

REVIEW

Healthy Function of Plant-Based Foods Fermented by Lactic Acid Bacteria

Qianqian Guan^{1,2}, Shijin Xiong¹, Tao Xiong¹, Mingyong Xie^{1,*}

¹ State Key Laboratory of Food Science and Resources, Nanchang University, Nanchang, 330047, China

² College of Food Science & Technology Nanchang University, Nanchang, 330031, China

Abstract

Chronic diseases, including cardiovascular diseases, cancer, diabetes, and hypertension, pose significant threats to human health. Epidemiological studies have shown that insufficient dietary fiber intake is closely related to an imbalance in the intestinal flora, jointly driving the high incidence of chronic diseases. The intake of lactic acid bacteria (LAB) and dietary fiber has been proven to help improve dietary patterns and restore gut microbiota balance. LAB-fermented plant-based foods, which integrate LAB and dietary fiber through microbial fermentation of plant substrates, exhibit substantial potential for chronic disease prevention and management. This paper systematically summarizes the fundamental theories, key technologies, as well as engineering challenges involved in the development of LAB-fermented plant-based foods, then focuses on introducing the healthy function of plant-based foods fermented by LAB, and finally looks forward to the future prospects and challenges of this innovative industry.

Keywords: Chronic diseases, Plant-based foods, LAB-fermentation technology, Nutritional health, Industrial applications

*Corresponding Author:

Email: myxie@ncu.edu.cn

About this Article

Received: 09 June 2025

Accepted: 27 June 2025

Published: 15 July 2025

Cite this Article:

Guan, Q.Q., Xiong, S.J., Xiong, T., et al. Healthy Function of Plant-Based Foods Fermented by Lactic Acid Bacteria. *Adv Funct Foods*. 2025;1(1):126–149. doi:10.64187/aff.2025010106

1. Introduction

Despite global advancements in public health, chronic diseases, including cardiovascular disorders, cancer, chronic respiratory diseases, and diabetes, remain the leading cause of global morbidity and mortality, presenting substantial challenges for preventive strategies and clinical management. According to data released by the World Health Organization (WHO) in December 2024, non-communicable diseases (chronic diseases) caused at least 43 million deaths in 2021, accounting for 75% of global deaths unrelated to pandemics.¹ Concurrently, the global incidence of chronic diseases has been steadily increasing these years, with a notable trend toward younger age groups. Studies have identified inadequate dietary patterns as a critical factor contributing to the high prevalence of chronic diseases. A 2019 Lancet study encompassing dietary surveys from 195 countries revealed that one-fifth of global deaths in 2017 were attributable to suboptimal dietary habits, particularly high sodium intake, insufficient whole grain consumption,

and inadequate fruit intake.² Diet-induced gut microbiota dysbiosis has been closely associated with the pathogenesis of chronic diseases, as microbial imbalance can trigger insulin resistance and chronic inflammation, which are the key mechanisms underlying metabolic syndrome, obesity, diabetes, and even cancer.^{3–6} Dietary fiber, a class of indigestible carbohydrate polymers predominantly derived from plant-based foods, plays a pivotal role in modulating gut microbiota and maintaining human health despite providing no direct energy. Extensive epidemiological investigations and clinical trials have demonstrated that increased dietary fiber intake exerts beneficial metabolic effects through gut microbiota modulation, effectively reducing risks of cardiovascular diseases, diabetes, colorectal cancer, overweight, and hypertension.^{7–12}

Plant-based foods, broadly defined as food products derived from plant sources, have evolved into an emerging sector within the global food industry, owing to their health attributes such as low fat and cholesterol content.¹³ These plant-derived ingredients are inherently rich in diverse phytochemicals, including flavonoids, polyphenolic compounds, and dietary fiber, which confer multiple health benefits to plant-based foods, such as antioxidant, anti-inflammatory, and gut health maintenance.^{14–16} Large-scale cohort studies have demonstrated that diets abundant in plant-derived foods, including whole grains, fruits, vegetables, nuts, and legumes, can significantly reduce the risks of chronic conditions, such as type 2 diabetes, hyperlipidemia, and cardiovascular diseases.^{17,18} LAB-fermentation, an advanced food processing technology with over a century of application in dairy industries, has established a substantial global market for fermented dairy products. In contrast to other fermentation technologies (e.g., yeast fermentation), LAB fermentation technology has unique advantages in the development of functional foods, distinguished by its significant healthy function, distinctive flavor profiles, and highly controllable fermentation process. In recent years, alongside the global expansion of plant-based food markets, the application of LAB fermentation technology in plant-based food systems has garnered increasing attention. This growing interest stems from the dual benefits of LAB fermentation: it not only enhances the nutritional profile and flavor characteristics of plant-based foods but also significantly amplifies their health-promoting properties, which holds critical importance for improving public nutritional health status and advancing strategies for chronic disease prevention and mitigation.

Over recent years, a variety of LAB-fermented plant-based food products have emerged in the market, including LAB-fermented fruit and vegetable products, LAB-fermented plant protein-based products, LAB-fermented cereal-based products, and LAB-fermented medicinal-edible homologous products (Table 1). These innovations not only substantially meet consumers' growing demand for health-oriented foods but also create novel development opportunities for the food industry.

Overall, the development of LAB-fermented plant-based foods constitutes an intricate process involving multiple stages such as strain screening, starter culture preparation, fermentation process development, and engineering scale-up. Several key scientific and technological challenges will be involved during this process, such as: 1) How to screen high-performance LAB strains suitable for the fermentation of plant-based substrates? 2) How to prepare highly active plant-based starter cultures? 3) How to establish a direct vat inoculation (DVI) process for plant-based fermentation and achieve industrial-scale production? 4) How to evaluate the health functionalities and safety profiles of both the LAB strains and their fermented products? etc. Addressing these challenges will provide crucial scientific foundations for developing LAB-fermented plant-based foods with demonstrable healthy function.

In this study, the fundamental theories (e.g., microbial community succession, flavor formation mechanisms), key technologies (e.g., high-efficiency strain screening, high-activity LAB agents preparation), as well as the engineering challenges related to the development of LAB-fermented plant-based foods were reviewed, the potential healthy function of LAB-fermented plant-based foods was summarized, and the future research directions of this innovative industry were discussed, aiming to offer references to drive innovative research and foster the creation of novel LAB-fermented plant-based food products.

Table 1. Some commercial LAB-fermented plant-based products in the market.

Product Category	LAB-Fermented Plant-Based Foods	Manufacturing Company/Brand
LAB-fermented fruit and vegetable products	Fermented coconut juice/Triple berry juice/Composite fruit and vegetable juice	GoodBelly
	Multiple fermented fruit and vegetable juices	Fresh Del Monte Produce Inc
	Fermented cranberry juice	Ocean Spray
	Fermented lemon juice/Fermented pitaya (dragon fruit) juice/ Fermented tangerine juice	Bio-E
	Fermented pineapple juice/Fermented orange juice/Fermented carrot juice	Golden Circle
	Composite fermented vegetable juice (beetroot, carrots, potatoes, celery root, etc.)	Biotta
	Fermented carrot juice/Fermented mulberry juice/Fermented mango juice/Fermented pomegranate juice/ Fermented bitter melon juice/Fermented mulberry jelly/ Fermented mango jelly	JIANGZHONG FOOD THERAPY
	Fermented fruit juice jelly	Labixiaoxin (Fujian) Foods Industrial Co., Ltd
	Fermented banana milk	Beijing Sanyuan Foods Co., Ltd/Jiangxi Sunshine Dairy Co., Ltd
	Fermented fruit and vegetable puree; Fermented carrot juice/Fermented mango juice/ Fermented pear juice/ Fermented mulberry juice	Jiangxi Kuangda Biotechnology Co., Ltd
	Fermented fruit and vegetable ice cream	Jiangxi Yiweier Food Co., Ltd
	Fermented Korla pear juice	Xinjiang Avatina Agricultural Development Co., Ltd
	Fermented Vegetable products	1.8 Meters Technology Holding Limited/Yunnan Hongbin Green Food Group Co., Ltd
	Fermented fruit and vegetable juice	PERFECT (CHINA) CO., LTD
LAB-fermented plant protein-based products	Fermented soy milk	Marusan/Soybio
	Plant-based yogurt made from coconut cream, pea protein, and potato protein	Daiya
	Cashew-based plant yogurt	Danone
	Coconut cream-based plant yogurt	Chobani/KoKo/Coyo
	Almond-based plant yogurt	Good Plants
	Plant-based yogurt made from soy, almonds, and coconut milk	Stonyfield Organic
	Soy-based plant yogurt	Dali Foods Group Company Limited
	Soy-based plant yogurt	Nongfu Spring
	Coconut and soy-based plant yogurt	Beijing Sanyuan Foods Co., Ltd.
	Fermented walnut beverage	Hebeiyangyuanzhahui Beverage Co.,Ltd.
LAB-fermented cereal-based products	Oat-based plant yogurt	Valio/Hälsa Foods/OATLY
	Fermented rice beverage	JIANGZHONG FOOD THERAPY
	Fermented cereal beverage	Shandong Gu Gan Food Co., Ltd.
LAB-fermented medicinal-edible homologous products	Fermented beverage made from natural plants that are both food and traditional medicinal ingredients, such as hawthorn, ginkgo nut, cassia seed, lily bulb, malt, kelp, goji berry, lotus seed, and pueraria root	Jiangsu Hengkang Biotechnology Co.,Ltd.
	Fermented beverage made from natural plants that are both food and traditional medicinal ingredients, such as Inula britannica, Coix seed, red beans, ginseng, and dried tangerine peel	Jiangsu LiJian Life Science & Technology Development Co., Ltd.
	Fermented ginkgo nut beverage	Lunan Pharmaceutical Group Co., Ltd
	Fermented ginseng beverage	Nuspower Greatsun (Guangdong) Biotechnology Co., Ltd

2. Basic Theory Research Related to LAB-Fermented Plant-Based Foods

2.1 Diversity of LAB and Their Succession Rules in Traditional Fermented Plant-Based Foods

During the maturation process of fermented foods, the microbial community structure showed regular dynamic changes with the prolongation of time and changes in environmental parameters, which directly determined the stability of product quality.¹⁹ Therefore, it is important to reveal the microbiota succession patterns during the fermentation of traditional fermented foods for the control of fermented food quality. In recent years, with the wide application of high-throughput sequencing and multi-omics technologies, there have been more and more reports on the diversity of LAB and their succession patterns in traditional plant-based fermented foods. The understanding of the complex microbial community structure and its dynamic changes during the fermentation process has also gradually deepened. For instance, many studies have found that *Serratia*, *Bacillus*, and *Rhizobium* dominated in the pre-fermentation stage and gradually shifted to heterofermentative LAB (e.g. *Leuconostoc mesenteroides*, *Lactobacillus sakei*, and *Weissella koreensis*) in the mid- and late-fermentation stages^{20–22}; the microbiota gradually evolved from *Pseudomonas* in the early fermentation stage to *Lactococcus* spp. and *Lactobacillus* spp. in the later fermentation stage during the fermentation of the Germany sauerkraut.^{23,24} We have revealed the universal pattern of microbial succession during the fermentation process of Chinese traditional fermented vegetables by systematically analyzing the microbial diversity in many typical Chinese traditional fermented vegetables, such as Sichuan Paocai^{25,26}, Jiangshui²⁷, Suansun²⁸, Laotan Suancai²⁹, Yancai³⁰, Chinese spicy cabbage³¹, and Dongbei Suancai³²: Heterofermentative microbiota (e.g. *Leuconostoc*, *Lactococcus*, and *Pediococcus*) with the facultative anaerobic ability dominated in the initial fermentation stage, and gradually succeeded to acid-resistant homofermentative LAB with the decrease of pH and the accumulation of metabolites. In addition, in some fermented foods with higher salinity, the microbial communities change towards a trend of being more tolerant of high-salt environments. For example, during the industrial fermentation of mustard Paocai, *Halomonas* and *Lactiplantibacillus* replaced the salt-sensitive microbiota through competitive proliferation in the initial stage (salt concentration 5%–6%), and the proportion of extreme salt-tolerant bacteria *Halanaerobium* was significantly increased and gradually became the dominant genus in the second stage (salt concentration 6%–7%).³³ This dual driving mechanism of metabolic type transition (heterolactic fermentation → homolactic fermentation) and environmentally adapted evolution (generalized bacteria → extremophiles) essentially reflects the dynamic response strategy of microbial communities to the fermentation microenvironment. The microbial diversity and succession process of traditional plant-based fermented food are jointly regulated by biotic and abiotic factors, where biotic factors include microbial interactions, domestication, and lifestyle, and abiotic factors include environmental selection pressures such as temperature, salinity, pH, and substrate. The process of microbial community assembly can be classified as drift, diversification, dispersal and selection based on the neutral theory and the ecological niche theory. The dynamic succession of microbial communities during the fermentation of traditional plant-based fermented foods can be systematically elucidated by community assembly theory, which is driven by dispersal and selection. Understanding the microecological succession of traditional plant-based fermented foods contributes to the consistency and safety of product quality in industrial production.

2.2 Mechanistic Insights into Microbial-Mediated Flavor Formation in Traditional Fermented Plant-Based Foods

The formation of characteristic flavors in traditional fermented foods essentially results from synergistic metabolism of complex microbial consortia, involving intricate precursor transformation networks and metabolic regulation mechanisms. Elucidating the microbial-driven flavor formation mechanisms in plant-based fermented products and identifying functionally important microorganisms during fermentation provides crucial theoretical foundations for modernizing traditional fermentation technologies. Over the past years, a growing number of researchers have employed foodomics technologies, particularly metagenomics,

metatranscriptomics, and metabolomics, combined with multivariate statistical analysis methods, to elucidate the flavor formation mechanisms in plant-based fermented foods. For instance, Hu et al.³⁴ identified four fungal genera (*Kodamaea*, unclassified Dipodascaceae, *Geotrichum*, and *Trichosporon*) and nine bacterial genera (*Lysinibacillus*, *Enterococcus*, *Acidipropionibacterium*, *Bifidobacterium*, *Corynebacterium*, *Lactococcus*, *Pseudomonas*, *Enterobacter*, and *Acinetobacter*) as core functional microorganisms contributing to the characteristic flavor of fermented stinky tofu using amplicon sequencing and statistical methods. Additionally, Xiang et al.³⁵ revealed positive correlations between key flavor components (phenylethanol, phenylacetaldehyde, furfural, and various organic acids) and specific microbial species (*Lactobacillus agilis*, *Kocuria koreensis*, *Lactobacillus delbrueckii*, *Lactobacillus brevis*, and *Lactobacillus curvatus*), and elucidated the metabolic pathways of these key aroma compounds through metagenomics and multivariate statistical analysis in Pixian doubanjiang. Our research team has previously reconstructed the metabolic regulatory networks of flavor quality, revealed the formation mechanisms of characteristic flavors, and identified the core functional microorganisms involved in flavor development in traditional Chinese fermented plant-based foods, including Sichuan paocai³⁶, Laotan Suancai³⁷, sour bamboo shoots³⁸, and soy sauce³⁹, using metagenomics, metatranscriptomics, and metabolomics approaches. The metabolic pathways of characteristic flavor of Laotan Suancai were reconstructed, and the *Companilactobacillus alimentarius*, *Weissella cibaria*, *Lactiplantibacillus plantarum*, and *Loigolactobacillus coryniformis* were identified as the core functional microbes and engaged in the formation of characteristic flavor compounds via the metatranscriptome and metabolome.³⁷ As exemplified by soy sauce fermentation studies, based on the relevant fermentative microorganisms, FAAs, annotated enzymes, and detected BAs during soy sauce fermentation, we constructed a metabolic network of biogenic amine synthesis during brewing (as shown in Figure 1) by integrating metagenomic and metabolomic datasets with KEGG pathway mapping, revealing that histamine-related genes were primarily encoded by *Klebsiella* spp., tyramine-related genes were mainly produced by *Bacillus* spp., and phenylethylamine-related genes were predominantly derived from *Enterobacter*, *Staphylococcus*, *Klebsiella*, and *Bacillus*. Although current studies have established a preliminary “microbiota-metabolite-flavor characteristics” correlation framework, most conclusions remain based on correlation analyses. These correlations still need to be confirmed by further experimental validation. For example, the ability of different strains to express key flavor synthesis-related enzymes and to generate key flavor compounds can be quantified at the metabolic and transcriptional levels under pure culture conditions. In addition, confirmation of the ability of core functional microbes to regulate the formation of characteristic flavors in real fermentation systems by synthetic microbial community fermentation is important for the precise regulation of flavor-directed fermentation processes in industrial production.

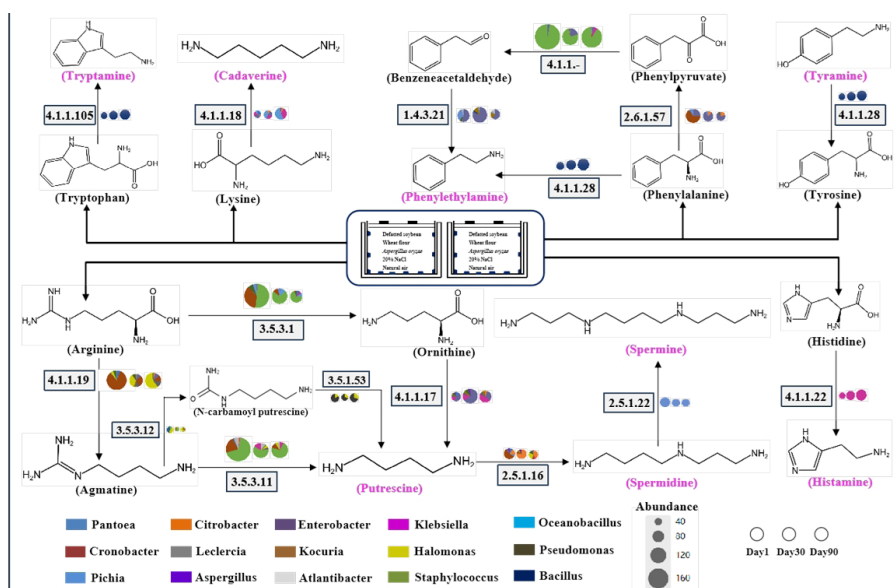


Figure 1. Biosynthesis pathways of biogenic amines in soy sauce and the expression of genes encoding amine-producing enzymes.

2.3 Functional Genes Exploration of Elite Fermentative Microbial Strains for Traditional Fermented Plant-Based Foods

The genomic resources of plant-based fermentative microbial strains harbor the genetic basis driving metabolic diversity. Systematic characterization of their functional genes holds strategic significance for optimizing fermentation processes, developing functional products, and enabling synthetic biology applications. Through whole-genome sequencing analysis, our research team has conducted pioneering genomic characterization of three high-performance plant-based fermentation strains: *Lactiplantibacillus plantarum* NCU116, *Lactobacillus acidophilus* NCU402, and *Lacticaseibacillus paracasei* NCU215. The genomic investigations revealed that all three strains possess conserved genetic features, including extracellular polysaccharide (EPS) biosynthesis gene clusters, class II bacteriocin (e.g., plantaricin) biosynthetic operons, and carbohydrate-active enzyme (CAZyme) gene families encoding galactosidases and pectate lyases.^{40,41} These genetic elements not only account for the strains' plant biomass degradation capabilities but also elucidate molecular mechanisms underlying their ability to enhance product texture and functional properties. Recent studies have further substantiated strong genotype-phenotype correlations in fermentative microbes. For instance, Beck et al.⁴² employed comparative genomic analysis to demonstrate that *Lactiplantibacillus plantarum* ATG-K2, isolated from kimchi, exhibits significantly reduced abundance of carbohydrate metabolism genes compared to its phylogenetic relatives ATG-K6 and ATG-K8. This genomic characteristic correlates with its distinct growth phenotype in saccharide-rich matrices. Furthermore, the observed capacity of ATG-K8 to elicit elevated TNF- α production concomitant with reduced IL-10 levels was mechanistically linked to genomic variations within specific immunomodulatory gene clusters. Furthermore, Tamang et al.⁴³ conducted a comprehensive whole-genome analysis of *Bacillus subtilis* Tamang, a strain isolated from the traditional fermented food kinema, which elucidated the genetic determinants underlying its high-yield production of γ -polyglutamic acid (γ -PGA), fibrinolytic enzymes, and vitamins, as well as its probiotic functionalities. The study further substantiated the strain's potential as a food-grade microbial culture through rigorous safety assessments. Despite the establishment of preliminary genotype-phenotype-function correlation frameworks in current research, two critical challenges remain unresolved: Firstly, the metabolic regulatory networks of most functional genes await experimental validation through targeted gene knockout or overexpression studies; secondary, comprehensive characterization of cross-species genetic resources and advancement of synthetic biology toolkits are still in early developmental phases. Future studies should combine CRISPR gene editing and other technologies to deeply analyze the spatiotemporal expression patterns of key genetic elements, which will provide theoretical support for the precise design of high-efficiency fermentation strains.

3. Key Technological Breakthroughs in LAB-Fermented Plant-Based Foods

3.1 Screening of Superior LAB Strains Specifically for Plant-Based Foods Fermentation

Traditional plant-based fermented foods (e.g., kimchi, sauerkraut, and fermented soybean milk) harbor abundant microbial resources, which can provide scientific support for the industrialization and modernization of the production of traditional plant-based fermented foods. To address the challenges of strain specificity, extensive research has focused on screening LAB strains from traditional plant-based fermented foods. For example, Molina et al.⁴⁴ isolated two LAB strains from bees, namely *Leuconostoc pseudomesenteroides* NFICC 2004 and *Lactococcus lactis* NFICC 2005, and found that the co-fermentation of these two strains could increase the acidification rate of plant-based materials, including soybeans, peas, oats, and potatoes, and effectively remove the main off-flavor compounds originally present in the plant-based materials. Xiao et al.⁴⁵ isolated 136 LAB strains from 73 naturally fermented plant-based food samples. These strains were inoculated into plant-based materials such as coconut, oats, rice, hemp, peas, hazelnuts, and soy milk for fermentation, and the results showed that *Enterococcus casseliflavus*

and *Lactobacillus sakei* were identified as efficient butter aroma producers in most plant-based materials, indicating that the two strains can be used as excellent plant-based fermentative strains for the development of LAB fermented plant-based foods. Bocchi et al.⁴⁶ screened *Lactobacillus* and *Bifidobacterium* strains with excellent fermentation properties and used these two strains to ferment oats, results showed that after fermentation, the contents of specific amino acids, vitamins, and polyphenols (flavonoids and phenolic acids) in the oat beverage significantly increased, while the content and structure of the oligosaccharides rich in oats remained unchanged.

With the development of the LAB-fermented plant-based food industry, an increasing number of enterprises have begun to pay more attention to the development of plant-based fermentation starters. For instance, Chr. Hansen A/S has developed the VEGA™ Culture Kit specifically for the production of fermented plant-based foods, which included fermentative strains for optimizing the taste and texture, as well as probiotic strains such as *Bifidobacterium bifidum* BB-12 and *Lactobacillus rhamnosus* LGG.⁴⁷ DuPont Danisco, another company of significant standing in the probiotics field, has developed a series of plant-based fermentation agent named Danisco® VEGE Cultures, which can be used for the fermentation of a variety of plant-based raw materials such as soybeans, coconuts, nuts, oats, corn, rice, fruits, and vegetables.⁴⁸ Weikang Probiotics (Suzhou) Co., Ltd, a Chinese company specializing in the probiotics industry, has selected several LAB strains with excellent plant-based fermentation properties, such as the soy-based fermentation strain PLF-101, which could reduce beany flavor, the high-acid-producing soy-based fermentation strain PLF-201, the coconut milk fermentation strain PLF-102, the oat milk fermentation strain PLF-103, etc. These strains can be widely applied in the production of various plant-based fermented foods, including fermented soy drinks, coconut milk, oat drinks, and so on.⁴⁹

Our research team has developed a high-throughput screening system tailored for LAB strains in plant-based fermentation. To date, over 8,000 plant-based fermentation-specific strains have been isolated from more than 2,000 traditional fermented plant samples, among which 386 strains with outstanding functional properties were identified. Some typical examples with healthy function isolated and preserved by our team are listed in Table 2.

Table 2. Some typical LAB strains with healthy function isolated and preserved by our team.

The LAB strains	Healthy Function	References
<i>Lactiplantibacillus plantarum</i> NCU116	immune-regulatory effects, constipation relief, hyperlipidemia inhibition, and gut microbiota modulation	[50–58]
<i>Lactocaseibacillus rhamnosus</i> NCU2217	alleviate constipation and suppress fatty liver development	[59,60]
<i>Limosilactobacillus reuteri</i> NCUH003/ <i>Lactiplantibacillus plantarum</i> NCUH046 / <i>Limosilactobacillus fermentum</i> NCUH068	weight-loss and lipid-lowering activities	[61]
<i>Limosilactobacillus fermentum</i> NCU001464/ <i>Limosilactobacillus fermentum</i> NCU003018/ <i>Lactocaseibacillus rhamnosus</i> NCUH061012/ <i>Limosilactobacillus fermentum</i> NCU326	uric acid-lowering effects	[62–66]
<i>Lactiplantibacillus plantarum</i> NCUH001003	antagonize <i>Helicobacter pylori</i>	[67–69]
<i>Lactocaseibacillus paracasei</i> NCUH012072/ <i>Limosilactobacillus fermentum</i> NCUH003081/ <i>Limosilactobacillus reuteri</i> NCUH064006	blood glucose-lowering effects	[70]
<i>Lactiplantibacillus plantarum</i> NCU0011098/ <i>Lactiplantibacillus plantarum</i> NCUH001084/ <i>Lactiplantibacillus plantarum</i> NCU0011129	antagonistic activity against colorectal cancer	[71]

3.2 Preparation of High-Activity LAB Agents for Plant-Based Foods Fermentation

High-density cultivation is an essential foundation for the large-scale production of high-activity direct vat-set starter. High-density fermentation technology creates the optimal growth environment for LAB strains by optimizing the composition of the culture medium, precisely controlling the culture temperature, real-time adjusting the pH value, and timely supplementing nutrients to the bioreactor, thereby maintaining a high growth rate of the bacterial cells.^{72–74} Currently, this technology can achieve a bacterial density of LAB that is more than ten times higher than that of static culture. Furthermore, personalized optimization strategies tailored to specific LAB strains, such as refining culture conditions for high-density fermentation

and adjusting medium composition can significantly enhance LAB viability. For instance, Wang et al.⁷⁵ achieved a 9-fold increase in *Lacticaseibacillus rhamnosus* LS-8 density (4.50×10^9 CFU·mL⁻¹) by simplifying the culture medium and controlling key fermentation parameters (constant pH, neutralizer type, aeration rate, and agitation speed); While Ding et al.⁷⁶ reported a 6-fold improvement in *Lactiplantibacillus plantarum* Y44 density (3.36×10^{10} CFU·mL⁻¹) through medium formula optimization and precise fermentation condition control.

Preserving the long-term viability of LAB strains and extending their shelf life remain critical challenges in the production of high-activity direct vat-set starter. In industrial applications, vacuum freeze-drying is the gold-standard technique, removing $\geq 95\%$ of cellular moisture under low-temperature and anaerobic conditions, rendering the LAB strains extremely “dry” and inducing a state of deep dormancy. This effectively halts cellular metabolic activities, which only resume upon rehydration, thus restoring the cells’ activity. Thus, this method not only preserves the activity of LAB strains but also enhances their stability during long-term storage.

However, the extreme cold during freeze-drying can elicit a stress response in bacterial cells. This leads to increased cell membrane permeability⁷⁷, decreased membrane fluidity⁷⁸, denaturation of enzymes and proteins⁷⁹, and changes in genetic material⁸⁰, all of which may cause cell inactivation. Therefore, improving the survival rate of LAB during freeze-drying remains a critical technical hurdle to be addressed in the industrialization of LAB. Currently, two primary strategies have been reported to enhance the activity of bacterial cells during the freeze-drying process. The first one involves modulating the intrinsic physiological state of the strains, which can be achieved by optimizing the culture medium to promote biofilm formation⁸¹ or by altering the ratio of unsaturated fatty acids in the bacterial cell membrane.^{82,83} Additionally, pre-treatment methods such as cold stress, heat stress, acid stress, or a combination of these stresses can be applied to enhance the freeze tolerance of LAB.^{84–86} The second strategy focuses on minimizing the damage caused by freeze-drying, and it can be done by identifying the optimal formulation of cryoprotectants^{87,88}, optimizing the parameters of pre-freezing and freeze-drying processes^{89–91}, and utilizing high-quality freeze-drying equipment.

3.3 The Engineering Challenges of LAB-Fermented Plant-Based Foods

Our team has been engaged in the research and development of LAB-fermented plant-based foods for over 20 years, achieving a series of breakthroughs in this field. Particularly in the area of LAB-fermented fruits and vegetables, we have constructed a new technology for the direct production of LAB-fermented fruit and vegetable and achieved its industrialization, developed a series of new products, such as LAB-fermented fruit and vegetable puree, beverage, etc. Proudly, these products are currently selling well in the market and have won the deep affection of consumers. Nevertheless, critical challenges continue to exist in the industrial-scale production of LAB-fermented plant-based foods.

3.3.1 The Stability Issue of the Product During Large-scale Fermentation

Plant-based substrates differ from dairy in their compositional complexity and variability. During large-scale fermentation, inconsistent parameters (e.g., the consistency of the fermentation liquid, tank pressure, and pH value) between the upper and lower parts of the fermentation tank exacerbate quality control challenges. To address this issue, in addition to ensuring the stability of plant-based raw materials, it is also necessary to focus on screening strains with robust tolerance to fluctuating environmental conditions as well as deploying real-time monitoring systems (e.g., pH, dissolved oxygen) and dynamic agitation strategies to ensure homogeneity.

3.3.2 Post-Acidification Control

Post-acidification poses a significant challenge in the large-scale production of yogurt, and it is equally problematic in the large-scale fermentation of plant-based materials. In live-bacteria products, LAB continue to grow and reproduce slowly during transportation and sales, leading to further fermentation and acid production. This post-acidification can negatively impact the taste and flavor of the product, resulting in a decline in sensory quality and potentially compromising the overall product quality and shortening its shelf

life. Thus, screening for acid-sensitive strains with growth arrest at predefined pH thresholds is crucial for addressing this issue effectively.

4. Research on the Healthy Function of LAB-Fermented Plant-Based Foods

LAB fermentation can improve the flavor and texture of plant-based raw materials, enhance their nutritional value, boost the health attributes, endowing LAB-fermented plant-based foods with more diverse health benefits. On the one hand, LAB fermentation can effectively degrade anti-nutritional factors in plant-based raw materials such as phytic acid, tannins, and protease inhibitors, thereby significantly improving the bioavailability of nutrients.⁹² On the other hand, during the fermentation process, LAB can secrete enzymes like pectin lyases (EC 4.2.2.10), feruloyl esterases (EC 3.1.1.73) and cellulases (EC 3.2.1.4) to break down cellulose, hemicellulose, and lignin in plant cell walls, facilitating the release of natural bioactive compounds such as flavonoids (e.g., quercetin aglycones with enhanced bioactivity from glycosides), glycosides, and alkaloids via ester bond cleavage and other mechanisms.^{93,94} For example, Pectin lyases can catalyze the β -elimination of ester bonds in pectin, releasing galacturonic acid oligomers, while cellulases can degrade cellulose microfibrils via endo- and exo-acting mechanisms, with β -glucosidases (EC 3.2.1.21) hydrolyzing cellobiose to glucose. In addition, the production of bioactive substances such as short-chain fatty acids (SCFAs), exopolysaccharides (EPSs), and ACE-inhibiting bioactive peptides during fermentation can further enhance their health benefits.⁹⁴ The current research reports on the healthy function of LAB-fermented plant-based foods were summarized in Table 3, including immunomodulatory, anti-obesity, antihyperuricemic, blood glucose regulatory, and anti-tumor activities. However, it should be noted that current reports on these healthy functions are almost entirely based on animal or cell experiments, further clinical trials are needed to validate these functions.

4.1 Immunomodulatory Activity

Immune imbalance, defined as disordered immune system function, manifests as abnormal enhancement or attenuation of immune responses, thereby disrupting physiological homeostasis and often triggering or exacerbating inflammatory reactions, including persistent or excessive inflammation. Research has demonstrated that LAB-fermented plant-based foods can modulate systemic immunity by mitigating blood inflammatory markers and alleviating inflammatory responses. For example, WASTYK et al.¹³⁰ conducted a 17-week randomized prospective trial with 36 healthy volunteers aged 39-61 and found that fermented foods could reduce the levels of inflammatory cytokines such as IL-6, IL-18, and IL-12b in the subjects' serum, inhibit the overreaction of immune cells, and the decline of inflammatory markers was consistent with the increase in microbial diversity. Another study by Zhao et al.⁹⁹ found that gavage administration of fermented fig extract could enhance the immune response in mice, improve their body weight, immune organ indices (liver, thymus, spleen), and the histopathological condition of immune organs, boost the production of immune-related cytokines such as IL-4, IL-6, TNF- α , and IFN- γ in mice, and alleviate the damage to immune organs. Moreover, bioactive substances such as SCFAs produced from fermentation have also been reported to have the effect of activating the immune system, enhancing the activity of immune cells, and promoting the balanced secretion of cytokines, thereby enhancing the body's immune defense capabilities. Fu et al.¹⁰⁰ found that fermented sea buckthorn juice could increase the SCFAs in tumor-bearing mice, improve gut microbiota dysbiosis (promote the proliferation of beneficial bacteria and inhibit the generation of harmful bacteria), and promote the balanced secretion of cytokines (increase TNF- α , INF- γ , and decrease IL-1 β , IL-6, IL-10, etc.), thereby activating the anti-tumor immune response in tumor-bearing mice and inhibiting tumor-promoting reactions. What's more, LAB-fermented oats were also reported to significantly improve the levels of serum immune-inflammatory factors in healthy adults, with notable decreases in pro-inflammatory cytokines such as IL-1 β , IL-6, and TNF- α , and an increase in the anti-inflammatory cytokine IL-10. Additionally, this fermentation process also significantly promoted the proliferation of beneficial gut bacteria, including *Bifidobacterium*, *Lactobacillus*, *Akkermansia muciniphila*, and *Faecalibacterium prausnitzii*.¹³¹

Our team utilized *Lactiplantibacillus plantarum* NCU137, which was previously screened from traditional fermented vegetables for its superior plant fermentation capabilities, to ferment adlay seeds, investigating the immunomodulatory and intestinal barrier-regulating effects of the fermented product. Results showed that fermented adlay seeds significantly increased the spleen and thymus indexes of immunosuppressed mice, up-regulated the cluster of differentiation(CD)4+/CD8+ratio of spleen t lymphocytes, while down-regulated the levels of spleen pro-inflammatory cytokines, and increased serum immunoglobulin(Ig)M and IgG levels, indicating that the ferment adlay seeds have the potential to regulate immune and intestinal mucosal barrier function.¹³²

Table 3. Healthy function of LAB-fermented plant-based foods in the literature studies.

Beneficial Health Effects	Fermented Plant-Based Foods	Animal/Cell Model	Main Conclusion	References
Immunomodulatory Activity	Cheonggukjang (fermented soybean food)	Cyclophosphamide-treated immunosuppressed rat	regulate Firmicutes/Bacteroidetes ratio, promote the IL-2, IL-12, IFN- γ and IgG productions in immunosuppression status, increase proliferation of splenocyte and NK cell activity, activate MAPKs and NF κ B pathways	[95]
	Cheonggukjang (fermented soybean food)	Immunosuppressed SPF KM male mice	restore the decreased lymphocytes proliferation, natural killer cell activity, and white blood cell count	[96]
	Fermented sweet potato	Common carp	affect the normal morphology or structure of the head, kidney, spleen or intestine of the common carp, and to a certain extent, and induce a non-specific immune response	[97]
	Fermented liquid derived from Aloe vera leaves	LPS-induced RAW 264.7 cells	decrease the synthesis of IL-1 β , IL-6, and TNF- α at both the mRNA and protein levels	[98]
	Fermented fig (<i>Ficus carica</i> L.) fruit extracts	CTX-treated male KM male mice	improved immune organ indexes, alleviated immune organ injuries, promoted the production of immune-related cytokines, improved the histopathological state of immune organs, and modulated the composition of the gut microbiota	[99]
	Ferment sea buckthorn juice	A CT26 xenograft tumor-bearing murine model	increased the TNF- α and INF- γ and decreased the IL-1 β , IL-6, and IL-10, increased SCFAs levels and improved intestinal microbiota dysbiosis	[100]
	Rosa roxburghii Tratt Juice (fermented juice)	STZ-induced type 2 diabetes mellitus KM male mice	reverse dyslipidemia, relieve oxidative stress, increase SCFAs levels, and regulate the composition of gut microbiota	[101]
	Fermented sorghum	STZ-induced type 2 diabetes mellitus C57BL/6 male mice	ameliorate hyperglycemia, promote the growth of beneficial bacteria, decrease the serum concentration of microbial metabolites, and regulated the bile acid metabolism	[102]
	Fermented dietary fiber from soy sauce residue	STZ-induced type 2 diabetes mellitus C57BL/6 male mice	enhance hepatic glucose metabolism via the IRS-1/PI3K/AKT/mTOR pathway, regulate gut microbiota composition, and restore the G-protein-coupled receptors (GPRs) expression	[103]
	Kombucha (fermented tea soup)	STZ-induced type 2 diabetes mellitus KM male mice	increase the abundance of SCFAs-producing bacteria, reduce the damage of intestinal barrier, reduce the displacement of LPS, increase the SCFAs and improve islet β cell function by promoting the secretion of gastrointestinal hormones (GLP-1/PYY)	[104]
Blood Glucose Regulatory Activity	Bambusa nutans fermented shoot extracts	STZ-induced type 2 diabetes mellitus LACA male mice	improve body weight loss, reduce LDH activity and LPO level, decrease the liver enzymes (SGPT, SGOT, ALP, and bilirubin levels), increase the albumin and A/G ratio, enhance antioxidant activities and improve the hepatocytes and central vein structure	[105]
	Fermented polygonatum sibiricum	STZ-induced type 2 diabetes mellitus SPF C57BL/6 male mice	protect against glucose intolerance and insulin resistance, ameliorate the lipid accumulation in liver and white adipose tissue (WAT), enhance lipolysis and fatty acid oxidation, strike anti-inflammatory effect and enhance the activation of AMPK	[106]
	Two peptides from soy-fermented douchi	STZ-induced type 2 diabetes mellitus SPF C57BL/6 male mice	reduce insulin resistance, hyperglycemia, inflammation, liver injury, and lipid accumulation, regulate insulin and AMPK signaling pathways and reverse HFD-induced gut dysbacteriosis	[107]
	The phenolic extract from fermented <i>Psidium guajava</i> leaves	STZ-induced type 2 diabetes mellitus KM male mice	improve the serum glucose-lipid profiles as well as insulin resistance, modulate the gut microbiota, increase levels of SCFA, activate G protein-coupled receptor signaling, and restore serum metabolite disorders	[108]

Beneficial Health Effects	Fermented Plant-Based Foods	Animal/Cell Model	Main Conclusion	References
Anti-Obesity Activity	Fermented mixed vegetable juice	High-Fat Diet-induced obese C57BL/6J mice	decrease fat mass, reduce levels of TC, TG, leptin, and hepatic lipid accumulation, and downregulated expression of lipogenesis-related genes	[109]
	Fermented blueberry pomace liquid	High-Fat Diet-induced obese C57BL/6J mice	decrease fat mass, reduce levels of TC, TG, and LDL-C, decrease inflammation levels, and downregulate expression of lipid synthesis-related proteins	[110]
	<i>Lactobacillus plantarum</i> -fermented aloe vera juice	High-Fat Diet-induced obese C57BL/6J mice	reduce fat accumulation, decrease levels of TC, ALT, and IL-10, and improve gut microbiota structure	[111]
	<i>Lactobacillus</i> OPC1-fermented lemon juice	High-Fat Diet-induced obese Wistar rats	decrease levels of TC and TG, downregulated expression of lipid metabolism-related genes such as SREBP-1c, PPAR γ , and ACC, and improve gut microbiota	[112]
	<i>Lactobacillus kisonensis</i> -fermented black barley	High-Fat Diet-induced obese SD rats	decrease levels of TC, TG, and unsaturated fatty acids in serum and adipose tissue, and improve oxidative stress and liver metabolism	[113]
	<i>Lactobacillus brevis</i> FZU0713-fermented kelp liquid	High-Fat Diet-induced obese SD rats	decrease liver and fat mass, reduce serum TC and TG levels, and increase fecal SCFAs	[114]
	Probiotic fermented blueberry juice	High-Fat Diet-induced obese C57BL/6J mice	decrease TG levels, increased HDL-C levels, improve insulin resistance, inflammation, lipid metabolism, and gut microbiota, and elevate fecal SCFAs levels	[115]
	<i>Lactobacillus plantarum</i> EM-fermented cabbage-apple juice	High-Fat Diet-induced obese SD rats	decrease fat mass, reduce levels of TC, TG, LDL-C, and downregulate expression of the FAS and ACC genes	[116]
	<i>Lactobacillus plantarum</i> S-811-fermented prickly pear juice	High-Fat Diet-induced obese C57BL/6J mice	decrease fat mass, reduce levels of TC, TG, and blood glucose, and improve insulin resistance	[117]
	Anti-tumor activity	Fermented kimchi	AOM+DSS induced male C57BL/6 mice	concerte anti-inflammatory, antioxidative, and anti-mutagenic actions
Fermented So-Cheong-Ryong-Tang		Athymic nu/nu female mice	induce apoptosis via the activation of caspases and the regulation of MAPK activity in AGS cells, enhance the inhibition of tumor formation	[119]
<i>Lactobacillus acidophilus</i> -Fermented Germinated Brown Rice		DMH induced male F344 rats	inhibit preneoplastic lesions of the colon in rats treated with DMH/DSS	[120]
Fermented guava		AOM+DSS induced male C57BL/6J mice	suppresse chronic inflammation, reinforce intestinal barrier integrity, increase colonic SCFA levels, restructure the intestinal microbiota	[121]
Shanxi aged vinegar		The 4T1 tumor-bearing mice	chelate Zn ²⁺ ions in the tumor microenvironment and inhibit the activity of MMP 2/9, thereby blocking lung metastasis	[122]

Beneficial Health Effects	Fermented Plant-Based Foods	Animal/Cell Model	Main Conclusion	References
Antihyperuricemic Activity	Polysaccharide purified from fermented barley	lung cancer mice	BF-I had the highest immunostimulatory effect, secretion of cytokines by macrophages, activation of the complement system, and enhancement of NK (or CTL)-mediated cytotoxicity	[123]
	Fermented apple juice	Hyperuricemia mice	reduce Urea, Creatinine and Uric acid levels, inhibit xanthine oxidase activity and the expression of pro-inflammatory factors, reverse gut microbiota dysbiosis and raise the abundance of beneficial bacteria	[124]
	Fermented dandelion	Hyperuricemia mice	reduce serum UA levels, inhibited XO activity, decrease expressions of GLUT9 and URAT1 transporters, and reverse the F/B ratio	[125]
	Phenolic compounds from fermented radish	Hyperuricemia mice	reduce UA levels and XO activity, ameliorate renal dysfunction, regulate gut microbiota	[126]
	Flavonoids from fermented <i>Astragalus membranaceus</i>	Hyperuricemia mice	decrease serum UA levels, reduce renal inflammation, promote the abundance of probiotics and butyrate-producing bacteria	[127]
	Raw soy sauce	hyperuricemic rats	reduce the serum UA levels and XO activities	[128]
	Fermented barley extract	hyperuricemia rats	reduce serum UA by increasing urinary excretion of UA	[129]

4.2 Anti-Obesity Activity

Obesity, characterized by excessive adipose tissue accumulation, induces abnormalities in endocrine, metabolic, and immune systems, thereby escalating the risk of chronic diseases. An increasing number of studies have confirmed that LAB-fermented plant-based foods, including mixed fermented vegetable juice¹⁰⁹, fermented lychee juice¹³³, fermented wheat bran¹³⁴, fermented blueberry pomace liquid¹¹⁰, and fermented buckwheat¹³⁵, all have the potential to alleviate obesity and its complications.

Phenolic compounds (e.g., phenolic acids, flavonoids), abundant in fruits and vegetables, are reported to be the pivotal anti-obesity components.¹³⁶ For instance, Wang et al.¹³⁷ demonstrated that mixed-probiotic-fermented *Cerasus humilis* reduced hepatic lipid deposition and gut microbiota dysbiosis in high-fat-diet-induced SD rats, potentially attributed to the increased content of phenolic compounds and lactic acid after fermentation. Some studies have pointed out that probiotic-derived hydrolases (e.g., glycosidases, tannases) could hydrolyze complex bound phenolics into bioavailable forms, which might be the reason for the increase of phenolic compounds during the fermentation process.^{137,138} Additionally, bioactive components such as β -glucans and essential amino acids which were rich in fermented grains are also considered to have the anti-obesity potential. Xiao et al.¹³⁹ found that after fermentation by *Lactiplantibacillus Plantarum* dy-1, the molecular weight of barley β -glucan was reduced, and it exhibited a flaky microstructure, which provided an opportunity for cholesterol binding. Moreover, fermentation also enhanced the inhibitory ability of β -glucan against α -amylase, α -glucosidase, and lipase activities, and showed stronger cholesterol adsorption capacity than unfermented β -glucan. In addition, other studies have pointed out that γ -aminobutyric acid and rutin in fermented buckwheat¹³⁵, genistein in fermented soybean paste¹⁴⁰, and ginsenosides in fermented ginseng¹⁴¹ may all have some correlation with the alleviation of obesity symptoms.

Our team previously screened a strain of *Lactobacillus plantarum* NCUH001046 with excellent anti-obesity effects and utilized it to ferment tomatoes, finding that the fermented tomato can significantly reduce weight gain and fat mass, improve dyslipidemia, alleviate inflammatory states and gut microbiota dysbiosis in obese mice. Further research revealed that the fermented tomato may alleviate the development of obesity potentially via the gut microbiota-fat-liver axis. On the one hand, it regulated the gut microbiota and systemic metabolic disorders by modulating the key genera and metabolite levels associated with obesity. On the other hand, the fermented tomato could activate the AMPK and PPAR signaling pathways by increasing the levels of key metabolites such as adiponectin and SCFA, thereby reducing hepatic lipid

synthesis and alleviating the development of obesity as well as its complications. Specifically, it significantly promoted AMPK phosphorylation, which facilitated subsequent ACC phosphorylation and the expression of CPT-1, as well as that of PPAR α , which is an upstream protein that stimulates CPT-1 expression to promote the β -oxidation of FFAs. Non-targeted metabolomics further identified five phenolic compounds, including chlorogenic acid, capsiate, tiliroside, irisfloreantin, and homoeriodictyol, as potential bioactive agents driving anti-obesity and lipid-regulatory effects.^{142,143}

4.3 Antihyperuricemic Activity

Hyperuricemia has emerged as the second most prevalent metabolic disorder after diabetes. A variety of polyphenolic compounds in plant-based raw materials have been proven to have urate-lowering effects, such as caffeic acid, chlorogenic acid, chicoric acid, rosmarinic acid, and sinapic acid. LAB fermentation enhances the bioavailability of these compounds by releasing bound phenols from plant matrices, thereby amplifying their uric acid-lowering efficacy. Xanthine oxidase (XOD) is the key enzyme that catalyzes the conversion of hypoxanthine to xanthine and subsequently to uric acid in purine metabolism. Researches have indicated that LAB-fermented plant-based foods can curb uric acid production by dampening the activity of XOD. Song et al.¹⁴⁴ showed that *Lactocaseibacillus rhamnosus* L08-fermented honeysuckle increased XOD inhibitory activity by 2.08-fold, which was correlated with elevated flavonoid and phenolic content. Similarly, Cui et al.¹⁴⁵ demonstrated that LAB fermentation could enhance the XOD inhibitory activity of Sophora flowers by significantly increasing the contents of total flavonoids and phenols, thereby increasing their anti-hyperuricemia activity. In addition to enzymatic inhibition, LAB-fermented foods can also modulate uric acid homeostasis through gut-kidney axis mechanisms. Li et al.¹²⁴ discovered that LAB-fermented apple juice can reduce serum uric acid, urea, and creatinine in hyperuricemic mice by inhibiting XOD activity, suppressing pro-inflammatory cytokines, and restoring gut microbiota balance (e.g., increasing Firmicutes and reducing pathogenic taxa). Another study further illustrated this pathway, phenolic compounds in fermented dandelion can promote beneficial gut bacteria (e.g., Akkermansia), inhibit renal uric acid transporters (GLUT9, URAT1), and reduce uric acid reabsorption.¹²⁵ Furthermore, SCFAs produced during fermentation also contribute indirectly by regulating metabolic pathways, enhancing intestinal barrier function, and dampening inflammation.¹⁴⁶

Our team previously screened a strain of *Lactobacillus rhamnosus* NCUH061012 that can significantly reduce hyperuricemia levels in mice and employed it to ferment carrots, yielding a product with significantly enhanced XOD inhibition and urate-lowering activities. Human trials further confirmed its efficacy in reducing serum uric acid levels. Results of multi-omics analysis showed that the product reduced serum uric acid levels mainly through pathways such as regulating gut microbiota, intestinal metabolites, and serum metabolites, alleviating systemic inflammation and kidney damage, as well as regulating the production and excretion of uric acid.¹⁴⁷

4.4 Blood Glucose Regulatory Activity

Diabetes, a metabolic disorder characterized by pancreatic β -cell dysfunction or insulin signaling pathway obstruction, frequently culminates in complications such as cardiovascular disease, retinopathy, nephropathy, and neurodegeneration. An increasing number of studies have shown that a variety of fermented plant-based foods, including fermented oats¹⁴⁸, fermented kombucha¹⁰⁴, fermented prickly pear juice¹⁰¹, fermented sorghum¹⁰², and fermented soy milk¹⁴⁹, all demonstrated good effects in reducing insulin resistance and improving diabetes complications.

Dietary fiber in plant-based foods has been proven to reduce blood glucose levels by increasing the diversity and abundance of the gut microbiota in patients with type 2 diabetes, while fermentation can alter the structure and function of dietary fiber, further enhancing its blood glucose-lowering effects. For instance, fermented dietary fiber extracted from soy sauce residue can alleviate hyperglycemia and insulin resistance by modulating the PI3/AKT pathway and the gut microbiota-SCFAs-GPR axis, which may be related to the structural changes in dietary fiber caused by biofermentation.¹⁰³ Meanwhile, hydrolases such as feruloyl esterase and β -glucosidase produced during fermentation can hydrolyze conjugated phenolic acids and release phenolic compounds bound to dietary fiber, thereby changing the phenolic composition in fermented

plant-based foods, increasing phenolic content, and enhancing their potential for blood glucose reduction.¹⁵⁰ Huang et al.¹⁵¹ reported that polyphenol extracts from fermented pomegranate leaves can significantly improve blood glucose, lipid levels, and antioxidant capacity in diabetic mice, while also markedly alleviating liver, kidney, and pancreatic damage. In addition, peptides generated from fermented grains and legumes are also believed to hold potential for regulating diabetes. For instance, peptides in the fermented food natto can inhibit the DPP-IV site to improve hyperglycemia¹⁵², while peptides in fermented rice bran can inhibit α -glucosidase activity¹⁵³, thereby slowing carbohydrate absorption and alleviating diabetes symptoms. These multi-mechanistic effects, ranging from microbiota modulation to phenolic compound liberation and peptide-mediated enzyme inhibition, position LAB-fermented plant-based foods as promising adjuncts in diabetes management.

Our team has isolated *Lactiplantibacillus plantarum* NCU116 for its hypoglycemic properties and used it to ferment carrots¹⁵⁴ and bitter melon.¹⁵⁵ It was found that compared with unfermented carrots and bitter melon, both fermented carrots and fermented bitter melon demonstrated good effects in lowering fasting blood glucose, glycated serum protein, serum insulin, and oxidative stress levels in type 2 diabetic rats, as well as in regulating the lipid profile and repairing pathological damage to the islets, liver, and kidneys.

4.5 Anti-Tumor Activity

Cancer is a disease that results from the interplay of multiple complex factors, such as chronic inflammation, genetic factors, environmental exposure, lifestyle, and abnormal hormone levels. Recent investigations have unveiled that plant-based foods fermented by LAB exhibit promising potential in the realm of anti-tumor activity. For instance, Quyang et al.¹⁵⁶ found that a fermented soy beverage (Q-CAN® PLUS) reduced viability and increased apoptosis of cancer cells in a concentration- and fermentation-dependent manner. In another study, Yim N et al.¹¹⁹ fermented So-Cheong-Ryong-Tang (CY), a traditional Korean herbal formula using lactic acid bacteria, and compared its anti-tumor effects before and after fermentation. It was found that the fermented CY could induce cell apoptosis by activating caspase-3, caspase-8, and caspase-9, enhance the growth inhibitory activity against cancer cells, and significantly inhibit tumor formation. Additionally, *Lactobacillus acidophilus*-fermented germinated brown rice was found to reduce serum pro-inflammatory markers (e.g., IL-6, TNF- α), decrease aberrant crypt foci, and activate cancer cell apoptosis pathways to suppress colorectal precancerous lesions in DMH/DSS-induced rat models.¹²⁰

Our research team applied the plant-derived *Lactiplantibacillus plantarum* NCU11129, a probiotic strain previously demonstrated to exhibit in vitro anti-colorectal cancer potential⁷¹, for the fermentation of guava. We then evaluated the preventive effects of fermented guava against azoxymethane/dextran sodium sulfate (AOM/DSS)-induced CRC in mice. It was demonstrated that the fermented guava could significantly improve survival rates, reduce tumor burden, mitigate colon shortening, and restore colonic mucosal integrity, which were mediated by upregulating tight junction proteins and promoting SCFA production.¹²¹

5. Future Prospects and Challenges of LAB-Fermented Plant-Based Foods

LAB-fermented plant-based foods cater to the consumer demands for “safe, nutritious, delicious, and healthy” products, demonstrating substantial potential in preventing and managing chronic diseases. Thus, the industry is poised to embrace enormous market opportunities in the future. However, numerous challenges remain to be addressed in the future development of this industry, including a limited variety of products, unstable flavor profiles, inconsistent shelf-life performance, etc. To accelerate industrialization, future research should prioritize the following directions: (1) Elucidating the mechanisms underlying flavor formation in various LAB-fermented plant-based foods, as well as the biological mechanisms by which LAB fermentation enhanced the healthy function of plant-based raw materials; (2) Identifying more suitable plant-based raw materials for fermentation, exploring superior LAB strains, developing stable direct-set starters, and optimizing fermentation processes; (3) Developing new types of LAB-fermented plant-based foods targeting chronic disease risk reduction (e.g., uric acid-lowering, blood sugar-lowering, blood pressure-lowering, lipid-lowering, anti-*Helicobacter pylori*, sleep-promoting and anti-tumor products); and (4)

Establishing standards for LAB-fermented plant-based foods and conducting clinical trials to improve the scientific evaluation system for the safety and functionality of LAB strains as well as their fermented plant-based products.

Author Contributions

Qianqian Guan: Writing–Original Draft Preparation; **Shijin Xiong:** Writing–Review & Editing; **Tao Xiong:** Supervision, Project Administration; **Mingyong Xie:** Conceptualization, Resources, Funding acquisition.

Conflicts of Interest

All authors declare that they have no conflict of interest or financial conflicts to disclose.

Data Availability Statement

Not applicable.

Funding

This work was supported by the National Natural Science Foundation of China (Project No. 32130082), Key Research and Development Program of Guangdong Province (2023B0202030002), Key Research and Development Program of Jiangxi Province (Project No. 20243BCC31004, 20232BBF60024), National Key Laboratory Foundation of China (20232BCD44005), Key Core Agricultural Technology Tackling Project of Jiangxi Province (Project No. JXNK22303-05).

References

- [1] Liu, X., Yin, P., Qi, J., et al. Burden of non-communicable diseases in China and its provinces, 1990-2021: Results from the Global Burden of Disease Study. *Chin Med J.* 2021;137(19):2325–2333. <https://doi.org/10.1097/CM9.00000000000003270>
- [2] GBD 2017 Diet Collaborators. Health effects of dietary risks in 195 countries, 1990-2017: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet.* 2019;393(10184):1958–1972. [https://doi.org/10.1016/S0140-6736\(21\)01342-8](https://doi.org/10.1016/S0140-6736(21)01342-8)
- [3] Liu, K., Owens, J., Saeedi, B., et al. Microbial metabolite delta-valerobetaine is a diet-dependent obesogen. *Nat Metab.* 2021;3(12):1694–1705. <https://doi.org/10.1038/s42255-021-00502-8>
- [4] Seo, D., O'Donnell, D., Jain, N., et al. ApoE isoform- and microbiota-dependent progression of neurodegeneration in a mouse model of tauopathy. *Sci.* 2023;379(6628):155. <https://doi.org/10.1126/science.add1236>
- [5] Ye, S., Shah, B., Li, J., et al. A critical review on interplay between dietary fibers and gut microbiota. *Trends Food Sci Tech.* 2022;124:237–249. <https://doi.org/10.1016/j.tifs.2022.04.010>
- [6] Desai, M., Seekatz, A., Koropatkin, N., et al. A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility. *Cell.* 2016;167(5):1339–1353. <https://doi.org/10.1016/j.cell.2016.10.043>
- [7] Reynolds, A., Mann, J., Cummings, J., et al. Carbohydrate quality and human health: a series of systematic reviews and meta-analyses. *Lancet.* 2019;393(10170):405–414. [https://doi.org/10.1016/S0140-6736\(18\)31809-9](https://doi.org/10.1016/S0140-6736(18)31809-9)
- [8] Ma, W., Nguyen, L., Song, M., et al. Dietary fiber intake, the gut microbiome, and chronic systemic inflammation in a cohort of adult men. *Genome Med.* 2021;13(1):102. <https://doi.org/10.1186/s13073-021-00921-y>
- [9] Aune, D., Sen, A., Norat, T., et al. Dietary fibre intake and the risk of diverticular disease: a systematic review and meta-analysis of prospective studies. *Eur J Nutr.* 2020;59(2):421–432. <https://doi.org/10.1007/s00394-019-01967-w>
- [10] Ojo, O., Ojo, O.O., Zand, N., et al. The Effect of Dietary Fibre on Gut Microbiota, Lipid Profile, and Inflammatory Markers in Patients with Type 2 Diabetes: A Systematic Review and Meta-Analysis of Randomised Controlled Trials. *Nutrients.* 2021;13(6):1805. <https://doi.org/10.3390/nu13061805>

- [11] Lairon, D., Arnault, N., Bertrais, S., et al. Associations between dietary fiber intake and cardiovascular risk factors: An umbrella review of meta-analyses of randomized controlled trials. *Cardiol Res.* 2022;9(103):972399. <https://doi.org/10.3389/fnut.2022.972399>
- [12] Jiang, J., Liu, Y., Yang, H., et al. Dietary fiber intake, genetic predisposition of gut microbiota, and the risk of metabolic dysfunction-associated steatotic liver disease. *Food Res Int.* 2025;116497. <https://doi.org/10.1016/j.foodres.2025.116497>
- [13] Lei, S. and Xiong, Y. Plant protein-based alternatives of reconstructed meat: Science, technology, and challenges. *Trends Food Sci Tech.* 2020;102:51–61. <https://doi.org/10.1016/j.tifs.2020.05.022>
- [14] Mozaffarian, D. Plant-Based Diets and Diabetes Risk: Which Foods, What Mechanisms? *Diabetes Care.* 2024;47(5):787–789. <https://doi.org/10.2337/dci24-0011>
- [15] Fackelmann, G., Manghi, P., Carlino, N., et al. Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals. *Nat Microbiol.* 2025;10(1):41–52. <https://doi.org/10.1038/s41564-024-01870-z>
- [16] Shuai, Z., Cao, Y., Huang, Y., et al. Aqueous *M. oleifera* leaf extract alleviates DSS-induced colitis in mice through suppression of inflammation. *J Ethnopharmacol.* 2023;318:116929. <https://doi.org/10.1016/j.jep.2023.116929>
- [17] Satija, A., Bhupathiraju, S., Rimm, E., et al. Plant-based dietary patterns and incidence of type 2 diabetes in US men and women: results from three prospective cohort studies. *Plos Med.* 2016;13(6):e1002039. <https://doi.org/10.1371/journal.pmed.1002039>
- [18] Schwingshackl, L., Schwedhelm, C., Hoffmann, G., et al. Food groups and risk of all-cause mortality: a systematic review and meta-analysis of prospective studies. *Am J Clin Nutr.* 2017;105(6):1462–1473. <https://doi.org/10.3945/ajcn.117.153148>
- [19] Wang, Y., Zhang, C., Liu, F., et al. Ecological succession and functional characteristics of lactic acid bacteria in traditional fermented foods. *Crit Rev Food Sci Nutr.* 2022;63(22):5841–5855. <https://doi.org/10.1080/10408398.2021.2025035>
- [20] Song, H., Lee, S., Ahn, S., et al. Effects of the main ingredients of the fermented food, kimchi, on bacterial composition and metabolite profile. *Food Res Int.* 2021;149:110668. <https://doi.org/10.1016/j.foodres.2022.110946>
- [21] Jung, J., Lee, S., Jin, H., et al. Metatranscriptomic analysis of lactic acid bacterial gene expression during kimchi fermentation. *Int J Food Microbiol.* 2013;163(2–3):171–179. <https://doi.org/10.1016/j.ijfoodmicro.2013.02.022>
- [22] Kim, J., Park, S., Kim, E., et al. Long-term population dynamics of viable microbes in a closed ecosystem of fermented vegetables. *Food Res Int.* 2022;154:111044. <https://doi.org/10.1016/j.foodres.2022.111044>
- [23] Świder, O., Roszko, M., Wójcicki, M., et al. Non-aminobiogenic starter cultures in a model system of cucumber fermentation. *LWT.* 2023;177:114574. <https://doi.org/10.1016/j.lwt.2023.114574>
- [24] Müller, A., Rösch, N., Cho, G., et al. Influence of iodized table salt on fermentation characteristics and bacterial diversity during sauerkraut fermentation. *Food Microbiol.* 2018;76:473–480. <https://doi.org/10.1016/j.fm.2018.07.009>
- [25] Xiong, T., Guan, Q., Song, S., et al. Dynamic changes of lactic acid bacteria flora during Chinese sauerkraut fermentation. *Food Control.* 2012;26(1):178–181. <https://doi.org/10.1016/j.foodcont.2012.01.027>
- [26] Xiao, Y., Xiong, T., Peng, Z., et al. Correlation between microbiota and flavours in fermentation of Chinese Sichuan Paocai. *Food Res Int.* 2018;114(235):123–132. <https://doi.org/10.1016/j.foodres.2018.06.051>
- [27] Liu, Z., Peng, Z., Huang, T., et al. Bacterial community dynamics and physicochemical characteristics in natural fermentation of jiang-shui, a traditional food made in northwest China. *J Sci Food Agric.* 2019;99(7):3391–3397. <https://doi.org/10.1002/jsfa.9556>
- [28] Guan, Q., Zheng, W., Huang, T., et al. Comparison of microbial communities and physicochemical characteristics of two traditionally fermented vegetables. *Food Res Int.* 2020;128:108755. <https://doi.org/10.1016/j.foodres.2019.108755>
- [29] Xiong, S., Qiu, D., Xu, X., et al. Heterogeneity of microbiome and flavor profiles of industrial-scale Laotan Suancai: Fermentation craft plays important roles. *Food Biosci.* 2023;55:102928. <https://doi.org/10.1016/j.fbio.2023.102928>
- [30] Liu, Z., Li, J., Huang, T., et al. Comparison of the bacterial communities in home-made Nanfeng yancai with and without salt. *Food Res Int.* 2019;125(235):108509. <https://doi.org/10.1016/j.foodres.2019.108509>
- [31] Liu, Z., Peng, Z., Huang, T., et al. Comparison of bacterial diversity in traditionally homemade paocai and Chinese spicy cabbage. *Food Microbiol.* 2019;83(235):141–149. <https://doi.org/10.1016/j.fm.2019.02.012>
- [32] Xiao, Y., Huang, T., Huang, C., et al. The microbial communities and flavour compounds of Jiangxi

- yancai, Sichuan paocai and Dongbei suancai: Three major types of traditional Chinese fermented vegetables. *LWT*. 2020;121:108865. <https://doi.org/10.1016/j.lwt.2019.108865>
- [33] Wang, D., Chen, G., Tang, Y., et al. Correlation between autochthonous microbial communities and flavor profiles during the fermentation of mustard green paocai (*Brassica juncea* Coss.), a typical industrial-scaled salted fermented vegetable. *Lwt-food Sci Technol*. 2022;172:114212. <https://doi.org/10.1016/j.lwt.2022.114212>
- [34] Hu, X., Liu, S., Li, E. Microbial community succession and its correlation with the dynamics of flavor compound profiles in naturally fermented stinky sufu. *Food Chem*. 2023;427:136742. <https://doi.org/10.1016/j.foodchem.2023.136742>
- [35] Xiang, Y., Zhou, B., Jiang, C., et al. Revealing the formation mechanisms of key flavors in fermented broad bean paste. *Food Res Int*. 2024;177:113880. <https://doi.org/10.1016/j.foodres.2023.113880>
- [36] Xiao, M., Huang, T., Xu, Y., et al. Metatranscriptomics reveals the gene functions and metabolic properties of the major microbial community during Chinese Sichuan Paocai fermentation. *Food Microbiol*. 2021;98:103573. <https://doi.org/10.1016/j.fm.2020.103573>
- [37] Xiong, S., Xu, X., Zhang, L., et al. Integrated metatranscriptomics and metabolomics reveal microbial succession and flavor formation mechanisms during the spontaneous fermentation of Laotan Suancai. *Food Res Int*. 2024;177:113865. <https://doi.org/10.1016/j.foodres.2023.113865>
- [38] Guan, Q., Kang, X., Qin, X., et al. Metagenomic analysis of microbial-community structure and function during the fermentation of suansun, a Chinese traditional bamboo shoot. *Food Biosci*. 2023;54. <https://doi.org/10.1016/j.fbio.2023.102908>
- [39] Zhang, L., Xiong, S., Du, Xu Y., et al. Unraveling the core functional microbiota involved in metabolic network of characteristic flavor development during soy sauce fermentation. *Food Biosci*. 2024;58:103697. <https://doi.org/10.1016/j.fbio.2024.103697>
- [40] Huang, T., Peng, Z., Hu, M., et al. Interactions between *Lactobacillus plantarum* NCU116 and its environments based on extracellular proteins and polysaccharides prediction by comparative analysis. *Genomics*. 2020;112(5):3579–3587. <https://doi.org/10.1016/j.ygeno.2020.04.008>
- [41] Huang, T., Xiong, T., Peng, Z., et al. Genomic analysis revealed adaptive mechanism to plant-related fermentation of *Lactobacillus plantarum* NCU116 and *Lactobacillus* spp. *Genomics*. 2020;112(1):703–711. <https://doi.org/10.1016/j.ygeno.2019.05.004>
- [42] Beck, R., Park, S., Lee, H., et al. Whole genome analysis of *Lactobacillus plantarum* strains isolated from kimchi and determination of probiotic properties to treat mucosal infections by candida albicans and gardnerella vaginalis. *Front Microbiol*. 2019;10:433. <https://doi.org/10.3389/fmicb.2019.00433>
- [43] Tamang, P., Kharnaor, P., Pariyar, P. Whole genome sequencing of the poly- γ -glutamic acid-producing novel *Bacillus subtilis* Tamang strain, isolated from spontaneously fermented kinema. *Food Res Int*. 2024;190:114655. <https://doi.org/10.1016/j.foodres.2024.114655>
- [44] Molina, G., Shetty, R. Synergistic effect of the coculture of *Leuconostoc pseudomesenteroides* and *Lactococcus lactis*, isolated from honeybees, on the generation of plant-based dairy alternatives based on soy, pea, oat, and potato drinks. *Food Microbiol*. 2024;118:104427. <https://doi.org/10.1016/j.fm.2023.104427>
- [45] Xiao, H., Sedó, G., Tovar, M., et al. Isolation and characterization of plant-based lactic acid bacteria from spontaneously fermented foods using a new modified medium. *Lwt-food Sci Technol*. 2024;192:115695. <https://doi.org/10.1016/j.lwt.2023.115695>
- [46] Bocchi, S., Rocchetti, G., Elli, M., et al. The combined effect of fermentation of lactic acid bacteria and in vitro digestion on metabolomic and oligosaccharide profile of oat beverage. *Food Res Int*. 2021;142:110216. <https://doi.org/10.1016/j.foodres.2021.110216>
- [47] CHR. Hansen has launched the Vega Culture Kit to support plant-based innovation. Available online: <https://m.baobei360.com/articles/detail-180373.html>
- [48] Danisco® VEGE fermentation strains: The most widely used fermentation strain products for plant-based foods and beverages. Available online: <https://www.industrysourcing.cn/article/352605>
- [49] The application of Probiotics in Fermented Plant-based industrial beverages. Available online: <https://www.wecare-bio.com/review/305.html>
- [50] Li, C., Nie, S., Ding, Q., et al. Cholesterol-lowering effect of *Lactobacillus plantarum* NCU116 in a hyperlipidaemic rat model. *Food Res Int*. 2014;8(1):340–347. <https://doi.org/10.1016/j.jff.2014.03.031>

- [51] Ding, Q., Li, C., Zhu, k., et al. Protective Effect of *Lactobacillus plantarum* NCU116 on Renal Injury in Rats Fed a High-Fat Diet. *Food science*. 2014;35(19):236–240. <https://doi.org/10.7506/spkx1002-6630-201419047>
- [52] Li, C., Nie, S., Zhu, K., et al. Lactobacillus plantarum NCU116 improves liver function, oxidative stress and lipid metabolism in rats with high fat diet induced non-alcoholic fatty liver disease. *Food Funct*. 2014;5(12):3216–3223. <https://doi.org/10.1039/c4fo00549j>
- [53] Li, C., Cao, J., Nie, S., et al. Serum metabolomics analysis for biomarker of *Lactobacillus plantarum* NCU116 on hyperlipidaemic rat model feed by high fat diet. *J Funct Foods*. 2018;42:171–176. <https://doi.org/10.1016/j.jff.2017.12.036>
- [54] Zhou, X., Hong, T., Yu, Q., et al. Exopolysaccharides from *Lactobacillus plantarum* NCU116 induce c-Jun dependent Fas/FasL-mediated apoptosis via TLR2 in mouse intestinal epithelial cancer cells. *Sci Rep*. 2017;7:14247. <https://doi.org/10.1038/s41598-017-14178-2>
- [55] Li, C., Nie, S., Zhu, K., et al. Effect of *Lactobacillus plantarum* NCU116 on loperamide-induced constipation in mice. *Int J Food Sci Nutr*. 2015;66(5):533–538. <https://doi.org/10.3109/09637486.2015.1024204>
- [56] Xie, J., Nie, S., Yu, Q., et al. *Lactobacillus plantarum* NCU116 Attenuates Cyclophosphamide-Induced Immunosuppression and Regulates Th17/Treg Cell Immune Responses in Mice. *Int J Food Sci Nutr*. 2016;64(6):1291–1297. <https://doi.org/10.1021/acs.jafc.5b06177>
- [57] Xie, J., Yu, Q., Nie, S., et al. Effects of *Lactobacillus plantarum* NCU116 on Intestine Mucosal Immunity in Immunosuppressed Mice. *J Agric Food Chem*. 2015;63(51):10914. <https://doi.org/10.1021/acs.jafc.5b04757>
- [58] Xie, J., Fan, S., Nie, S., et al. *Lactobacillus plantarum* NCU116 attenuates cyclophosphamide-induced intestinal mucosal injury, metabolism and intestinal microbiota disorders in mice. *Food Funct*. 2016;7(3):1584–1592. <https://doi.org/10.1039/c5fo01516b>
- [59] Xiong, T., Xie, M., Guan, Q., et al. “A strain of *Lactobacillus rhamnosus* with constipation relieving effect and its application”. CN201810978544.3. 2018-08-27. Available online: <http://epub.cnipa.gov.cn/>
- [60] Xiong, T., Xie, M., Guan, Q., et al. “The application of *Lactobacillus rhamnosus* in the preparation of compositions with the effect of inhibiting fatty liver lesions”: CN201810978415.4. 2018-08-27. Available online: <http://epub.cnipa.gov.cn/>
- [61] Wei, B., Peng, Z. Modulation of the Microbiome-Fat-Liver Axis by Lactic Acid Bacteria: A Potential Alleviated Role in High-Fat-Diet-Induced Obese Mice. *J Agr Food Chem*. 2023;71(27):10361–10374. <https://doi.org/10.1021/acs.jafc.3c03149>
- [62] Lin, X., Xiong, T., Peng, Z., et al. Novel lactic acid bacteria with anti-hyperuricemia ability: Screening and in vitro probiotic characteristics. *Food Biosci*. 2022;49:101840. <https://doi.org/10.1016/j.fbio.2022.101840>
- [63] Xiong, T., Xie, M., Peng, F., et al. A strain of *Lactobacillus fermentum* NCU001464, CN2022 1 0287684.2X. 2022-03-22. Available online: <http://epub.cnipa.gov.cn/>
- [64] Zhao, T., Peng, F., Liu, Z., et al. Lactic acid bacteria with anti-hyperuricemia ability: Screening in vitro and evaluating in mice. *Food Biosci*. 2023;52:102411. <https://doi.org/10.1016/j.fbio.2023.102411>
- [65] Zhao, T., Cai, P., Xiong, J., et al. *Lacticaseibacillus rhamnosus* NCUH061012 alleviates hyperuricemia via modulating gut microbiota and intestinal metabolites in mice. *Food Biosci*. 2024;58:103699. <https://doi.org/10.1016/j.fbio.2024.103699>
- [66] Xiong, T., Xie, M. A strain of *Lactobacillus fermentum* NCU326 with uric acid-lowering effect and its application, CN202310144684.1. 2023-02-21. Available online: <http://epub.cnipa.gov.cn/>
- [67] Huang, H., Peng, F., Li, J., et al. Isolation and characteristics of lactic acid bacteria with antibacterial activity against *Helicobacter pylori*. *Food Biosci*. 2021;44:101446. <https://doi.org/10.1016/j.fbio.2021.101446>
- [68] Li, J., Peng, F., Huang, H., et al. Characterization, mechanism and in vivo validation of *Helicobacter pylori* antagonism by probiotics screened from infants’ feces and oral cavity. *Food Funct*. 2024;15(3):1055–1722. <https://doi.org/10.1039/d3fo04592g>
- [69] Li, J., Xu, X., Yang, S., et al. *Helicobacter pylori* Inhibition, Gastritis Attenuation, and Gut Microbiota Protection in C57BL/6 Mice by *Ligilactobacillus salivarius* NCUH062003. *Microorganisms*. 2024;12(12):2521. <https://doi.org/10.3390/microorganisms12122521>
- [70] Xu, Y., Xiong, T., Zhang, L., et al. Novel lactic acid bacteria with anti-hyperglycaemic properties: In vitro screening and probiotic assessment. *Food Biosci*. 2025;63:105696. <https://doi.org/10.1016/j.fbio.2024.105696>
- [71] Xu, X., Xiong, S., Du, T., et al. In vitro screening of *Lactiplantibacillus plantarum* with

- probiotic properties and anti-colon cancer potential. *Front Bioeng Biotechnol.* 2024;62:105569. <https://doi.org/10.1016/j.fbio.2024.105569>
- [72] Ichinose, R., Yamasaki-Yashiki, S., Katakura, Y. Analysis of the effects of specific growth rate of *Lactococcus lactis* MG1363 on aerobic metabolism and its application to high-density culture. *J Biosci Bioeng.* 2023;136(2):129–135. <https://doi.org/10.1016/j.jbiosc.2023.05.005>
- [73] Li, L., Zhang, H., Meng, D., et al. Transcriptomics of *Lactobacillus paracasei*: metabolism patterns and cellular responses under high-density culture conditions. *Front Bioeng Biotechnol.* <https://doi.org/10.3389/fbioe.2023.1274020>
- [74] Schiraldi, C., Adduci, V., Valli, V., et al. High cell density cultivation of probiotics and lactic acid production. *Biotechnol Bioeng.* 2010;82(2):213–222. <https://doi.org/10.1002/bit.10557>
- [75] Wang, T., Lu, Y., Yan, H., et al. Fermentation optimization and kinetic model for high cell density culture of a probiotic microorganism: *Lactobacillus rhamnosus* LS-8. *Bioprocess Biosyst Eng.* 2020;43(5):515–528. <https://doi.org/10.1007/s00449-019-02246-y>
- [76] Ding, X., Qian, F., Mu, G., et al. Optimization of medium composition of *Lactobacillus plantarum* Y44 using Plackett-Burman and Box-Behnken designs. *Prep Biochem Biotech.* 2023;53(9):1058–1066. <https://doi.org/10.1080/10826068.2023.2166957>
- [77] Wang, G., Chen, P., Yu, X., et al. C18:1 improves the freeze drying resistance of *Lactobacillus plantarum* by maintaining the cell membrane. *ACS Appl Bio Mater.* 2020;3(8):4933–4940. <https://doi.org/10.1021/acsabm.0c00444>
- [78] Brga, G., Sophi, F., Catherineet, C., et al. Effect of hydroxypropyl- β -cyclodextrin on lipid membrane fluidity, stability and freeze-drying of liposomes–ScienceDirect. *J Drug Deliv Sci Tec.* 2018;44:101–107. <https://doi.org/10.1016/j.jddst.2017.12.009>
- [79] Lim, J., Lim, D., Kim, K., et al. Effects of the annealing on the physical properties of therapeutic proteins during freeze drying process. *Int J Biol Macromol.* 2017;107:730–740. <https://doi.org/10.1016/j.ijbiomac.2017.09.041>
- [80] Santivarangan, C., Wenning, M., Foperst, P., et al. Damage of cell envelope of *Lactobacillus helveticus* during vacuum drying. *J Appl Microbiol.* 2007;102(3):748–756. <https://doi.org/10.1111/j.1365-2672.2006.03123.x>
- [81] E, J., Rongze, M., Chen, C., et al. Improving the freeze-drying survival rate of *Lactobacillus plantarum* LIP-1 by increasing biofilm formation based on adjusting the composition of buffer salts in medium. *Food Chem.* 2021;338:128134. <https://doi.org/10.1016/j.foodchem.2020.128134>
- [82] E, J., Ma, L., Chen, Z., et al. Effects of buffer salts on the freeze-drying survival rate of *Lactobacillus plantarum* LIP-1 based on transcriptome and proteome analyses. *Food Chem.* 2020;326:126849. <https://doi.org/10.1016/j.foodchem.2020.126849>
- [83] Xia, Y., Wang, Y., Pu, J., et al. The protective effect of oleic acid on *Lactiplantibacillus plantarum* during freeze-drying. *Food Sci Hum Wellness.* 2023;12(6):2355–2361. <https://doi.org/10.1016/j.fshw.2023.03.039>
- [84] Zheng, Y., Yang, Y., Wang, R., et al. Effects of Cross Stress on the Survival of *Lactiplantibacillus plantarum* LIP-1 After Freeze-Drying. *Food Bioprocess Technol.* 2025;18(1):1029–1041. <https://doi.org/10.1007/s11947-024-03512-y>
- [85] Zhen, N., Zeng, X., Wang, H., et al. Effects of Heat Shock Treatment on the Survival Rate of *Lactobacillus acidophilus* after Freeze-drying. *Food Res Int.* 2020;136:109507. <https://doi.org/10.1016/j.foodres.2020.109507>
- [86] E, J., Chen, J., Chen, Z., et al. Effects of different initial pH values on freeze-drying resistance of *Lactiplantibacillus plantarum* LIP-1 based on transcriptomics and proteomics. *Food Res Int.* 2021;149:110694. <https://doi.org/10.1016/j.foodres.2021.110694>
- [87] Liu, L., Xie, S., Zhu, Y., et al. Sodium carboxymethyl celluloses as a cryoprotectant for survival improvement of lactic acid bacterial strains subjected to freeze-drying. *Int J Biol Macromol.* 2024;260:129468. <https://doi.org/10.1016/j.ijbiomac.2024.129468>
- [88] Cheng, Z., Yan, X., Wu, J., et al. Effects of freeze drying in complex lyoprotectants on the survival, and membrane fatty acid composition of *Lactobacillus plantarum* L1 and *Lactobacillus fermentum* L2. *Cryobiology.* 2022;105:1–9. <https://doi.org/10.1016/j.cryobiol.2022.01.003>
- [89] Yang, Y., Wang, R., Yang, Y., et al. Effects of different pre-freezing temperatures on the freeze-drying survival rate and stability during room temperature storage of *Lactiplantibacillus plantarum* LIP-1. *Food Biosci.* 2022;50:102087. <https://doi.org/10.1016/j.fbio.2022.102087>
- [90] Wang, G., Pu, J., Yu, X., et al. Influence of freezing temperature before freeze-drying on the viability of various *Lactobacillus plantarum* strains. *J Dairy Sci.* 2020;103(4):3066–3075. <https://doi.org/10.3168/jds.2019-17685>

- [91] Wang, G., Yu, X., Lu, Z., et al. Optimal combination of multiple cryoprotectants and freezing -thawing conditions for high Lactobacilli survival rate during freezing and frozen storage. *LWT*. 2018;99:217–223. <https://doi.org/10.1016/j.lwt.2018.09.065>
- [92] Erem, E. and Kilic, A. The role of fermentation with lactic acid bacteria in quality and health effects of plant - based dairy analogues. *Compr Rev Food Sci F*. 2024;23(4):e3402. <https://doi.org/10.1111/1541-4337.13402>
- [93] Aloo, S., Park, S., Oh, D. Impacts of germination and lactic acid bacteria fermentation on anti-nutrients, bioactive compounds, and selected functional properties of industrial hempseed (*Cannabis sativa* L.). *Food Chem*. 2023;428:136722. <https://doi.org/10.1016/j.foodchem.2023.136722>
- [94] Zhang, X., Miao, Q., Pan, C., et al. Research advances in probiotic fermentation of Chinese herbal medicines. *iMeta*. 2023;2(2):e93. <https://doi.org/org/10.1002/imt2.93>
- [95] Hak, Y., Young, M., Dong, Y., et al. Immune-enhancing effect of fermented soybean food, Cheonggukjang on cyclophosphamide-treated immunosuppressed rat. *Heliyon*. 2024;10(18). <https://doi.org/10.1016/j.heliyon.2024.e37845>
- [96] Cho, C.W., Han, C.J., Rhee, Y.K., et al. Cheonggukjang polysaccharides enhance immune activities and prevent cyclophosphamide-induced immunosuppression. *Int J Biol Macromol*. 2015;72:519–525. <https://doi.org/10.1016/j.ijbiomac.2014.09.010>
- [97] Feng, Y., Cai, H., Liu, X., et al. Effects of fermented sweet potato residue on growth performance, immune organ morphology, antioxidant capacity and nonspecific immunity in common carp (*Cyprinus carpio*). *Aquac Rep*. 2024;36(000). <https://doi.org/10.1016/j.aqrep.2024.102153>
- [98] Jiang, M., Deng, K., Jiang, C., et al. Evaluation of the Antioxidative, Antibacterial, and Anti-Inflammatory Effects of the Aloe Fermentation Supernatant Containing *Lactobacillus plantarum* HM218749.1. *Mediat Inflamm*. 2016;2016(2):1–8. <https://doi.org/10.1155/2016/2945650>
- [99] Zhao, J., Gong, L., Wu, L., et al. Immunomodulatory effects of fermented fig (*Ficus carica* L.) fruit extracts on cyclophosphamide-treated mice. *J Funct Foods*. 2020;75:104219. <https://doi.org/10.1016/j.jff.2020.104219>
- [100] Fu, Y., Liu, Z., Wang, K., et al. Fermented sea buckthorn compound juice inhibits colorectal cancer growth by regulating immunity and the gut microbiome. *J Funct Foods*. 2024;121, 106408. <https://doi.org/10.1016/j.jff.2024.106408>
- [101] Wei, M., Feng, D., Zhang, Y., et al. Effect and Correlation of Rosa roxburghii Tratt Juice Fermented by *Lactobacillus paracasei* SR10-1 on Oxidative Stress and Gut Microflora Dysbiosis in Streptozotocin (STZ)-Induced Type 2 Diabetes Mellitus Mice. *Foods*. 2023;12:3233. <https://doi.org/10.3390/foods12173233>
- [102] Ofofu, F.K., Elahi, F., Daliri, E.B.-M., et al. Fermented sorghum improves type 2 diabetes remission by modulating gut microbiota and their related metabolites in high fat diet-streptozotocin induced diabetic mice. *J Funct Foods*. 2023;107:105666. <https://doi.org/10.1016/j.jff.2023.105666>
- [103] Mo, Z., Zhan, M., Yang, X., et al. Fermented dietary fiber from soy sauce residue exerts antidiabetic effects through regulating the PI3K/AKT signaling pathway and gut microbiota-SCFAs-GPRs axis in type 2 diabetic mellitus mice. *Int J Biol Macromol*. 2024;270:132251. <https://doi.org/10.1016/j.ijbiomac.2024.132251>
- [104] Xu, S., Wang, Y., Wang, J., et al. Kombucha Reduces Hyperglycemia in Type 2 Diabetes of Mice by Regulating Gut Microbiota and Its Metabolites. *Foods*. 2022;11:754. <https://doi.org/10.3390/foods11050754>
- [105] Indira, A., Joshi, B., Koul, A., et al. Comparative hepato-ameliorative effects of Bambusa nutans fresh and fermented shoot extracts on STZ induced diabetic LACA mice. *Talanta*. 2024;274:126035. <https://doi.org/10.1016/j.talanta.2024.126035>
- [106] Li, C., Li, J., Shang, Y., et al. Hypoglycemic and Hypolipidemic Activity of Polygonatum sibiricum Fermented with Lactobacillus brevis YM 1301 in Diabetic C57BL/6 Mice. *J Med Food*. 2021;24:720–731. <https://doi.org/10.1089/jmf.2021.k.0034>
- [107] Yu, S., Wang, W., Wang, H., et al. Douchi Peptides VY and SFLLR Improve Glucose Homeostasis and Gut Dysbacteriosis in High - Fat Diet - Induced Insulin Resistant Mice. *Mol Nutr Food Res*. 2023;67:2200681. <https://doi.org/10.1002/mnfr.202200681>
- [108] Huang, Z., Fang, Z., Wu, A., et al. Fermented Psidium guajava leaves regulate the gut microbiota and improve metabolic alterations in diabetic mice. *Food Biosci*. 2023;51:102201. <https://doi.org/10.1016/j.fbio.2022.102201>
- [109] Lee, M., Yun, Y., Choi, E., et al. Anti-obesity effect of vegetable juice fermented with lactic acid bacteria isolated from kimchi in C57BL/6J mice and human mesenchymal stem cells. *Food Funct*. 2023;14(3):1349–1356. <https://doi.org/10.1039/d2fo02998g>

- [110] Chai, Z., Yan, Y., Zan, S., et al. Probiotic-fermented blueberry pomace alleviates obesity and hyperlipidemia in high-fat diet C57BL/6J mice. *Food Res Int.* 2022;157:111396. <https://doi.org/doi.org/10.1016/j.foodres.2022.111396>
- [111] Fu, S., Dang, Y., Xu, H., et al. Aloe Vera-Fermented Beverage Ameliorates Obesity and Gut Dysbiosis in High-Fat-Diet Mice. *Foods.* 2022;11(22):3728. doi.org/10.3390/foods11223728
- [112] Wu, C., Huang, Y., Hou, C., et al. Lemon fermented products prevent obesity in high-fat diet-fed rats by modulating lipid metabolism and gut microbiota. *JFST.* 2023;60(3):1036–1044. <https://doi.org/10.1007/s13197-022-05445-w>
- [113] Guan, Q., Ding, X., Zhong, L., et al. Beneficial effects of *Lactobacillus*-fermented black barley on high fat diet-induced fatty liver in rats. *Food Funct.* 2021;12(14):6526–6539. <https://doi.org/10.1039/D1FO00290B>
- [114] Zhang, Q., Fan, X., Cao, Y., et al. The beneficial effects of *Lactobacillus brevis* FZU0713-fermented *Laminaria japonica* on lipid metabolism and intestinal microbiota in hyperlipidemic rats fed with a high-fat diet. *Food Funct.* 2021;12(16):7145–7160. <https://doi.org/10.1039/D1FO00218J>
- [115] Zhong, H., Abdullah, A., Deng, L., et al. Probiotic-fermented blueberry juice prevents obesity and hyperglycemia in high fat diet-fed mice in association with modulating the gut microbiota. *Food Funct.* 2020;11(10):9192–9207. <https://doi.org/10.1039/D0FO00334D>
- [116] Park, S., Son, H., Chang, H., et al. Effects of Cabbage-Apple Juice Fermented by *Lactobacillus plantarum* EM on Lipid Profile Improvement and Obesity Amelioration in Rats. *Nutrients.* 2020;12(4):1135. <https://doi.org/10.3390/nu12041135>
- [117] Verón, H., Gauffin, C., Fabersani, E., et al. Cactus pear (*Opuntia ficus-indica*) juice fermented with autochthonous *Lactobacillus plantarum* S-811. *Food Funct.* 2019;10(2):1085–1097. <https://doi.org/10.1039/c8fo01591k>
- [118] Han, Y., Kang, E., Min, J., et al. Dietary intake of fermented kimchi prevented colitis-associated cancer. *J Clin Biochem Nutr.* 2020;67(3):263–273. <https://doi.org/10.3164/jcbn.20-77>
- [119] Yim, N., Kim, A., Jung, Y. P., et al. Fermented So-Cheong-Ryong-Tang (FCY) induces apoptosis via the activation of caspases and the regulation of MAPK signaling pathways in cancer cells. *Bmc Complement Altern M.* 2015;15:336. <https://doi.org/org/10.1186/s12906-015-0821-2>
- [120] Li, S.-C., Lin, H.-P., Chang, J.-S., & Shih, C.-K.. *Lactobacillus acidophilus*-Fermented Germinated Brown Rice Suppresses Preneoplastic Lesions of the Colon in Rats. *Nutrients.* 2019;11(11):2718. <https://doi.org/org/10.3390/nu1112718>
- [121] Xu, X., Xiong, S., Du, T., et al. Fermented guava (*psidium guajava*) by *Lactiplantibacillus plantarum* NCU0011129 attenuates azoxymethane/dextran sodium sulfate-induced colorectal cancer in mice: Restructuring gut microbiota and enhancing intestinal barrier function. *Food Biosci.* 2025;68:106672. <https://doi.org/org/10.1016/j.fbio.2025.106672>
- [122] Liu, P., Dai, R., Li, J., et al. Simple theranostics nanoagent for precision suppression of tumor growth and metastasis: A traditional fermented product having a novel functional breakthrough. *Chem Eng J.* 2024;500:156545. <https://doi.org/org/10.1016/j.cej.2024.156545>
- [123] Son, S., Kim, H., Park, M., et al. Effects of intravenous administration of polysaccharide purified from fermented barley on tumor metastasis inhibition via immunostimulating activities. *Food Biosci.* 2022;49:101833. <https://doi.org/org/10.1016/j.fbio.2022.101833>
- [124] Li, H., Shen, N., Ren, J., et al. Biotransformation characteristics of urate-lowering probiotic fermented apple juice and potential regulatory mechanisms for ameliorating hyperuricemia via mediating gut microbiota and metabolic pathways. *Food Chem.* 2024;460:140462. <https://doi.org/10.1016/j.foodchem.2024.140462>
- [125] Ma, Q., Chen, M., Liu, Y., et al. *Lactobacillus acidophilus* fermented dandelion improves hyperuricemia and regulates gut microbiota. *Fermentation.* 2023;9(4):352. <https://doi.org/10.3390/fermentation9040352>
- [126] Liu, X., Zhang, L., Wu, D., et al. Three dietary phenols from pickled radish improve uric acid metabolism disorder in hyperuricemia mice associated with the altered gut microbiota composition. *Food Biosci.* 2024;61:104802. <https://doi.org/10.1016/j.fbio.2024.104802>
- [127] Wang, R., Lin, F., Ye, S. Multi-omics analysis reveals therapeutic effects of *Bacillus subtilis*-fermented *Astragalus membranaceus* in hyperuricemia via modulation of gut microbiota. *Food Chem.* 2023;399:133993. <https://doi.org/10.1016/j.foodchem.2022.133993>
- [128] Li, H., Zhao, M., Su, G., et al. Effect of soy sauce on serum uric acid levels in hyperuricemic rats and identification of flazin as a potent xanthine oxidase inhibitor. *J Agric Food Chem.* 2016;64:4725–4734. <https://doi.org/10.1021/acs.jafc.6b01094>

- [129] Hokazono H, T., Omori, K. Anti-hyperuricemic effect of fermented barley extract is associated with increased urinary uric acid excretion. *Food Sci Technol Res.* 2010;16:295–304. <https://doi.org/10.3136/fstr.16.295>
- [130] Wastyk, H., Fragiakis, G., Pereln, D., et al. Gut-microbiota-targeted diets modulate human immune status. *Cell.* 2021;184(16):4137–4153. <https://doi.org/10.1016/j.cell.2021.06.019>
- [131] Yan, X., Xia, H., Xia, J., et al. The Regulatory Effects of Fermented Oats on Immune Cytokines and Gut Health in Healthy Adults. *Food Sci.* 2025;1–13. <https://doi.org/10.7506/spkx1002-6630-20250116-119>
- [132] Yin, H., Xia, S., Zhong, Y., et al. Adlay Seeds Fermented by *Lactobacillus plantarum* NCU137 Regulates Immunity and Intestinal Mucosal Barrier Function in Immunosuppressed Mice. *Food Sci.* 2024;45(11):136–143. <https://doi.org/10.7506/spkx1002-6630-20230613-110>
- [133] Wang, D., Deng, Y., Zhao, L., et al. GABA and fermented litchi juice enriched with GABA promote the beneficial effects in ameliorating obesity by regulating the gut microbiota in HFD-induced mice. *Food Funct.* 2023;14(18):8170–8185. <https://doi.org/10.1039/d2fo04038g>
- [134] Wu, Q., Zhuang, M., Guo, T., et al. Gut microbiota, host lipid metabolism and regulation mechanism of high-fat diet induced mice following different probiotics-fermented wheat bran intervention. *Food Res Int.* 2023;174:113497. <https://doi.org/10.1016/j.foodres.2023.113497>
- [135] Yan, J., Xue, Q., Chen, W., et al. Probiotic-fermented rice buckwheat alleviates high-fat diet-induced hyperlipidemia in mice by suppressing lipid accumulation and modulating gut microbiota. *Food Res Int.* 2022;155:111125. <https://doi.org/10.1016/j.foodres.2022.111125>
- [136] Redan, B., Buhman, K., Novotny, J., et al. Altered Transport and Metabolism of Phenolic Compounds in Obesity and Diabetes: Implications for Functional Food Development and Assessment. *Adv Nutr.* 2016;7(6):1090–1104. <https://doi.org/10.3945/an.116.013029>
- [137] Wang, Y., Han, C., Cheng, J., et al. Fermented *Cerasus humilis* fruits protect against high-fat diet induced hyperlipidemia which is associated with alteration of gut microbiota. *J Sci Food Agric.* 2023;103(5):2554–2563. <https://doi.org/10.1002/jsfa.12377>
- [138] Meng, J., Wang, J., Hao, Y., et al. Effects of *Lactobacillus fermentum* GD01 fermentation on the nutritional components and flavor substances of three kinds of bean milk. *LWT - Food Sci Technol.* 2023;184,115006. <https://doi.org/10.1016/j.lwt.2023.115006>
- [139] Xiao, X., Tan, C., Sun, X., et al. Effects of fermentation on structural characteristics and in vitro physiological activities of barley β -glucan. *Carbohydr Polym.* 2020;231:115685. <https://doi.org/10.1016/j.carbpol.2019.115685>
- [140] Kwak, C., Lee, M., Park, S. Higher antioxidant properties of Chungkookjang, a fermented soybean paste, may be due to increased aglycone and malonylglycoside isoflavone during fermentation. *Nutr Res.* 2007;27(11):719–727. <https://doi.org/10.1016/j.nutres.2007.09.004>
- [141] Nan, B., Liu, Y., You, Y., et al. Protective effects of enhanced minor ginsenosides in *Lactobacillus fermentum* KP-3-fermented ginseng in mice fed a high fat diet. *Food Funct.* 2018;9(11):6020–6028. <https://doi.org/10.1039/c8fo01056k>
- [142] Wei, B., Zheng, W., Peng, Z., et al. Probiotic-fermented tomato with hepatic lipid metabolism modulation effects: analysis of physicochemical properties, bioactivities, and potential bioactive compounds. *Food Funct.* 2024;15(9):4874–4886. <https://doi.org/10.1039/d3fo05535c>
- [143] Wei, B., Peng, Z., Zheng, W., et al. Probiotic-fermented tomato alleviates high-fat diet-induced obesity in mice: Insights from microbiome and metabolomics. *Food Chem.* 2024;436,;137719. <https://doi.org/10.1016/j.foodchem.2023.137719>
- [144] Song, Y., Liu, Q., Munir, M., et al. Effect of *Lactocaseibacillus rhamnosus* L08 fermentation on xanthine oxidase inhibitory activity and flavour profile of honeysuckle (*Lonicera japonica* thunb.). *Lwt-food Sci Technol.* 2024;200:116196. <https://doi.org/10.1016/j.lwt.2024.116196>
- [145] Cui, R., Zhang, C., Pan, Z., et al. Potential of probiotic-fermented *Flos sophorae* as a functional food: Enhanced anti-hyperuricemic activity and modulation of volatile components. *Food Biosci.* 2025;63:105640. <https://doi.org/10.1016/j.fbio.2024.105640>
- [146] Cleophas, M., Cri?an, T., Lemmers H, et al. Suppression of monosodium urate crystal-induced cytokine production by butyrate is mediated by the inhibition of class I histone deacetylases. *Ann Rheum Dis.* 2016;75:593–600. <https://doi.org/10.1038/s41423-019-0284-3>
- [147] Zhao, X. The effect and mechanism of alleviating hyperuricemia by *Lactocaseibacillus rhamnosus*

- NCUH061012 and fermented carrots. Doctoral dissertation. NanChang University, Jiangxi Nanchang. 2024. <https://doi.org/10.27232/d.cnki.gnchu.2024.000033>
- [148] Alharbi, H., Algonaiman, R., Barakat, H. Ameliorative and Antioxidative Potential of *Lactobacillus plantarum*-Fermented Oat (*Avena sativa*) and Fermented Oat Supplemented with Sidr Honey against Streptozotocin-Induced Type 2 Diabetes in Rats. *Antioxidants*. 2022;11(6):1122. <https://doi.org/10.3390/antiox11061122>
- [149] Marazza, J., LeBlanc, J., Giori, G., et al. Soymilk fermented with *Lactobacillus rhamnosus* CRL981 ameliorates hyperglycemia, lipid profiles and increases antioxidant enzyme activities in diabetic mice. *J Funct Foods*. 2013;5(4):1848–1853. <https://doi.org/10.1016/j.jff.2013.09.005>
- [150] Septembre-Malaterre, A., Remize, F., Poucheret, P. Fruits and vegetables, as a source of nutritional compounds and phytochemicals: Changes in bioactive compounds during lactic fermentation. *Food Res Int*. 2018;104:86–99. <https://doi.org/10.1016/j.foodres.2017.09.031>
- [151] Huang, Z., Luo, Y., Xia, X., et al. Bioaccessibility, safety, and antidiabetic effect of phenolic-rich extract from fermented *Psidium guajava* Linn. leaves. *J Funct Foods*. 2021;86:104723. <https://doi.org/10.1016/j.jff.2021.104723>
- [152] Sato, K., Miyasaka, S., Tsuji, A., et al. Isolation and characterization of peptides with dipeptidyl peptidase IV (DPPIV) inhibitory activity from natto using DPPIV from *Aspergillus oryzae*. *Food Chem*. 2018;261:51–56. <https://doi.org/10.1016/j.foodchem.2018.04.029>
- [153] Hu, J., Lai, X., Wu, X., et al. Isolation of a Novel Anti-Diabetic α -Glucosidase Oligo-Peptide Inhibitor from Fermented Rice Bran. *Foods*. 2023;12:183. <https://doi.org/10.3390/foods12010183>
- [154] Li, C., Nie, S., Zhua, K., et al. *Lactobacillus plantarum* NCU116 fermented carrot juice evokes changes of metabolites in serum from type 2 diabetic rats. *Food Res Int*. 2016;80:36–40. <https://doi.org/10.1016/j.foodres.2015.12.025>
- [155] Gao, H., Wen, J., Hu, J., et al. Fermented *Momordica charantia* L. juice modulates hyperglycemia, lipid profile, and gut microbiota in type 2 diabetic rats. *Food Res Int*. 2019;121:367–378. <https://doi.org/10.1016/j.foodres.2019.03.055>
- [156] Ouyang, X., Chen, Y., Tejaswi, B., et al. Fermented Soy Drink (Q-CAN® PLUS) Induces Apoptosis and Reduces Viability of Cancer Cells. *Nutr Cancer*. 2022;74(10):3670–3678. <https://doi.org/10.1080/01635581.2022.2077385>

Copyright: © 2025 by the author(s). Published by LumoScience Publishing, Singapore. This is an Open Access article distributed under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author(s) and the source are properly credited, and any changes made are indicated.

Disclaimer: All statements, views, and opinions expressed in this article are solely those of the author(s) and do not necessarily reflect those of their affiliated institutions, the editors, reviewers, or LumoScience Publishing. Any products, methods, or claims mentioned are not guaranteed or endorsed by LumoScience Publishing. The publisher and editors disclaim any responsibility for harm to people or property resulting from the use of any information, procedures, or materials discussed in the publication. The publisher remains neutral with regard to jurisdictional claims in maps and affiliations, and does not guarantee or endorse any products, methods, or claims mentioned.