

Microbial Fermentation of *Gardenia Jasminoides*: Biotransformation Mechanisms and Development of Value-Added Functional Products

Teo Chee Loong^{1,3*}, Zeng Qiu²

¹Agri Season Sdn Bhd, Malaysia

²Kanghong Biotechnology Group Co., Ltd. CHINA

³UNITAR University College Kuala Lumpur, Wisma Hong Leong, 18 Jalan Perak, 50450 Kuala Lumpur, MALAYSIA

Email: anthony1109@hotmail.my

Abstract: *Gardenia jasminoides* is a traditional medicinal and functional plant rich in iridoid glycosides and bioactive compounds, particularly geniposide. However, the biological efficacy of native *Gardenia* phytochemicals is often limited by their glycosylated structure and low bioavailability, creating a need for effective bioactivation strategies. This mini-review aims to summarize recent advances in microbial fermentation of *Gardenia jasminoides*, with emphasis on biotransformation mechanisms, enhancement of biological activities, and development of value-added functional products. Relevant studies published on microbial fermentation of *Gardenia*-derived materials were critically reviewed and synthesized to evaluate microbial species, enzymatic pathways, transformation products, and reported functional outcomes. The reviewed evidence demonstrates that lactic acid bacteria, filamentous fungi, and symbiotic microbial consortia convert geniposide into genipin and other bioactive metabolites primarily through β -glucosidase-mediated hydrolysis. Fermentation enhanced anti-inflammatory, antioxidant, antimicrobial, and metabolic regulatory activities. Probiotic strains such as *Levilactobacillus* and *Lactiplantibacillus plantarum* improved anti-inflammatory responses through suppression of nitric oxide and pro-inflammatory cytokines, while *Aspergillus niger* fermentation generated novel antibacterial derivatives with increased bioactivity. Furthermore, fermentation applied in kombucha beverages and fermented dairy products promoted the formation of functional metabolites and improved physiological outcomes, including glycemic regulation. Overall, microbial fermentation transforms *Gardenia jasminoides* into a promising platform for value-added functional foods, natural bioactive compounds, and nutraceutical applications. Future research integrating microbial genomics, metabolomics, and controlled fermentation design may further expand its industrial and biomedical potential.

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*Corresponding Author:

Teo Chee Loong

Department of Research and Development

Kanghong Biotechnology Group Co., Ltd.

Email: anthony1109@hotmail.my

1. Introduction

Gardenia jasminoides Ellis (Rubiaceae) is a traditional medicinal plant widely cultivated

across East Asia and has been used for centuries in herbal medicine for the treatment of inflammatory disorders, metabolic diseases, fever, and hepatic dysfunction. Increasing

scientific interest in this species arises from its rich phytochemical composition and broad pharmacological potential. The fruit of *G. jasminoides* contains diverse bioactive constituents, including iridoid glycosides, crocins, and related secondary metabolites, among which geniposide represents the predominant compound, while genipin serves as its biologically active aglycone derivative. These compounds have been associated with multiple health-promoting properties, including anti-inflammatory, antioxidant, antimicrobial, and antidiabetic activities, supporting the growing application of Gardenia-derived materials in functional foods and nutraceutical development. Some studies demonstrate that Gardenia extracts can regulate inflammatory mediators, improve metabolic parameters, and enhance antioxidant defense systems, highlighting their therapeutic relevance in modern biomedical research [1, 2].

Despite these promising biological activities, the functional efficacy of native Gardenia phytochemicals is often constrained by their chemical form. Geniposide, the major iridoid glycoside naturally present in Gardenia fruits, exhibits lower bioactivity compared with genipin due to the presence of a sugar moiety that limits cellular absorption and biological interaction. Conversion into genipin typically occurs through hydrolysis mediated by intestinal microorganisms, meaning that bioactivation depends strongly on an individual's gut microbiota composition. Variability in microbial metabolism therefore leads to inconsistent therapeutic outcomes, creating a need for controlled and reproducible strategies capable of enhancing the bioavailability and activity of Gardenia-derived compounds before consumption [1, 3].

Microbial fermentation has emerged as an effective bioactivation technology capable of overcoming these limitations by enabling targeted phytochemical transformation through microbial enzymatic systems. During fermentation, microorganisms such as lactic acid bacteria, fungi, and mixed microbial

consortia metabolize plant substrates and catalyze structural modifications via enzymes including β -glucosidases, esterases, and reductases. These enzymatic reactions convert complex glycosides into more bioavailable aglycones and generate novel metabolites with enhanced biological functions. For example, fermentation of Gardenia extracts by probiotic lactic acid bacteria promotes the hydrolytic conversion of geniposide into genipin, resulting in improved suppression of inflammatory mediators and increased antioxidant activity. Similarly, microbial transformation processes have been shown to produce new antibacterial derivatives and enhance overall functional properties of fermented products [3, 4]. Consequently, microbial fermentation represents a promising strategy for transforming *G. jasminoides* from a traditional herbal material into a value-enhanced platform for functional foods and bioactive product development. Therefore, this mini review aims to summarize current advances in microbial fermentation of *G. jasminoides*, focusing on biotransformation mechanisms, enhancement of biological activities, and the generation of value-added products derived from microbial metabolism.

2. Microbial Biotransformation Mechanisms in Gardenia Fermentation

2.1 Geniposide as the Central Biotransformation Substrate

Geniposide is the major iridoid glycoside in *Gardenia jasminoides* and is commonly present at relatively high abundance in the raw plant material, whereas its aglycone genipin is typically present at much lower concentration, despite being widely reported as functionally stronger in multiple bioactivity contexts [1, 3]. A recurring mechanistic theme across the previous studies is that fermentation creates a controlled biological route to convert geniposide into genipin and, in some cases, into additional downstream metabolites beyond genipin. Whole-cell lactic acid bacteria bioconversion increased the genipin fraction in

Gardenia extracts and was accompanied by measurable enhancement of anti-inflammatory performance in macrophage models [1]. In parallel, fungal fermentation demonstrated that geniposide can be transformed through alternative reactions into structurally distinct metabolites with improved antibacterial potency relative to the parent compound, indicating that geniposide is not only a precursor to genipin but also a hub substrate for broader microbial chemical diversification [4].

2.2 β -Glucosidase-Mediated Hydrolysis Pathways

Across lactic acid bacteria driven fermentations, β -glucosidase activity is positioned as the key enzymatic driver of the geniposide to genipin conversion. In a large strain screening study, lactic acid bacteria isolated from kimchi were evaluated for bioconversion performance, and the better performing *Levilactobacillus* isolate achieved substantial conversion activity; docking analysis and an esculin-based assay supported β -glucosidase involvement [1]. Complementing this phenotype-level evidence, transcriptional profiling during fermentation provided a gene-level basis for β -glucosidase-mediated biotransformation. In *Lactiplantibacillus plantarum* SN13T, multiple putative β -glucosidase genes were identified in the complete genome, and expression analysis during fermentation of *Gardenia fructus* extract revealed that two adjacent 6-phospho- β -glucosidase genes were transcribed markedly more than other candidates, supporting their functional involvement in geniposide hydrolysis during fermentation [3]. These converging results indicate that enzymatic cleavage of the glycosidic linkage is a central bioactivation step, and that fermentation can be designed as a controllable upstream process to enrich genipin and strengthen downstream bioactivity outcomes.

2.3 Microbial Metabolic Diversity in Gardenia Fermentation

Microbial fermentation of Gardenia is not mechanistically uniform, because different

microbial platforms apply distinct enzymatic toolkits and metabolic routes, yielding different transformation products and functional endpoints.

In lactic acid bacteria systems, whole-cell bioconversion provides a practical route to increase genipin content while maintaining a food-compatible microbial chassis. A *Levilactobacillus* strain with strong conversion capacity was also characterized as probiotic-friendly, including tolerance to acid, bile, and phenol, supporting feasibility for functional food positioning while enhancing anti-inflammatory effects after fermentation [1]. In *Lactiplantibacillus plantarum* SN13T fermentation, the mechanistic narrative is strengthened by transcriptional evidence linking increased bioactivity to β -glucosidase-mediated conversion, alongside suppression of inflammatory mediators such as nitric oxide, reactive oxygen species, IL-6, and TNF- α in LPS-stimulated macrophages [3].

In fungi fermentation, transformation outcomes can extend beyond simple hydrolysis. Fermentation of *Gardenia fructus* with *Aspergillus niger* DQWM-G11 increased antibacterial activity of the fermented product relative to the raw material, and a newly described transformation route converted geniposide into a distinct metabolite, 1 β -methoxyl-4-epigardendiol, which exhibited stronger antibacterial performance than the parent geniposide [4]. This demonstrates that fungal systems can introduce alternative chemical reactions that generate value-added antibacterial molecules rather than only enriching genipin.

In symbiotic fermentation systems, kombucha represents a multi-species microbial ecosystem whose bacteria and yeasts collectively reshape the chemical and functional profile of the beverage. The kombucha SCOBY contains bacteria such as *Acetobacter* and *Gluconacetobacter* that contribute to organic acid formation, lactic acid bacteria such as *Lactobacillus*, and yeasts including *Saccharomyces* and related genera that convert

sugars to alcohol and produce aromatic compounds [2]. Using this platform, kombucha fermented with *Gardenia jasminoides* displayed strong antioxidant and antimicrobial profiles and measurable cytotoxic effects in tested cell lines, with experimental designs that separated acidity effects from other bioactivities via pH-adjusted controls [2].

In food-matrix fermentation, dairy-based fermentation provides another route to translate *Gardenia* substrates into consumer-ready functional products. Fermented milk supplemented with *Gardenia jasminoides* water extracts showed improved fermentation-associated quality indicators and higher antioxidant capacity, and *in vivo* testing in a diabetic mouse model indicated improvements in glycemic and lipid-related outcomes, with reported involvement of AMP-activated protein kinase (AMPK) and acetyl-CoA carboxylase (ACC) phosphorylation in the mechanistic readout [5]. Collectively, these studies show that the same botanical substrate can yield different value-added outcomes depending on whether the microbial system is a single-strain probiotic platform, a fungal biotransformation platform, a symbiotic consortium, or a complex food-matrix fermentation.

3. Enhancement of Bioactivity through Fermentation

3.1 Anti-Inflammatory Enhancement

Microbial fermentation significantly enhances the anti-inflammatory potential of *Gardenia jasminoides* by converting inactive or weakly active phytochemicals into more bioavailable metabolites. A central mechanism underlying this improvement is the microbial hydrolysis of geniposide into genipin, which exhibits stronger biological activity. Fermentation using probiotic lactic acid bacteria has been shown to suppress inflammatory mediators, including nitric oxide (NO), reactive oxygen species (ROS), and pro-inflammatory cytokines such as interleukin-6 (IL-6) and tumor necrosis

factor- α (TNF- α) in lipopolysaccharide-stimulated macrophage models [3]. The enhanced activity observed after fermentation is attributed to β -glucosidase-mediated cleavage of the glycosidic bond in geniposide, generating genipin, which more effectively modulates inflammatory signaling pathways and reduces oxidative stress at the cellular level. Similarly, whole-cell bioconversion using *Levilactobacillus* strains demonstrated improved anti-inflammatory responses following fermentation, confirming that microbial transformation directly contributes to functional enhancement rather than simple extraction effects [1].

3.2 Antioxidant and Antimicrobial Improvements

Fermentation also promotes antioxidant and antimicrobial activities through metabolite enrichment and structural modification of phytochemicals. Microbial metabolism increases the availability of phenolic compounds and bioactive derivatives, resulting in improved radical scavenging capacity and enhanced biological efficacy. In fermented *Gardenia* systems, increased antioxidant activity has been associated with microbial enzymatic transformation and accumulation of functional metabolites produced during fermentation [2]. Furthermore, fungal fermentation using *Aspergillus niger* generated previously unreported transformation products derived from geniposide, which exhibited stronger antibacterial activity compared with the native compound, demonstrating that microbial metabolism can produce novel antimicrobial agents [4]. These findings indicate that fermentation functions not only as a bioactivation process but also as a biosynthetic platform capable of expanding the chemical diversity and antimicrobial potential of *Gardenia*-derived compounds.

3.3 Metabolic and Antidiabetic Effects

Beyond antioxidant and anti-inflammatory benefits, fermentation enhances metabolic

regulatory effects of *Gardenia jasminoides*, particularly in functional food matrices. Fermented milk supplemented with *Gardenia* water extracts showed improved probiotic growth characteristics and elevated antioxidant capacity, accompanied by significant physiological benefits in streptozotocin-induced diabetic mice [5]. Fermented formulations reduced blood glucose levels, improved lipid profiles by decreasing total cholesterol, triglycerides, and low-density lipoprotein cholesterol while increasing high-density lipoprotein levels, and enhanced hepatic antioxidant enzyme activities. Mechanistically, these improvements were linked to activation of the AMP-activated protein kinase (AMPK) signaling pathway and phosphorylation of acetyl-CoA carboxylase (ACC), alongside inhibition of fatty acid synthase activity, suggesting improved lipid metabolism and energy regulation after fermentation [5]. These results highlight the importance of microbial fermentation in transforming *Gardenia* extracts into metabolically active functional ingredients.

3.4 Cytotoxic and Functional Health Properties

Fermented *Gardenia* products also demonstrate promising cytotoxic and functional health properties, particularly in fermented beverage systems. Kombucha fermentation incorporating *Gardenia jasminoides* significantly enhanced antioxidant and antimicrobial performance while exhibiting measurable cytotoxic effects against tested human cell lines [2]. Fermentation promoted the production of bioactive metabolites that reduced cancer cell viability while maintaining controlled experimental conditions that distinguished bioactivity from acidity effects. The symbiotic microbial ecosystem of kombucha, composed of bacteria and yeasts, contributes to the formation of organic acids, phenolic derivatives, and fermentation metabolites that collectively enhance functional properties. These findings support the potential of *Gardenia*-based fermented beverages as multifunctional health products

and illustrate how fermentation can convert traditional plant materials into value-added functional drinks with antimicrobial, antioxidant, and potential anticancer applications [2].

4. Formation of Value-Added Products from *Gardenia* Fermentation

4.1 Functional Food Applications

Microbial fermentation enables *Gardenia jasminoides* to be incorporated into functional food systems by improving both bioactivity and compatibility with food-grade microbial platforms. Probiotic fermentation using lactic acid bacteria represents one of the most practical approaches for producing value-added functional ingredients. Whole-cell bioconversion by *Levilactobacillus* strains not only enhanced the conversion of geniposide into genipin but also demonstrated probiotic characteristics such as tolerance to acidic and bile conditions, supporting their application in functional food formulations [1]. Fermented dairy systems further illustrate this translational potential, where milk supplemented with *Gardenia jasminoides* extracts showed improved antioxidant properties and physiological benefits in diabetic animal models, indicating feasibility for functional fermented dairy products targeting metabolic health [5]. In parallel, fermented beverage systems such as kombucha provide a symbiotic microbial environment that promotes metabolite diversification. Kombucha fermented with *Gardenia* tea exhibited enhanced antioxidant and antimicrobial activities together with measurable functional bioactivities, highlighting the potential development of fermented botanical beverages as health-promoting products [2]. Collectively, these studies demonstrate that fermentation converts *Gardenia* from a traditional herbal material into a food-compatible functional ingredient suitable for probiotic foods, fermented drinks, and dairy-based health products.

4.2 Natural Pigments and Industrial Metabolites

Beyond functional foods, microbial fermentation plays an important role in generating industrially valuable pigments and secondary metabolites from *Gardenia* substrates. *Gardenia* fruits are naturally rich in yellow pigments derived from crocin-type carotenoids, which can undergo microbial transformation to form structurally modified pigments with improved stability and application potential. Microbial processing has enabled the conversion of *Gardenia* pigment residues into blue pigments through microbial metabolic activity, demonstrating an environmentally friendly strategy for pigment valorization and waste utilization. Transformation using specific microbial strains produced *Gardenia*-derived blue pigments with enhanced physicochemical stability, suggesting potential applications as natural colorants in food, cosmetics, and biotechnology industries [6]. In addition to pigment modification, fungal fermentation by *Aspergillus niger* generated new metabolites derived from geniposide transformation, including structurally modified antibacterial compounds with stronger activity than the native precursor, indicating that microbial fermentation can function as a biosynthetic platform for industrial metabolite generation [4]. These findings emphasize fermentation as a sustainable route to expand the chemical diversity and commercial value of *Gardenia*-derived materials.

4.3 Pharmaceutical and Nutraceutical Potential

Microbial fermentation also enhances the pharmaceutical and nutraceutical relevance of *Gardenia jasminoides* by improving bioavailability and generating novel bioactive molecules. The glycosylated structure of geniposide limits absorption in its native state, whereas fermentation-mediated hydrolysis produces genipin, a more bioactive and readily absorbable compound associated with anti-inflammatory and metabolic regulatory effects

[1, 3]. Controlled microbial biotransformation therefore mimics and standardizes intestinal microbial activation, reducing variability associated with host-dependent metabolism. Furthermore, microbial systems introduce additional biochemical pathways capable of producing previously unreported metabolites, expanding the pharmacological potential of *Gardenia* fermentation products [4]. Functional fermentation matrices such as probiotic foods and kombucha beverages further demonstrate that fermentation-derived metabolites can exert antioxidant, antimicrobial, and cytotoxic activities, supporting applications in nutraceutical development and functional therapeutics [2]. Overall, microbial fermentation provides a bridge between traditional herbal medicine and modern pharmaceutical innovation by enabling scalable production of bioactivated compounds and value-added biofunctional ingredients.

5. Microbial Platforms and Fermentation Strategies

5.1 Probiotic-Based Bioconversion

Probiotic microorganisms represent one of the most practical and industrially applicable platforms for *Gardenia jasminoides* fermentation due to their established safety profiles and compatibility with food systems. Lactic acid bacteria, particularly strains belonging to *Levilactobacillus* and *Lactiplantibacillus*, have demonstrated efficient whole-cell bioconversion of geniposide into genipin through endogenous β -glucosidase activity. These microorganisms possess advantages including Generally Recognized As Safe (GRAS) status, tolerance to gastrointestinal conditions, and suitability for incorporation into functional foods. Probiotic-based fermentation enables simultaneous enhancement of bioactivity and development of consumer-ready products such as fermented beverages and dairy systems. Studies have shown that *Levilactobacillus*-mediated fermentation significantly increases anti-inflammatory efficacy while maintaining

probiotic viability, supporting dual functionality as both a bioactivation process and a delivery system for beneficial microbes [1]. Similarly, transcriptional analyses of *Lactiplantibacillus plantarum* fermentation highlight regulated expression of β -glucosidase genes during substrate utilization, indicating that probiotic strains can be optimized at the genetic and metabolic levels to improve biotransformation efficiency [3].

5.2 Fungal Fermentation Systems

Fungi provide an alternative fermentation platform characterized by strong enzymatic transformation capability and metabolic flexibility. Compared with probiotic bacteria, fungal systems possess broader enzyme repertoires, allowing not only hydrolysis reactions but also oxidation, reduction, and structural rearrangement of phytochemicals. Fermentation of *Gardeniae Fructus* using *Aspergillus niger* demonstrated the formation of novel metabolites derived from geniposide transformation, including antibacterial compounds exhibiting stronger biological activity than the native substrate [4]. These findings suggest that fungal fermentation can extend beyond bioactivation into true biotransformation, generating structurally new molecules with potential pharmaceutical or industrial applications. The ability of fungal strains to secrete extracellular enzymes also facilitates substrate accessibility and improves conversion efficiency, making them suitable for large-scale metabolite production.

5.3 Mixed Microbial Consortia

Mixed microbial systems introduce additional metabolic complexity through synergistic interactions among bacteria and yeasts. Kombucha fermentation represents a representative example of such a consortium, where symbiotic cultures of bacteria and yeast (SCOBY) collectively modify the chemical composition of plant substrates. In kombucha fermented with *Gardenia jasminoides*, acetic acid bacteria, lactic acid bacteria, and yeast species cooperatively metabolize sugars and

phytochemicals, producing organic acids, ethanol-derived intermediates, and secondary metabolites that enhance antioxidant and antimicrobial properties [2]. The coexistence of multiple microbial species enables sequential and complementary metabolic reactions that cannot be achieved by single strains alone. This synergistic metabolism contributes to diversified metabolite profiles and improved functional properties, highlighting the potential of complex fermentation ecosystems for developing multifunctional botanical products.

5.4 Key Process Parameters

The efficiency and outcome of *Gardenia* fermentation are influenced by several critical process parameters. Fermentation time plays a decisive role in determining metabolite accumulation, as insufficient duration limits enzymatic hydrolysis while excessive fermentation may lead to degradation of desired compounds. Microbial strain selection is equally important because different microorganisms possess distinct enzymatic capacities and metabolic pathways, resulting in varied transformation products and bioactivities. Studies comparing probiotic bacteria and fungal systems demonstrate that strain-specific enzymatic profiles directly determine conversion efficiency and metabolite diversity [1, 4]. Additionally, enzyme activity control, particularly regulation of β -glucosidase expression and activity, is essential for optimizing geniposide hydrolysis and maximizing genipin production. Transcriptional evidence indicates that enzyme expression levels fluctuate during fermentation stages, suggesting that process optimization through controlled environmental conditions can enhance biotransformation outcomes [3]. Together, these parameters highlight the importance of integrating microbial selection, fermentation design, and enzymatic regulation to achieve reproducible and scalable fermentation strategies for value-added *Gardenia* products.

6. Current Challenges, Research Gaps and Future Perspectives

Despite the growing body of research demonstrating the effectiveness of microbial fermentation in enhancing the functional value of *Gardenia jasminoides*, several scientific and technological challenges remain unresolved. One major limitation is the lack of mechanistic integration across existing studies. While individual investigations have confirmed geniposide conversion into genipin and other metabolites, most research focuses on isolated biological outcomes rather than connecting enzymatic pathways, microbial gene regulation, and downstream pharmacological effects into a unified mechanistic framework [1, 3]. Consequently, understanding of how specific microbial pathways translate into predictable bioactivity improvements remains incomplete, limiting rational process design.

Another important gap lies in the absence of standardized fermentation protocols. Current studies employ different microbial strains, fermentation durations, substrate concentrations, and environmental conditions, making cross-study comparisons difficult and hindering reproducibility. Variations in microbial composition, particularly between single-strain fermentation and mixed microbial ecosystems such as kombucha, produce markedly different metabolite profiles, yet systematic optimization strategies are rarely reported [2]. Establishing standardized parameters for strain selection, fermentation time, and enzymatic activity control is therefore essential for consistent bioactivation outcomes.

In addition, metabolite characterization remains insufficient. Although several studies have identified genipin formation and selected transformation products, comprehensive metabolomics analyses are still limited. Fungal fermentation research has revealed the formation of novel antibacterial derivatives beyond genipin, suggesting that many fermentation-generated compounds remain undiscovered [4]. Advanced analytical approaches integrating metabolomics, transcriptomics, and enzymatic profiling are needed to fully map metabolic pathways and

identify bioactive intermediates responsible for enhanced functionality.

From an industrial perspective, scale-up and commercialization present additional challenges. Laboratory-scale fermentation systems often demonstrate promising biological activity but lack validation under industrial processing conditions. Parameters such as microbial stability, product consistency, downstream purification, and regulatory compliance must be addressed before large-scale production becomes feasible. Functional food models, including fermented dairy systems, illustrate translational potential; however, industrial optimization and shelf-stability evaluation remain underexplored [5].

Future research directions are increasingly oriented toward precision fermentation and strain engineering. Advances in microbial genomics and synthetic biology offer opportunities to engineer strains with enhanced β -glucosidase activity or tailored metabolic pathways to selectively produce desired compounds such as genipin or novel derivatives. Omics-guided pathway discovery, particularly transcriptomic evidence linking gene expression to biotransformation efficiency, provides a foundation for rational fermentation design [3]. Integrating multi-omics datasets with controlled fermentation strategies could enable predictive optimization of metabolite production.

Finally, the concept of personalized microbiome-assisted bioactivation represents an emerging frontier. Since natural conversion of geniposide depends on intestinal microbiota, fermentation technologies may be developed to complement or standardize individual metabolic variability. Tailored fermented products designed to interact synergistically with host microbiomes could enhance therapeutic consistency and open new opportunities for precision nutraceutical development. Collectively, addressing these challenges will be critical for transforming *Gardenia* fermentation from experimental

research into scalable, mechanism-driven platforms for functional food, pharmaceutical, and industrial applications.

6.0 Conclusions

Microbial fermentation has emerged as a transformative strategy that shifts *Gardenia jasminoides* from a traditional phytochemical resource into a dynamic bioactive platform with enhanced functional and industrial value. Through targeted microbial metabolism, particularly β -glucosidase-mediated hydrolysis, fermentation converts geniposide and related glycosides into more bioavailable and biologically potent metabolites such as genipin. This enzymatic biotransformation underlies the consistent enhancement of anti-inflammatory, antioxidant, antimicrobial, and metabolic regulatory activities observed across diverse fermentation systems. Evidence from probiotic bacteria, fungi, and mixed microbial consortia demonstrates that microbial enzymes not only activate existing compounds but also generate structurally novel metabolites, thereby expanding the chemical diversity and functional potential of *Gardenia*-derived products. Importantly, fermentation enables the integration of *Gardenia* substrates into practical application platforms, including functional foods, fermented beverages, natural pigments, and nutraceutical formulations. The convergence of microbial biotechnology, food science, and natural product chemistry highlights significant opportunities for developing next-generation functional ingredients and bioactive products. With continued advances in fermentation optimization, omics-guided pathway discovery, and precision microbial engineering, *Gardenia* fermentation is positioned to play an increasingly important role in both functional food innovation and biopharmaceutical development. Microbial biotransformation provides a scalable and sustainable approach to unlocking the therapeutic and industrial potential of *Gardenia jasminoides*. However, it should be noted that most evidence discussed in this review is derived from in vitro studies, microbial fermentation systems, and animal

models. Further clinical studies are required to validate the efficacy, safety, and health benefits of fermented *Gardenia*-derived products in humans.

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