliminate risks associated with living microorganisms, such as bacterial migration, opportunistic infections, and unintended changes in host microbiota (Ozma et al., 2022). These risks are especially important for immunocompromised individuals, young children, and the elderly, and live probiotic products can cause health problems (Cohen, 2018). Postbiotics provide controlled and predictable health effects because they are composed of nonviable cells or purified metabolites (Mayorgas, Dotti, & Salas, 2021). Another advantage lies in the possibility of regulation and quality control (Yunes, Poluektova, Belkina, & Danilenko, 2022). The use of inanimate substances facilitates the standardization of dosage and functional components, addressing difficulties in probiotic labeling and claiming viability (Sanders & Levy, 2011). In addition, postbiotics do not face the same strain-specific regulatory hurdles, enabling a more streamlined approval process in the development of functional foods and supplements (Ayesiga et al., 2024). From an industrial point of view, the incorporation of postbiotics into functional food formulations eliminates the need for cold chain logistics and special delivery systems, thereby reducing production costs (Thorakkattu et al., 2022). This diversity also enables the development of new product formats such as fortified drinks, sauces, and capsules, which are not possible in living cultures (Puntillo, Segli, Champagne, Raymond, & Vinderola, 2022). Given these advantages, postbiotics can be a promising alternative to traditional probiotics in both research and applications (Rad, Abbasi, Kafil, & Ganbarov, 2020). Their stable, safe, and scalable properties are in good agreement with current trends in food innovation and consumer demand for scientifically supported, effective health products (Grover, Rashmi, Srivastava, & Batish, 2012).

4. DISCUSSION

The growing interest in postbiotics as health enhancers reflects the widespread shift in the development of functional foods to safety, stability, and mechanical clarity (Prajapati et al., 2023). This review highlights the different types of postbiotics derived from traditional Asian fermented soy foods and the potential mechanisms that support intestinal health (Rafique et al., 2023). However, to fully realize their applications in both research and industry, several limitations and challenges must be addressed. The main limitations are the lack of standardized definitions and classifications for postbiotic compounds in various studies (Vinderola, Sanders, Salminen, & Szajewska, 2022). While recent agreed-upon efforts have clarified the general definition, the exact identity, effective dose, and bioavailability of many postbiotic components are still poorly identified (Abbasi, Hajipour, Hasannezhad, Baghbanzadeh, & Aghebati-Maleki, 2022). For example, studies on polyglutamic acid or bacteriocin often differ in extraction methods, fermentation conditions, and functional analyses, making direct comparisons difficult (Isaac, Mohd Hashim, Faizal Wong, Mohamed Akbar, & Wan Ahmad Kamil, 2025). Another challenge is the limited availability of human clinical data (Liang & Xing, 2023). While in vitro and animal studies strongly support the intestinal regulatory effects of postbiotics, few well-controlled trials have investigated their efficacy in human subjects, especially in the context of fermented soybean foods (Guo et al., 2024; Maftei et al., 2024). Furthermore, most of the existing studies have focused on individual components or isolates, while actual consumption involves complex food matrices and microbial consortia (Kango & Nath, 2024). In terms of food development, the scalability of postbiotic production due to traditional fermentation remains an issue (Terefe, 2022). Traditional fermented soybean foods vary widely due to differences in microbial communities, fermentation times, and local practices. Further studies on the standardization of fermentation processes and identification of stable and reproducible postbiotic profiles are needed to enable consistent use in functional food formulations (Yang et al., 2017). Despite these limitations, the future of postbiotic research is promising (Sharafi, Divsalar, Rezaei, Liu, & Moradi, 2024). Advances in metabolomics, microbiome sequencing, and fermentation technologies provide new tools for identifying and verifying postbiotic compounds (Kumar, Green, & Rawat, 2024). Furthermore, exploring the combined effects of postbiotics and prebiotics or soybean phytochemicals can open new directions for intestinal-targeted nutritional strategies (Lázaro, Vila-Donat, & Manyes, 2024). Overall, the integration of postbiotic science into fermented food research provides a unique opportunity to link traditional dietary practices with modern functional food innovations (Abdul Manan, 2025; Zhang et al., 2025). Addressing the current gap through clinical verification, mechanical elucidation, and industrial standardization is essential for advancing applications in intestinal health care (Heniedy, Mahdy, Elenien, Mourad, & El-Kadi, 2024).

5. CONCLUSION

Traditional Asian fermented soybean foods such as soybean paste, natto, cheonggukjang, and tempeh are rich in a variety of postbiotic compounds such as short-chain fatty acids, polyglutamic acid, physiologically active peptides, and microbial metabolites. These compounds regulate intestinal microorganisms, enhance barrier integrity, and inhibit inflammation, resulting in several beneficial effects on intestinal health. Unlike live probiotics, postbiotics have improved stability, safety, and industrial feasibility, making them an attractive alternative in functional food applications. Due to their resistance to processing conditions and long shelf life, they can be used extensively in product development, especially in heat treatment or display-stable forms. However, further studies are needed to scientifically validate and standardize postbiotic profiles in fermented soybean foods. Clinical trials and mechanistic studies are required to establish evidence-based health claims and guide product design. In conclusion, fermented soybean-derived postbiotics represent a promising class of functional ingredients that can connect traditional diets with modern health sciences. These compounds can play a key role in next-generation strategies to promote intestinal health and overall well-being by increasing understanding of physiological roles and ensuring consistent production.

5.1. Implications

The findings of this review have important implications for food science and functional food development. The identification of postbiotic compounds in traditional Asian fermented soybean foods underscores their potential as stable and safe functional ingredients that can be incorporated into a wide range of food matrices. Compared with live probiotics, postbiotics offer advantages in processing tolerance, storage stability, and formulation flexibility, which are critical considerations for industrial-scale food production. In addition, improved technological understanding of the relationship between fermentation conditions and postbiotic profiles may support the optimization and standardization of traditional fermentation processes. Such advances could facilitate the development of value-added fermented soybean products with reproducible functional properties, thereby enhancing their competitiveness in modern functional food markets. Overall, fermented soybean-derived postbiotics provide a practical bridge between traditional food practices and contemporary food technology applications.

5.2. Limitations

This review has several limitations that should be acknowledged. As a structured narrative review, the synthesis relied on qualitative interpretation of existing studies rather than quantitative meta-analysis, which limits the ability to draw definitive conclusions regarding the magnitude of functional effects. In addition, heterogeneity among included studies, such as differences in fermentation methods, microbial strains, analytical techniques, and reported outcomes, may affect the comparability of findings. Furthermore, much of the available evidence is based on in vitro experiments or animal models, with relatively limited human data directly linking fermented soybean-derived postbiotics to intestinal health outcomes. Variability in the definition and characterization of postbiotics across studies also poses challenges for consistent interpretation.

5.3. Future Research Suggestions

Future research should focus on improving the standardization and characterization of postbiotic compounds in fermented soybean foods, particularly through harmonized analytical methods and clearly defined compositional profiles. Studies investigating the relationship between fermentation parameters and postbiotic yield would be valuable for optimizing production processes. Additionally, well-designed human intervention studies are needed to substantiate functional claims and clarify dose-response relationships and safety considerations. From a food technology perspective, further research on incorporating postbiotics into diverse food systems, including heat-treated and shelf-stable products, would support broader application. Addressing these research gaps will contribute to the evidence-based development of fermented soybean-derived postbiotics as next-generation functional food ingredients.

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