Natural Resources for Human Health
eISSN: 2583-1194

Original Research

Received 05 July 2026
Revised 13 Aug 2026
Accepted 30 Aug 2026

Natural Resources for Human Health 2026, Vol. 6 (20s): 1000–1014

KEYWORDS:
Indigenous fermented foods; North-East India; Microbial diversity; Nutritional transformation; Bioactive compounds; Functional foods.

Indigenous Fermented Plant Foods of North-East India: Microbial Diversity, Nutritional Transformation and Functional Properties

Ambarish Bhuyan

DHSK College Autonomous, Dibrugarh
ambhuyan22@gmail.com

ABSTRACT: Indigenous fermented plant foods of North-East India represent an important intersection of traditional knowledge, microbial biodiversity and nutritional resources. This review critically examines the ethnobotanical diversity, fermentation-associated microorganisms, biochemical transformations and functional properties of traditional plant-based fermented foods, with particular emphasis on bamboo shoot, soybean and leafy vegetable products. Recent studies reveal distinct microbial communities, with lactic acid bacteria predominantly associated with fermented bamboo shoots and Bacillus species playing a major role in alkaline soybean fermentation. Microbial enzymatic activities contribute to carbohydrate metabolism, protein hydrolysis, modification of secondary metabolites and reduction of selected antinutritional compounds, thereby influencing nutritional composition, sensory characteristics and potential bioactivity. Evidence also indicates antioxidant, antimicrobial and probiotic-associated properties, although their physiological relevance remains insufficiently established. Advances in metagenomics and metabolomics have improved understanding of microbial diversity and metabolic potential; however, limitations persist in functional validation, microbial safety assessment and fermentation standardization. Integrating indigenous knowledge with multi-omics approaches and controlled fermentation studies could facilitate the conservation of traditional food heritage and the development of safe, nutritionally valuable and scientifically validated functional foods.

1. INTRODUCTION

1.1. Historical and Cultural Significance of Fermented Foods

Fermentation is an age-old food preservation practice closely associated with the agricultural traditions, dietary habits and indigenous knowledge systems of India (Samantaray and Saha, 2026). In North-East India, the region's rich cultural diversity and abundance of locally available plant resources have given rise to numerous traditional fermented foods. Tamang et al. (2021) documented over 200 ethnic fermented foods and beverages across the Eastern Himalayan region, reflecting the close relationship between biodiversity and traditional food practices. Popular examples include fermented soybean products such as *hawaijar* of Manipur, *tungrymbai* of Meghalaya, *axone* of Nagaland and *bekang* of Mizoram, alongside fermented bamboo shoot preparations such as *khorisa* of Assam and *soibum* of Manipur (Tamang et al., 2021). Prepared through traditional methods involving naturally occurring microorganisms, these foods are valued for their distinctive flavours, preservation qualities and cultural significance. Beyond their dietary importance, they help sustain ethnic identity and knowledge passed down through generations (Mipun et al., 2026; Samantaray and Saha, 2026). Documenting these practices is therefore essential for preserving indigenous food heritage and exploring their potential in sustainable food processing and functional food development.

1.2. Diversity of Plant-Based Fermented Foods in North-East India

North-East India has a rich diversity of indigenous fermented plant foods prepared from locally available bamboo shoots, soybeans, cereals and leafy vegetables. Prominent bamboo shoot products include soibum and soidon of Manipur, mesu of

Sikkim, and ekung, eup and hirring of Arunachal Pradesh (Goyal et al., 2024). Traditional fermented soybean foods such as kinema of Sikkim, hawaijar of Manipur, tungrymbai of Meghalaya and bekang of Mizoram further reflect the region's distinct food traditions (Kumar et al., 2019; Deka et al., 2021). These foods are generally prepared through spontaneous fermentation using traditional containers and, occasionally, previously fermented material as an inoculum. Such practices preserve seasonal plant resources while imparting characteristic flavours, textures and aromas (Singhal et al., 2021; Goyal et al., 2024).

1.3. Scientific Importance of Traditional Plant Fermentation

Traditional plant fermentation involves microbial and enzymatic activities that modify the nutritional composition, phytochemical content and sensory properties of plant-based foods. Lactic acid bacteria and other microorganisms break down carbohydrates and complex compounds, producing organic acids and flavour-related metabolites that contribute to food preservation and quality (Wang et al., 2025). Fermentation may also improve nutrient accessibility, release bound phenolics and generate bioactive compounds, although these effects vary with the substrate, microbial strains and processing conditions (Qiao et al., 2022; Gunawardena et al., 2024). Metagenomic studies of fermented bamboo shoots from North-East India have identified diverse lactic acid bacteria and genes involved in carbohydrate metabolism, vitamin biosynthesis and secondary metabolite production (Das et al., 2026). A dietary intervention further associated fermented food consumption with increased gut microbial diversity and reduced inflammatory markers, although these findings cannot be directly applied to individual traditional products (Wastyk et al., 2021). These findings highlight the potential of indigenous fermented foods for functional food development, while emphasizing the need for product-specific nutritional and health-related validation.

1.4. Research Gaps and Objectives of the Review

Despite increasing scientific interest in traditional fermented foods, significant knowledge gaps remain concerning the microbial ecology, biochemical transformations, nutritional characteristics and functional properties of plant-based fermented foods indigenous to North-East India. Although previous investigations have documented diverse microbial communities and fermentation practices, the available information remains fragmented across individual food products and ethnic communities, limiting a comprehensive understanding of microbial succession, interspecies interactions and their contributions to fermentation outcomes (Saikia et al., 2026). Furthermore, comparative investigations examining changes in nutritional composition, phytochemical profiles and fermentation-derived metabolites across different plant substrates remain insufficient, particularly in relation to the influence of indigenous microbial communities and traditional processing conditions. Huang et al. (2026) highlighted persistent limitations in understanding microbial community assembly, metabolic interactions and their relationships with product quality, emphasizing the need for integrated microbiological and metabolomic investigations. Although traditional fermented foods are frequently associated with antioxidant, antimicrobial, probiotic and other health-promoting properties, much of the available evidence is derived from laboratory-based or preclinical investigations, while mechanistic studies and human clinical validation remain limited (Saikia et al., 2026). Moreover, variations in raw materials, fermentation conditions and indigenous processing techniques present additional challenges for establishing consistent nutritional quality, microbial safety and reproducible functional characteristics (Huang et al., 2026). Addressing these limitations requires an interdisciplinary approach integrating ethnobotanical documentation with culture-dependent microbiology, high-throughput sequencing, metagenomics and metabolomics, supported by experimental validation of microbial functions and bioactive compounds. Accordingly, the present review aims to critically synthesize existing knowledge on the diversity of traditional plant-based fermented foods of North-East India, examine their associated microbial communities and fermentation-mediated nutritional transformations, evaluate the scientific evidence supporting their functional and health-related properties, and identify research priorities for preserving indigenous fermentation knowledge while advancing the development of safe, standardized and scientifically validated functional foods.

2 METHODOLOGY

The present review was structured following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines (Page et al., 2021). Peer-reviewed articles published between January 2017 and October 2026 were considered through a literature search designed for Scopus, Web of Science, PubMed and Google Scholar, using keywords including "indigenous fermented foods," "Northeast India," "fermented bamboo shoots," "fermented soybean," "traditional fermentation," "microbial diversity," "metagenomics," "metabolomics," "nutritional composition" and "functional properties." Studies addressing traditional plant fermentation, microbial diversity, nutritional changes, bioactive compounds, food safety

and potential health benefits were considered, alongside relevant comparative studies from other regions. Duplicate, out-of-period and unrelated publications were designated for exclusion. The screening framework comprised title and abstract assessment followed by full-text evaluation. Information on food types, geographical origins, microbial communities, analytical methods and reported functional properties was organized for qualitative analysis. Given the differences in substrates, experimental designs and analytical approaches, a narrative synthesis was selected instead of a meta-analysis.

3. ETHNOBOTANICAL DIVERSITY OF INDIGENOUS FERMENTED PLANT FOODS

3.1. Fermented Bamboo Shoot Products

Fermented bamboo shoots are an important part of North-East India's traditional food culture, prepared from locally available species such as Bambusa tulda, Bambusa balcooa, Dendrocalamus hamiltonii and Dendrocalamus sikkimensis (Goyal et al., 2024). Popular products include soibum, soidon and soijim of Manipur, mesu of Sikkim, khorisa of Assam, lung-siej of Meghalaya, bastenga of Nagaland, and ekung, hirring and eup of Arunachal Pradesh (Goyal et al., 2024). These foods undergo spontaneous fermentation, largely involving lactic acid bacteria that contribute to acidification and preservation. Shotgun metagenomic analysis of 24 samples representing ten fermented bamboo shoot products from six North-Eastern states identified LactiplantiBacillus, LevilactoBacillus, LactoBacillus, Lactococcus and Pediococcus as prominent bacterial genera, with variations across products and locations (Das et al., 2026). Singhal et al. (2021) reported that 30-day fermentation of Bambusa vulgaris increased protein content by 17.28%, enhanced phenolic and flavonoid contents and antioxidant activity, and reduced cyanogenic compounds, although fat and vitamin C levels declined. Metagenomic studies have also identified genes associated with carbohydrate metabolism, vitamin biosynthesis and secondary metabolite production (Das et al., 2026). These findings highlight the nutritional and microbial significance of fermented bamboo shoots while emphasizing the need for further evaluation of their functional properties and safety.

3.2. Fermented Soybean Products

Traditional fermented soybean products include *kinema, hawaijar, tungrymbai* and *bekang* (Kumar et al., 2019; Mipun et al., 2026). Fermentation predominantly involves proteolytic *Bacillus* species (Kumar et al., 2019; Deka et al., 2021). In *kinema*, Firmicutes constituted 82.31–93.99% of bacterial communities (Kumar et al., 2019), with enzymes linked to carbohydrate metabolism and GABA production (Kumar et al., 2019). *Bekang* showed declining *Staphylococcus* abundance during fermentation (Deka et al., 2021). Although fermentation may generate bioactive metabolites (Kumar et al., 2019; Mipun et al., 2026), detection of potential pathogens in *kinema* highlights the need for safety assessment (Kumar et al., 2019).

3.3. Fermented Leafy Vegetables and Other Plant Materials

Gundruk, a traditional fermented leafy vegetable, is prepared from mustard, radish and cabbage leaves (Tamang, 2022; Das et al., 2026). Its spontaneous fermentation involves lactic acid bacteria (Tamang, 2022; Das et al., 2026), particularly *LactiplantiBacillus plantarum*. Das et al. (2026) reported substrate-dependent acidification, with *LactiplantiBacillus* dominating cabbage- and spinach-based products and *Lactococcus* enriched in radish-based preparations (Das et al., 2026). Other traditional products include *sinki* and *khalpi* (Tamang, 2022). These foods preserve indigenous fermentation knowledge, although their nutritional properties and potential for standardized production require further investigation (Das et al., 2026).

The botanical sources associated ethnic communities and traditional preparation methods of major indigenous fermented plant foods of North-East India are summarized in Table 1.

Table 1. Indigenous fermented plant foods of North-East India

Fermented food	Botanical source	Ethnic community / state	Traditional preparation method	References
Soibum	Tender shoots of *Bambusa* spp. and *Dendrocalamus* spp.	Meetei, Manipur	Bamboo shoots are peeled, sliced or shredded and packed into earthen pots or bamboo containers for spontaneous fermentation.	Acharya et al. (2023); Goyal et al. (2024)

Fermented food	Botanical source	Ethnic community / state	Traditional preparation method	References
Soidon	Bamboo shoots, particularly locally available *Bambusa* spp.	Meetei, Manipur	Tender shoots are prepared and fermented in traditional containers, sometimes using liquid from an earlier fermentation.	Goyal et al. (2024)
Mesu	Bamboo shoots, including *Dendrocalamus* spp.	Gorkha/Nepali communities, Sikkim	Tender shoots are peeled, sliced and tightly packed into hollow bamboo stems or other containers for natural fermentation.	Goyal et al. (2024)
Khorisa	Edible bamboo shoots, including *Bambusa* spp.	Assamese communities, Assam	Shoots are peeled and chopped or grated, then fermented in closed containers to develop their characteristic sour flavour.	Acharya et al. (2023); Goyal et al. (2024)
Ekung	Locally available edible bamboo shoots	Adi communities, Arunachal Pradesh	Processed bamboo shoots are packed into traditional containers and allowed to ferment spontaneously.	Goyal et al. (2024); Das et al. (2024)
Moiya koshak	Bamboo shoots	Debbarma and Uchoi communities, Tripura	Bamboo shoots are processed and fermented in traditional clay containers.	Acharya et al. (2023)
Mileye amileye	Bamboo shoots	Chakma community, Tripura	Tender bamboo shoots are prepared and allowed to ferment in traditional containers.	Acharya et al. (2023)
Kinema	Soybean	Nepali/Gorkha communities, Sikkim	Soybeans are soaked, boiled until soft, drained and subjected to spontaneous alkaline fermentation, traditionally using leaves or other local wrapping materials.	Kumar et al. (2019)
Hawaijar	Soybean	Meitei/Meetei, Manipur	Soaked and boiled soybeans are wrapped in leaves, traditionally including Ficus hispida, and fermented in bamboo baskets, often near household fireplaces.	Singh et al. (2023); Das et al. (2023)
Tungrymbai	Soybean	Khasi, Meghalaya	Soybeans are soaked, boiled and wrapped in locally available leaves, then fermented in baskets under warm conditions.	Mishra et al. (2019)
Akhone (Axone)	Soybean	Naga communities, Nagaland	Soybeans are boiled and fermented under warm conditions, traditionally using leaves and locally available containers.	Das et al. (2023)

3.4. Indigenous Fermentation Technologies

Natural Resources for Human Health
eISSN: 2583-1194

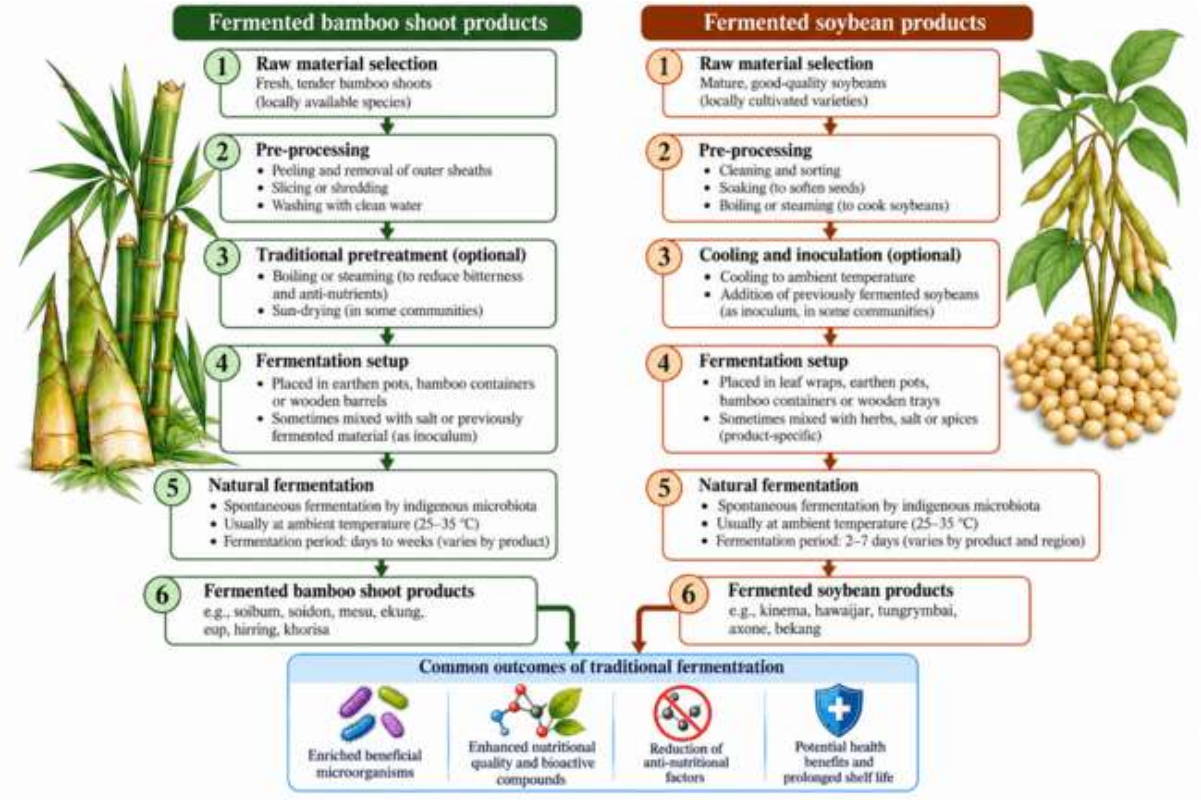


Figure 1. Traditional bamboo shoot and soybean fermentation processes in North-East India.

Indigenous fermentation in Northeast India combines traditional processing methods, plant materials and native microorganisms (Singh et al., 2023; Das et al., 2023). Hawaijar is prepared using boiled soybeans wrapped in Ficus hispida leaves and fermented in bamboo baskets (Singh et al., 2023). Similarly, tungrymbai involves Pyrnium leaves and fermentation near fireplaces (Mishra et al., 2019). Processing differences influence microbial communities and metabolites (Das et al., 2023). Rice-based apong uses herbal starters and traditional vessels (Loying et al., 2024). Selected Bacillus subtilis starters improve fermentation consistency (Singh et al., 2023), while Lactobacillus strains enhance selected properties of tungrymbai (Mishra et al., 2019). These practices warrant preservation alongside scientific standardization.

3.5. Traditional Knowledge and Conservation

Indigenous fermentation preserves ethnobotanical knowledge and cultural identity (Saikia et al., 2026; Talukdar et al., 2026). Women play a key role in transmitting these practices (Talukdar et al., 2026). An Assamese ethnobotanical study documented 41 plant species used in fermented beverages, approximately 85% collected from wild habitats (Talukdar et al., 2026). Traditional harvesting practices support biodiversity conservation (Talukdar et al., 2026), but urbanization and habitat degradation threaten this knowledge (Talukdar et al., 2026). Conserving plant and microbial resources is therefore essential (Saikia et al., 2026). Community-led documentation and scientific research can support sustainable livelihoods while safeguarding indigenous heritage (Saikia et al., 2026; Talukdar et al., 2026).

4. MICROBIAL DIVERSITY AND ECOLOGY OF INDIGENOUS FERMENTED PLANT FOODS

4.1. Microbial Diversity and Functional Roles in Indigenous Plant Fermentation

Indigenous fermented plant foods of Northeast India harbour diverse microbial communities, primarily comprising lactic acid bacteria (LAB), Bacillus species, yeasts and filamentous fungi. LAB, including *Lactiplantibacillus, Levilactobacillus, Lactobacillus, Lactococcus, Leuconostoc, Weissella* and *Pediococcus*, are particularly abundant in fermented bamboo shoots, contributing to acidification, carbohydrate metabolism and preservation (Das et al., 2023; Das et al., 2026). Deka et al. (2021) reported a decline in Lactobacillus abundance from 91.64% to 77.16% during tuaither fermentation. Similarly, *Lactiplantibacillus plantarum* predominated in four fermented bamboo shoot products from Tripura (Das et al., 2023), while analysis of 24 samples from six

northeastern states revealed distinct regional microbial communities (Das et al., 2026). Microbial succession may involve early hetero-fermentative genera such as *Leuconostoc* and *Weissella*, followed by acid-tolerant *Lactiplantibacillu*s and Pediococcus (Das et al., 2026). Metagenomic studies have also identified genes associated with carbohydrate metabolism, vitamin biosynthesis and antimicrobial compound production (Das et al., 2023; Das et al., 2026). In contrast, alkaline fermented soybean products such as kinema, hawaijar, bekang and akhone are mainly associated with proteolytic *Bacillus species*. B. *subtilis*, B. *amyloliquefaciens*, B. *licheniformis* and B. *pumilus* were identified in kinema (Kumar et al., 2019), while comparative studies revealed product-specific bacterial communities and metabolite profiles (Das et al., 2023). Protein hydrolysis and ammonia production contribute to their characteristic texture, flavour and alkalinity, although microbial–metabolite correlations do not establish causation (Das et al., 2023). The use of a native B. subtilis BCB-19 starter improved selected sensory properties of hawaijar (Tushir et al., 2026). However, detection of DNA from potentially harmful microorganisms, including B. cereus and *Staphylococcus aureus*, highlights the need for safety assessment without necessarily indicating viable pathogens (Kumar et al., 2019). Fungal diversity is also evident in fermented bamboo shoots. Das et al. (2024) isolated 95 yeast strains from eup, ekung and hirring, including *Meyerozyma, Candida, Pichia* and *Saccharomyces*, with 13 isolates exhibiting promising probiotic-associated properties. Fungal sequencing additionally identified Ascomycota, particularly *Pestalotiopsis* and *Penicillium* (Das et al., 2024), while Tripura samples contained representatives of Ascomycota, Basidiomycota and Glomeromycota (Das et al., 2023). Although these microorganisms may contribute to substrate transformation and flavour development, their metabolic activities, probiotic potential and safety require experimental confirmation (Das et al., 2024). Overall, microbial diversity underpins the distinctive characteristics of indigenous fermented foods, supporting further strain-level characterization, functional validation and controlled fermentation.

4.2. Microbial Succession During Fermentation

Microbial succession during fermentation depends on substrate composition, processing conditions and acidification, which favours acid-tolerant bacteria (Das et al., 2026). Deka et al. (2021) observed declining *Lactobacillus* abundance in tuaither (91.64–77.16%) and *Staphylococcus* in bekang (52.00–17.90%). Seasonal variations were reported in kinema (Kumar et al., 2019), while distinct microbial and metabolite profiles characterized hawaijar, bekang and akhone (Das et al., 2023). Fermentation vessels and *Bacillus subtilis* starters also influenced hawaijar quality (Tushir et al., 2026). Longitudinal studies combining microbial enumeration, sequencing and physicochemical measurements are needed to clarify succession mechanisms and their effects on food safety.

4.3. Modern Techniques for Microbial Identification

Molecular techniques have improved microbial characterization of indigenous fermented foods. Culture-dependent methods enable microbial isolation, while 16S rRNA sequencing reveals bacterial diversity. Deka et al. (2021) examined bacterial communities in Mizoram, whereas Das et al. (2023) combined sequencing and GC–MS to investigate microbial–metabolite associations. Shotgun metagenomics identified functional genes and seasonal microbial variations in kinema (Kumar et al., 2019). Similarly, Das et al. (2026) characterized microbial diversity, metabolic pathways and antimicrobial resistance determinants in fermented bamboo shoots. Fungal ITS sequencing and metatranscriptomics offer complementary insights, although DNA-based predictions require experimental validation.

4.4. Microbial Interactions and Fermentation Outcomes

Microbial interactions influence fermentation, metabolite production and food quality. In fermented bamboo shoots, lactic acid bacteria promote acidification, while metagenomic studies reveal genes associated with nutrient metabolism, quorum sensing and antimicrobial production (Das et al., 2026). Kumar et al. (2019) identified carbohydrate- and protein-metabolizing genes in *kinema*, including glutamate decarboxylase involved in GABA production. Distinct bacterial–metabolite associations were observed in *hawaijar, bekang* and *akhone* (Das et al., 2023). Deka et al. (2021) further linked microbial abundance with nutritional composition. However, microbial competition and metabolic cross-feeding require experimental validation through controlled fermentation and metabolomic studies.

5. NUTRITIONAL AND BIOCHEMICAL TRANSFORMATION DURING FERMENTATION

5.1. Changes in Carbohydrates

Natural Resources for Human Health
eISSN: 2583-1194

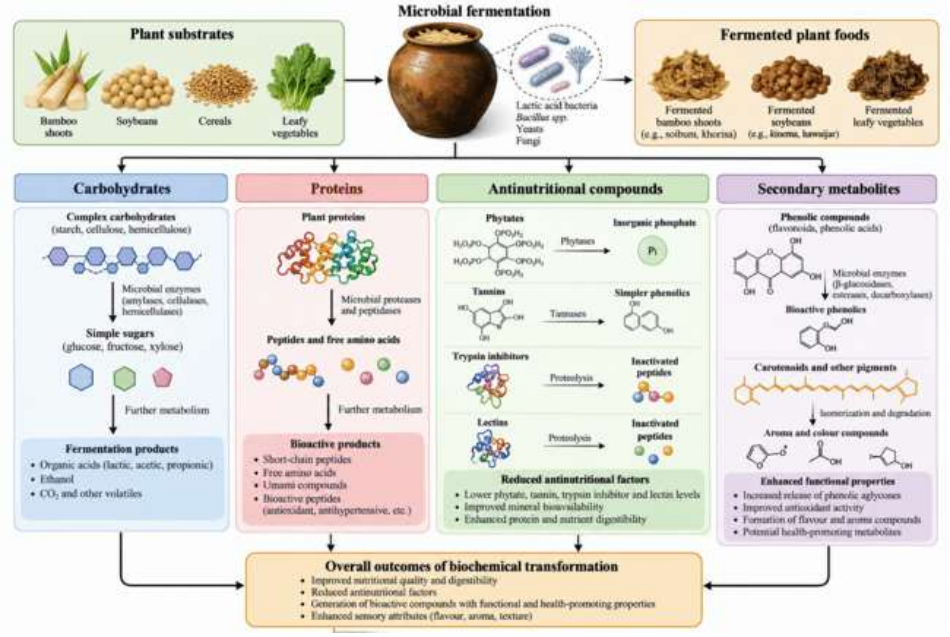


Figure 2. Schematic representation of biochemical transformations of carbohydrates, proteins, antinutritional compounds and secondary metabolites during plant fermentation.

Fermentation modifies plant carbohydrates through microbial enzymes, producing organic acids and other metabolites. Metagenomic analysis of fermented bamboo shoots identified genes associated with pectin degradation and carbohydrate metabolism (Das et al., 2023). Prativi et al. (2023) observed initial sugar accumulation followed by depletion during tempe fermentation. Similarly, Thai tuanao showed acetate accumulation and glucose-1-phosphate depletion alongside increasing Bacillus abundance (Dissook et al., 2025). Singhal et al. (2021) reported increased acidity during Bambusa vulgaris fermentation. These changes depend on microbial composition, substrate characteristics and fermentation duration, while improvements in carbohydrate digestibility require direct experimental confirmation..

5.2. Protein Degradation and Amino Acid Transformation

Microbial proteolysis transforms plant proteins into peptides and amino acids, influencing nutritional and sensory properties. Das et al. (2023) reported higher essential amino acid abundance in hawaijar than in other fermented soybean products. Similarly, tuanao fermentation increased free amino acids and oligopeptides through Bacillus-associated activity (Dissook et al., 2025). Conversely, Pediococcus pentosaceus fermentation reduced bitter dipeptides in bamboo shoot liquid (Huang et al., 2025). Singhal et al. (2021) observed a 17.28% increase in measured bamboo shoot protein content, although improved digestibility remains unconfirmed. Further biochemical and digestibility assessments are needed to establish nutritional benefits.

5.3. Changes in Vitamins and Minerals

Fermentation modifies micronutrient composition depending on microbial activity and substrate characteristics. Das et al. (2023) reported differences in vitamin profiles among hawaijar, bekang and akhone, without establishing increases over unfermented soybeans. Singhal et al. (2021) observed a 35.77% reduction in vitamin C in fermented bamboo shoots, while Kiczorowski et al. (2022) documented variable vitamin and mineral changes in fermented vegetables. Castro-Alba et al. (2019) reported reduced phytate levels and improved mineral accessibility in fermented pseudocereals. These findings indicate that fermentation does not uniformly enhance micronutrient availability, highlighting the need for product-specific nutritional evaluation..

5.4. Transformation of Plant Secondary Metabolites

Fermentation modifies plant secondary metabolites through microbial enzymatic activities. Xiang et al. (2022) reported 1.62-fold higher total isoflavones and 3.07-fold higher aglycones in fermented soybeans. Lee et al. (2022) identified 38 isoflavone derivatives, while Lee et al. (2021) observed distinct isoflavone and soyasaponin profiles across fermented soybean products.

In bamboo shoots, fermentation increased phenolic and flavonoid contents (Singhal et al., 2021). Huang et al. (2025) also reported changes in phenylpropanoid-related metabolites during bamboo shoot liquid fermentation. However, these transformations vary with substrates and processing conditions, requiring compound-specific analyses to establish their nutritional and functional significance.

5.5. Reduction of Antinutritional Compounds

Fermentation can reduce antinutritional compounds, although its effectiveness depends on substrate preparation and processing conditions. Castro-Alba et al. (2019) reported phytate reductions of 64–93% in fermented flour and 12–51% in whole grains, largely attributed to endogenous phytase activity. However, these findings cannot be directly generalized to indigenous soybean products. Evidence for tannin and trypsin inhibitor reduction in traditional fermented soybeans remains limited. In fermented *Bambusa vulgaris* shoots, cyanogenic content declined from 434.9 to 164.8 ppm after 30 days (Singhal et al., 2021). Nevertheless, reduced toxin levels do not necessarily establish food safety, highlighting the need for product-specific chemical assessment.

5.6. Fermentation and Antioxidant Properties

Fermentation modifies phenolic compounds, flavonoids and isoflavones, influencing antioxidant activity. Singhal et al. (2021) reported a 45.01% increase in phenolic content, alongside improved antioxidant capacity, in fermented *Bambusa vulgaris* shoots. In Korean meju, Song et al. (2020) associated isoflavones and soyasaponins with ABTS activity, while amino acids correlated with FRAP values. Similarly, *Bacillus subtilis* fermentation altered soybean isoflavone composition and antioxidant properties (Xiang et al., 2022). However, DPPH, ABTS and FRAP measure different chemical reactions, and their results do not establish antioxidant benefits in humans. Further metabolomic and biological validation is therefore necessary.

5.7. Metabolomic Approaches to Nutritional Transformation

Metabolomics reveals biochemical changes during fermentation using GC–MS, LC–MS and NMR spectroscopy. Das et al. (2023) identified distinct metabolite profiles in hawaijar, bekang and akhone. Lee et al. (2021) combined analytical platforms to characterize Korean fermented soybean products, while Prativi et al. (2023) examined metabolic changes during tempe fermentation. Dissook et al. (2025) integrated metagenomics, NMR and mass spectrometry to investigate microbial succession and metabolite accumulation in tuanao. Although these approaches link microbial diversity with biochemical transformations, correlations do not establish causation. Future studies require validated metabolite identification and time-resolved multi-omics analysis.

6. FUNCTIONAL PROPERTIES AND POTENTIAL HEALTH BENEFITS

6.1. Antioxidant Properties

Fermentation may enhance antioxidant properties through phenolic release, phytochemical transformation and peptide formation. Singhal et al. (2021) reported a 45.01% increase in phenolic content in fermented bamboo shoots. Mishra et al. (2019) observed antioxidant activity and isoflavone changes in tungrymbai. Hati et al. (2024) recorded 73.65 ± 0.54% antioxidative activity despite declining phenolic content, suggesting that antioxidant capacity depends on multiple compounds. Kumari et al. (2023) identified antioxidant-associated peptides produced by kinema-derived Bacillus strains. However, laboratory antioxidant activity does not establish physiological benefits, requiring further investigation of bioavailability and efficacy.

6.2. Antimicrobial Properties

Fermented plant foods may exhibit antimicrobial activity through organic acids, bacteriocins and other microbial metabolites. Ricci et al. (2019) demonstrated inhibition of several foodborne pathogens by fermented vegetable extracts. Nebbia et al. (2021) distinguished lactic acid-mediated inhibition from bacteriocin activity against Listeria monocytogenes. Metagenomic analysis of northeastern fermented bamboo shoots identified genes potentially involved in antimicrobial compound production (Das et al., 2026), although their expression remains unconfirmed. Detection of potentially pathogenic microorganisms in hawaijar further indicates that fermentation does not guarantee safety (Singh et al., 2023). Experimental validation and hygienic processing are therefore essential.

6.3. Probiotic Potential

Indigenous fermented plant foods contain microorganisms with potential probiotic properties, although benefits require strain-specific validation. Das et al. (2024) isolated 95 yeast strains from fermented bamboo shoots, including 13 showing favourable acid tolerance, bile resistance, aggregation and antimicrobial activity. These included *Meyerozyma, Pichia* and *Saccharomyces* species. Metagenomic investigations identified microbial genes associated with stress tolerance, carbohydrate metabolism and other potentially beneficial functions (Das et al., 2026). However, laboratory characteristics and genomic predictions cannot establish probiotic efficacy. Further studies should assess strain safety, antimicrobial resistance, gastro-intestinal survival and demonstrated health benefits before practical application.

6.4. Antidiabetic and Cardiometabolic Potential

Fermented soybean products contain metabolites with potential antidiabetic and cardiometabolic activities. Mishra et al. (2019) reported ACE-inhibitory activity in tungrymbai, while Hati et al. (2024) demonstrated inhibition of carbohydrate-digesting enzymes and pancreatic lipase. Das et al. (2024) observed improved glucose uptake and glycaemic parameters using hawaijar-derived fermented soybean preparations in cellular and animal models. Kumari et al. (2023) identified bioactive peptides from kinema-derived Bacillus strains, while comparative soybean studies reported ACE-inhibitory peptides (Wei et al., 2025; Jiang et al., 2026). However, these experimental findings require clinical validation before therapeutic benefits can be established.

6.5. Bioactive Peptides and Other Functional Metabolites

Microbial proteolysis during soybean fermentation generates potentially bioactive peptides. Kumari et al. (2023) identified antioxidant-associated peptides from kinema-derived Bacillus strains. Padhi et al. (2021) reported computationally predicted interactions of a soybean peptide with viral and immune-related targets, without biological validation. Wei et al. (2025) characterized ACE-inhibitory peptides from fermented soybean curds, while Jiang et al. (2026) demonstrated ACE inhibition and endothelial cell protection using fermented soybean peptides. Metagenomic analysis also identified secondary metabolite biosynthetic pathways in fermented bamboo shoots (Das et al., 2026). These findings warrant further structural, safety and physiological investigations.

7. FOOD SAFETY, QUALITY CONTROL AND STANDARDIZATION

7.1. Microbiological Safety

Spontaneous fermentation poses microbiological risks, particularly in alkaline soybean products lacking protective acidification. Singh et al. (2023) reported contamination concerns involving Bacillus cereus, Proteus mirabilis and toxin-associated genetic determinants in hawaijar. Vermeersch et al. (2026) demonstrated that rapid acidification and adequate holding periods help restrict Listeria monocytogenes in fermented vegetables, although these conditions may not apply to alkaline fermentation. Chin et al. (2024) highlighted pathogen contamination risks during spontaneous soybean fermentation. Ensuring safety requires hygienic processing, microbial monitoring, strain-level identification and targeted screening for pathogens and toxin-associated genes.

7.2. Chemical Safety

Chemical safety remains a concern in indigenous fermented foods. Biogenic amines may accumulate during soybean fermentation through microbial amino acid decarboxylation (Gao et al., 2023), potentially causing adverse health effects (Saha Turna et al., 2024). However, their concentrations in northeastern products remain insufficiently documented. Chen et al. (2023) demonstrated that selected Bacillus strains reduced biogenic amine accumulation in fermented soybeans. Bamboo shoots present additional risks from cyanogenic compounds. Singhal et al. (2021) reported a reduction in cyanogenic content from 434.9 to 164.8 ppm following fermentation. These findings emphasize the need for product-specific chemical safety assessment and validated processing methods.

7.3. Variability in Product Quality

Traditional fermented foods exhibit quality variations arising from differences in substrates, microbial communities and processing practices. Das et al. (2023) identified distinct bacterial and metabolite profiles in hawaijar, bekang and akhone, despite their shared soybean substrate. Tushir et al. (2026) demonstrated that fermentation vessels influenced hawaijar quality, while a native Bacillus subtilis starter improved selected sensory characteristics. Similarly, Gao et al. (2024) reported fermentation-

duration-dependent changes in peptides, amino acids and flavour compounds. These findings highlight the need for product-specific standardization of fermentation conditions, microbial quality and sensory attributes while preserving traditional characteristics.

7.4. Development of Safe Starter Cultures

Safe starter cultures can improve fermentation consistency while preserving traditional food characteristics. Elhalis et al. (2024) emphasized microbial ecology in starter development, while Chin et al. (2024) highlighted controlled inoculation for reducing fermentation hazards. Tushir et al. (2026) reported improved sensory properties of hawaijar using Bacillus subtilis BCB-19. Seo et al. (2025) demonstrated the importance of strain-specific genomic and safety assessments in Bacillus safensis, whereas Chen et al. (2023) identified biogenic amine-degrading Bacillus strains. Developing reliable starters therefore requires microbial identification, genomic screening, safety evaluation and controlled fermentation trials without compromising indigenous food characteristics.

8. EMERGING BIOTECHNOLOGICAL APPROACHES

8.1. Metagenomics and Microbial Community Profiling

Recent advances in high-throughput sequencing have improved our understanding of microbial diversity and functional potential in indigenous fermented plant foods of North-East India. Metagenomic analysis of Kinema revealed diverse microbial communities and genes associated with fermentation-related metabolic processes (Kumar et al., 2019). Similarly, shotgun metagenomic investigations of fermented bamboo shoots from Tripura identified lactic acid bacteria, including *LactiplantiBacillus plantarum*, *Leuconostoc mesenteroides* and *Pediococcus pentosaceus*, together with genes involved in carbohydrate and amino acid metabolism (Das et al., 2023a). More recently, genome-resolved metagenomic analysis of fermented bamboo shoots demonstrated product-specific microbial diversity and identified metabolic pathways, biosynthetic gene clusters and potential functional traits (Das et al., 2026). These approaches provide valuable information on microbial composition and genetic potential, although gene detection alone cannot establish metabolic activity.

8.2. Metabolomics and Functional Characterization

Metabolomics provides an important approach for understanding biochemical transformations during fermentation by identifying changes in amino acids, organic acids, fatty acids, phenolic compounds and other metabolites. Using GC-MS-based metabolite profiling alongside bacterial community analysis, Das et al. (2023b) demonstrated distinct biochemical characteristics among Hawaijar, Bekang and Akhone, suggesting that differences in microbial communities and traditional processing practices may influence product composition. Similarly, integrated metagenomic–metabolomic analysis of *Kinema* revealed diverse microbial and metabolic features associated with soybean fermentation (Kharnaior and Tamang, 2022). Techniques such as LC-MS, GC-MS and NMR could further clarify the transformation of plant-derived compounds and identify potential biochemical markers of fermentation quality. However, microbial–metabolite associations require experimental validation before causal relationships can be established.

8.3. Multi-Omics Approaches

Integrating metagenomics, metatranscriptomics, proteomics and metabolomics offers opportunities to understand the relationships between microbial communities and biochemical changes during fermentation. Kharnaior and Tamang (2023) employed genome-resolved metagenomics and metabolomics to investigate traditional fermented soybean foods of Arunachal Pradesh, identifying microbial genomes and diverse fermentation-associated metabolites. Such investigations demonstrate the potential of combining molecular and chemical analyses to characterize complex fermentation systems. Nevertheless, most existing studies primarily describe microbial composition and metabolite associations rather than directly establishing microbial functions. Future investigations incorporating gene-expression analysis, enzyme characterization and longitudinal metabolite profiling could help identify microorganisms responsible for specific nutritional transformations.

8.4. Precision Fermentation and Starter-Culture Development

The development of characterized starter cultures represents a promising strategy for improving the safety, consistency and nutritional characteristics of indigenous fermented plant foods. Functional characterization of lactic acid bacteria isolated from Indian fermented foods has identified microorganisms with potentially useful metabolic characteristics (Tamang et al., 2024).

Furthermore, metagenomic investigations of fermented bamboo shoots have provided information on microbial functional genes and potential safety-associated characteristics that may support the selection of candidate starter organisms (Das et al., 2026). Indigenous strains of *Bacillus* and lactic acid bacteria could be evaluated for proteolytic activity, carbohydrate metabolism, desirable metabolite production and fermentation stability. However, starter-culture development requires strain-level identification, assessment of antimicrobial resistance and toxigenic potential, and controlled fermentation trials. Standardisation should also preserve the distinctive sensory characteristics and traditional identity of indigenous foods.

8.5. Artificial Intelligence in Fermentation Optimisation

Artificial intelligence and machine learning offer emerging opportunities for predicting fermentation outcomes from microbial, biochemical and environmental data. Rocha et al. (2024) demonstrated machine-learning approaches for Arabica coffee fermentation, illustrating their potential to analyse relationships among fermentation conditions, chemical composition, and sensory characteristics. Similar approaches could be adapted to traditional fermented bamboo shoots and soybean products of North-East India to investigate the effects of temperature, pH, fermentation duration and microbial composition on product quality. However, direct applications of AI to these indigenous foods remain insufficiently documented. Future studies should therefore emphasise standardised datasets, independent model validation, and experimental confirmation of predicted fermentation outcomes.

9. CONCLUSION AND FUTURE PERSPECTIVES

Indigenous fermented plant foods of North-East India represent a valuable intersection of botanical diversity, microbial ecology and traditional knowledge. Studies on kinema and fermented bamboo shoots have revealed diverse microbial communities and metabolic pathways, with lactic acid bacteria contributing to bamboo shoot fermentation and Bacillus species playing important roles in alkaline soybean fermentation (Kumar et al., 2019; Das et al., 2023a). Comparative investigations of hawaijar, bekang and akhone have further identified product-specific microbial communities and metabolite profiles (Das et al., 2023b). Recent metagenomic studies have also demonstrated the functional potential of microorganisms associated with these traditional foods (Kumar et al., 2019; Das et al., 2023a, 2026). Nevertheless, most available findings establish microbial associations and predicted metabolic functions rather than experimentally confirmed nutritional or health benefits (Kharnaior and Tamang, 2022; Das et al., 2023b).

This review offers an integrated perspective on indigenous fermented plant foods of North-East India by examining the relationships between botanical substrate composition, traditional processing practices, microbial community dynamics and biochemical transformations. By bringing together ethnobotanical, metagenomic, metabolomic and functional evidence, it identifies potential links between plant–microbe interactions and nutritional outcomes, while highlighting the experimental approaches needed to establish these relationships. This perspective provides a basis for future substrate-specific investigations, safe starter-culture development and scientifically informed preservation of indigenous fermentation practices.. Unlike descriptive approaches focusing primarily on microbial diversity, this framework provides a testable basis for understanding how specific plant substrates and fermentation conditions influence product quality and nutritional properties. Existing multi-omics investigations provide a methodological foundation for this approach (Kharnaior and Tamang, 2022, 2023). Future studies should combine longitudinal microbial profiling, metatranscriptomics, metabolomics and controlled fermentation experiments to establish causal relationships between microbial activity and biochemical changes.

Further research should prioritize strain-level characterization, development of safe indigenous starter cultures, reduction of undesirable metabolites and experimental validation of reported bioactivities. Genomic safety screening, bioaccessibility studies and appropriately designed human trials are necessary before health-related claims can be substantiated. Emerging computational approaches, including machine learning, may also assist in predicting fermentation quality and processing outcomes when adequate experimental datasets become available (Rocha et al., 2024).

Importantly, scientific standardization should complement rather than replace traditional fermentation practices. Community participation, ethical benefit-sharing and preservation of indigenous knowledge must remain central to future research and commercialization. Integrating ethnobotany, microbial ecology, analytical biochemistry and food-safety research could therefore support the development of safer, nutritionally characterized fermented foods while safeguarding the distinctive biological and cultural heritage of North-East India.

CONFLICT OF INTEREST

The author declare that there is no conflict of interest.

ETHICS STATEMENT

Ethical approval was not required for this study.

REFERENCES

[1] Acharya, B., Behera, A., Sahu, P. K., Dilnawaz, F., Behera, S., Chowdhury, B., & Mishra, D. P. (2023). Bamboo shoots: An exploration into its culinary heritage in India and its nutraceutical potential. Journal of Ethnic Foods, 10, Article 22. https://doi.org/10.1186/s42779-023-00190-7

[2] Castro-Alba V, Lazarte CE, Perez-Rea D et al (2019) Fermentation of pseudocereals quinoa, canihua, and amaranth to improve mineral accessibility through degradation of phytate. J Sci Food Agric 99(11):5239–5248. https://doi.org/10.1002/jsfa.9793

[3] Chen Y, Luo W, Fu M et al (2023) Effects of selected *Bacillus* strains on the biogenic amines, bioactive ingredients and antioxidant capacity of shuidouchi. Int J Food Microbiol 388:110084. https://doi.org/10.1016/j.ijfoodmicro.2022.110084

[4] Chin XH, Elhalis H, Chow Y, Liu SQ (2024) Enhancing food safety in soybean fermentation through strategic implementation of starter cultures. Heliyon 10:e25007. https://doi.org/10.1016/j.heliyon.2024.e25007

[5] Das D, Kabir ME, Borah A et al (2024) Alpha-glucosidase inhibitory and glucoregulatory potential of soy protein fermented with a bacterium (*Bacillus subtilis* PM_NEIST_3) isolated from Hawaijar. Food Biosci 62:105465.

[6] Das R, Kumar R, Tamang B (2026) Microbial community structure, functional potential, probiotic signatures, and MAG reconstruction of fermented bamboo shoots from Northeast India. FEMS Microbes 7:xtag032. https://doi.org/10.1093/femsmc/xtag032

[7] Das R, Tamang B, Najar IN et al (2023a) First report on metagenomics and their predictive functional analysis of fermented bamboo shoot food of Tripura, North East India. Front Microbiol 14:1158411. https://doi.org/10.3389/fmicb.2023.1158411

[8] Das R, Tamang B, Najar IN et al (2024) Probiotic yeast characterization and fungal amplicon metagenomics analysis of fermented bamboo shoot products from Arunachal Pradesh, northeast India. Heliyon 10:e39500. https://doi.org/10.1016/j.heliyon.2024.e39500

[9] Das S, Bhattacharjee MJ, Mukherjee AK, Khan MR (2023b) Comprehensive bacterial-metabolite profiles of Hawaijar, Bekang, and Akhone: a comparative study on traditional fermented soybeans of north-east India. World J Microbiol Biotechnol 39:315. https://doi.org/10.1007/s11274-023-03773-3

[10] Das, R., Kumar, R., & Tamang, B. (2026). Microbial community structure, functional potential, probiotic signatures, and MAG reconstruction of fermented bamboo shoots from Northeast India. FEMS Microbes, 7, xtag032. https://doi.org/10.1093/femsmc/xtag032

[11] Das, R., Rai, P. K., Pandey, S., Das, N., Medhi, M. C., & Tamang, B. (2026). Lactiplanti*Bacillus* plantarum dominates the core microbiota of Gundruk across different leafy substrates: A culture-dependent and 16S rRNA amplicon study. Fermented Foods, 2, 100012. https://doi.org/10.1016/j.ferfo.2026.100012

[12] Das, R., Tamang, B., Najar, I. N., Bam, M., & Rai, P. K. (2024). Probiotic yeast characterization and fungal amplicon metagenomics analysis of fermented bamboo shoot products from Arunachal Pradesh, northeast India. Heliyon, 10(20), e39500. https://doi.org/10.1016/j.heliyon.2024.e39500

[13] Deka, P., et al. (2021). Metagenomic analysis of bacterial diversity in traditional fermented foods reveals food-specific dominance of specific bacterial taxa. Fermentation, 7(3), 167. https://doi.org/10.3390/fermentation7030167

[14] Deka, P., Mehetre, G. T., Lalnunmawii, E., Upadhyaya, K., Singh, G., Hashem, A., Al-Arjani, A.-B. F., Abd_Allah, E. F., & Singh, B. P. (2021). Metagenomic analysis of bacterial diversity in traditional fermented foods reveals food-specific dominance of specific bacterial taxa. Fermentation, 7(3), 167. https://doi.org/10.3390/fermentation7030167

[15] Dissook S, Thongkumkoon P, Noisagul P et al (2025) Insights into microbial and metabolite profiles in traditional Northern Thai fermented soybean (Tuanao) fermentation through metagenomics and metabolomics. Foods 14(17):3070. https://doi.org/10.3390/foods14173070

[16] Elhalis H, Chin XH, Chow Y (2024) Soybean fermentation: microbial ecology and starter culture technology. Crit Rev Food Sci Nutr 64(21):7648–7670. https://doi.org/10.1080/10408398.2023.2188951

[17] Gao X, Li C, He R et al (2023) Research advances on biogenic amines in traditional fermented foods: emphasis on formation mechanism, detection and control methods. Food Chem 405:134911. https://doi.org/10.1016/j.foodchem.2022.134911
[18] Gao Y, Hu M, Meng W et al (2024) Study on the quality of soybean proteins fermented by *Bacillus subtilis* BSNK-5: insights into nutritional, functional, safety, and flavor properties. Food Chem 443:138523. https://doi.org/10.1016/j.foodchem.2024.138523
[19] Goyal, A. K., Usha, T., Kalita, M., Hemavathi, K. N., Hemalatha, P., Mushahary, S., et al. (2024). Tradition meets technology: An overview of fermented bamboo shoots. Advances in Bamboo Science, 7, 100078. https://doi.org/10.1016/j.bamboo.2024.100078
[20] Gunawardena, S., Nadeeshani, H., Amarasinghe, V., & Liyanage, R. (2024). Bioactive properties and therapeutic aspects of fermented vegetables: A review. Food Production, Processing and Nutrition, 6, 31. https://doi.org/10.1186/s43014-023-00176-7
[21] Hati S, Basaiawmoit B, Ramanuj K et al (2024) Bio-functional properties and anti-inflammatory activity on the RAW macrophage cell line of Tungrymbai, a traditional fermented soy food of Meghalaya. Indian J Exp Biol 62:730–746. https://doi.org/10.56042/ijeb.v62i09.8299
[22] Huang J, Sun M, Guan X et al (2025) Metabolic variations in bamboo shoot boiled liquid during Pediococcus pentosaceus B49 fermentation. Foods 14(15):2731. https://doi.org/10.3390/foods14152731
[23] Huang, R., Fang, Y., Zhong, Y., Wang, D., Lu, W., Zhao, H., & Deng, Y. (2026). Advancing fermentation science: Microbial dynamics, metabolomics, and safety in fermented vegetables. Journal of Future Foods, 6(5), 780–795. https://doi.org/10.1016/j.jfutfo.2024.11.012
[24] Hung CM, Chu WC, Huang WY et al (2024) Safety assessment of a proprietary fermented soybean solution, Symbiota®, as an ingredient for use in foods and dietary supplements: non-clinical studies and a randomized trial. Food Sci Nutr 12:2346–2363. https://doi.org/10.1002/fsn3.3921
[25] Jiang M, Liu Y, Xue Y et al (2026) Angiotensin-converting enzyme inhibitory peptides from the soybean meal: screening, interaction, and their protective effects on Ang II-induced EA.Hy926 injury. J Agric Food Chem 74:10207–10219.
[26] Kaur P, Zalpouri R, Modi R et al (2023) Development and standardization of processing technique for ready-to-use lab fermented Kanji mix using refractance window dried black carrot powder. Sci Rep 13:185. https://doi.org/10.1038/s41598-023-27450-5
[27] Kefale B, Delele MA, Fanta SW, Abate S (2025) Effect of packaging materials and storage temperature on the shelf stability of Awaze paste. Front Nutr 11:1503328. https://doi.org/10.3389/fnut.2024.1503328
[28] Kharnaior P, Tamang JP (2022) Metagenomic-metabolomic mining of Kinema, a naturally fermented soybean food of the Eastern Himalayas. Front Microbiol 13:868383. https://doi.org/10.3389/fmicb.2022.868383
[29] Kharnaior P, Tamang JP (2023) Microbiome and metabolome in home-made fermented soybean foods of India revealed by metagenome-assembled genomes and metabolomics. Int J Food Microbiol 407:110417. https://doi.org/10.1016/j.ijfoodmicro.2023.110417
[30] Kiczorowski P, Kiczorowska B, Samolińska W et al (2022) Effect of fermentation of chosen vegetables on the nutrient, mineral, and biocomponent profile in human and animal nutrition. Sci Rep 12:13422. https://doi.org/10.1038/s41598-022-17782-z
[31] Kumar J, Sharma N, Kaushal G et al (2019) Metagenomic insights into the taxonomic and functional features of Kinema, a traditional fermented soybean product of Sikkim Himalaya. Front Microbiol 10:1744. https://doi.org/10.3389/fmicb.2019.01744
[32] Kumar, J., et al. (2019). Metagenomic insights into the taxonomic and functional features of Kinema, a traditional fermented soybean product of Sikkim Himalaya. Frontiers in Microbiology, 10, 1744. https://doi.org/10.3389/fmicb.2019.01744
[33] Kumar, J., Sharma, N., Kaushal, G., Samurailatpam, S., Sahoo, D., Rai, A. K., & Singh, S. P. (2019). Metagenomic insights into the taxonomic and functional features of kinema, a traditional fermented soybean product of Sikkim Himalaya. Frontiers in Microbiology, 10, 1744. https://doi.org/10.3389/fmicb.2019.01744
[34] Kumari R, Sharma N, Sharma S et al (2023) Production and characterization of bioactive peptides in fermented soybean meal produced using proteolytic *Bacillus* species isolated from kinema. Food Chem 421:136130. https://doi.org/10.1016/j.foodchem.2023.136130

[35] Lee S, Kwon RH, Kim JH et al (2022) Changes in isoflavone profile from soybean seeds during Cheonggukjang fermentation based on high-resolution UPLC-DAD-QToF/MS: new succinylated and phosphorylated conjugates. Molecules 27(13):4120. https://doi.org/10.3390/molecules27134120

[36] Lee SH, Lee S, Lee SH et al (2021) Integrated metabolomics and volatolomics for comparative evaluation of fermented soy products. Foods 10(11):2516. https://doi.org/10.3390/foods10112516

[37] Loying, R., Kalita, J., & Manna, P. (2024). Rice-based alcoholic fermented beverages of North-East India: Insight into ethnic preparation, microbial intervention, ethnobotany, and health benefits. Journal of Food Biochemistry, 2024, Article 7769743. https://doi.org/10.1155/2024/7769743

[38] Mipun, P., Sarma, P., Dey, G., Terangpi, L., Hajong, B., Chakraborty, D., Kshetriya, D., Mandal, S. M., Dinata, R., & Baindara, P. (2026). Ethnic fermentation secrets of Northeast India and emerging functional food insights. Food Research International, 228, 118431. https://doi.org/10.1016/j.foodres.2026.118431

[39] Mishra BK, Hati S, Das S (2019) Bio-nutritional aspects of Tungrymbai, an ethnic functional fermented soy food of Khasi Hills, Meghalaya, India. Clin Nutr Exp 26:8–22. https://doi.org/10.1016/j.yclnex.2019.05.004

[40] Nebbia S, Lamberti C, Lo Bianco G et al (2021) Antimicrobial potential of food lactic acid bacteria: bioactive peptide decrypting from caseins and bacteriocin production. Microorganisms 9(1):65. https://doi.org/10.3390/microorganisms9010065

[41] Padhi S, Sanjukta S, Chourasia R et al (2021) A multifunctional peptide from *Bacillus* fermented soybean for effective inhibition of SARS-CoV-2 S1 receptor binding domain and modulation of Toll Like Receptor 4: a molecular docking study. Front Mol Biosci 8:636647. https://doi.org/10.3389/fmolb.2021.636647

[42] Prativi MBN, Astuti DI, Putri SP et al (2023) Metabolite changes in Indonesian Tempe production from raw soybeans to over-fermented Tempe. Metabolites 13(2):300. https://doi.org/10.3390/metabo13020300

[43] Qiao, Y., et al. (2022). Fermented soybean foods: A review of their functional components, mechanism of action and factors influencing their health benefits. Food Research International, 158, 111575. https://doi.org/10.1016/j.foodres.2022.111575

[44] Ricci A, Bernini V, Maoloni A et al (2019) Vegetable by-product lacto-fermentation as a new source of antimicrobial compounds. Microorganisms 7(12):607. https://doi.org/10.3390/microorganisms7120607

[45] Rocha RAR et al (2024) Evaluation of Arabica coffee fermentation using machine learning. Foods 13(3):454. https://doi.org/10.3390/foods13030454

[46] Rocha RAR, Cruz MAD, Silva LCF et al (2024) Evaluation of Arabica coffee fermentation using machine learning. Foods 13(3):454. https://doi.org/10.3390/foods13030454

[47] Saha Turna N, Chung R, McIntyre L (2024) A review of biogenic amines in fermented foods: occurrence and health effects. Heliyon 10:e24501. https://doi.org/10.1016/j.heliyon.2024.e24501

[48] Saikia, L., Dutta, P. P., Gogoi, D., Talukdar, N. C., Sen, S., Sahariah, P., & Bharali, A. (2026). Indigenous fermented foods of Northeast India: Emerging opportunities in functional foods, microbiota-driven nutrition and safety perspectives. Food Bioscience, 80, 108992. https://doi.org/10.1016/j.fbio.2026.108992

[49] Samantaray, P., & Saha, S. (2026). Decoding the microbial diversity of Indian fermented foods: Integrating ethnobiology, multi-omics and functional insights. Foods, 15(4), 687. https://doi.org/10.3390/foods15040687

[50] Seo S, Jeong DW, Sul S, Lee JH (2025) Safety and amino acid profiles of *Bacillus* safensis in soybean fermentation. FEMS Microbiol Lett 372:fnaf063. https://doi.org/10.1093/femsle/fnaf063

[51] Singh TA, Nongthombam G, Goksen G et al (2023) Hawaijar – An ethnic vegan fermented soybean food of Manipur, India: a comprehensive review. Food Res Int 170:112983. https://doi.org/10.1016/j.foodres.2023.112983

[52] Singhal P, Satya S, Naik SN (2021) Fermented bamboo shoots: a complete nutritional, anti-nutritional and antioxidant profile of the sustainable and functional food to food security. Food Chem Mol Sci 3:100041. https://doi.org/10.1016/j.fochms.2021.100041

[53] Song DH, Chun BH, Lee S et al (2020) Metabolite profiling and microbial community of traditional Meju show primary and secondary metabolite differences correlated with antioxidant activities. J Microbiol Biotechnol 30(11):1697–1705. https://doi.org/10.4014/jmb.2007.07026

[54] Talukdar, S., Jyethi, D. S., Sarma, B., & Talukdar, H. (2026). Cultural ecology and conservation of traditional beverage practices among selected communities of Assam, Northeast India. Discover Food, 6, Article 376. https://doi.org/10.1007/s44187-026-01101-w

[55] Tamang JP, Kharnaior P, Halami PM (2024) Lactic acid bacteria in some Indian fermented foods and their predictive functional profiles. Braz J Microbiol 55:1745–1751. https://doi.org/10.1007/s42770-024-01251-y

[56] Tamang, J. P. (2022). "Ethno-microbiology" of ethnic Indian fermented foods and alcoholic beverages. Journal of Applied Microbiology, 133(1), 145–161. https://doi.org/10.1111/jam.15382

[57] Tamang, J. P., Jeyaram, K., Rai, A. K., & Mukherjee, P. K. (2021). Diversity of beneficial microorganisms and their functionalities in community-specific ethnic fermented foods of the Eastern Himalayas. Food Research International, 148, 110633. https://doi.org/10.1016/j.foodres.2021.110633

[58] Tushir S, Bidyalakshmi T, Bembem K et al (2026) Impact of fermentation containers and *Bacillus subtilis* BCB-19 starter culture on the microbial, sensory, and textural quality of Hawaijar. Food Humanit 7:101347. https://doi.org/10.1016/j.foohum.2026.101347

[59] Vermeersch M, Mayr C, Maes A et al (2026) Microbiological survey of spontaneous vegetable fermentations: a food safety perspective. Int J Food Microbiol 446:111541. https://doi.org/10.1016/j.ijfoodmicro.2026.111541

[60] Wang, X., et al. (2025). Microbial diversity and changes in flavor compounds during the fermentation of vegetables: A review. Journal of Food Science, 90, e70738. https://doi.org/10.1111/1750-3841.70738

[61] Wastyk HC, Fragiadakis GK, Perelman D et al (2021) Gut-microbiota-targeted diets modulate human immune status. Cell 184(16):4137–4153.e14. https://doi.org/10.1016/j.cell.2021.06.019

[62] Wei G, Zhao F, Zhang Z et al (2025) Identification and characterization of umami-ACE inhibitory peptides from traditional fermented soybean curds. Food Chem 465:142160. https://doi.org/10.1016/j.foodchem.2024.142160

[63] Xiang A, Wang J, Xie B et al (2022) Determination of 14 isoflavone isomers in Natto by UPLC-ESI-MS/MS and antioxidation and antiglycation profiles. Foods 11(15):2229. https://doi.org/10.3390/foods11152229