Review Article

Isolation sources and fermentation potential of lactic acid bacteria from plants, livestock and aquatic microbiota

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ABSTRACT

Lactic acid bacteria (LAB) constitute a wide range of bacteria that produce lactic acid as one of their main products. They are particularly important in the acidification of products, which is crucial in various food fermentation processes. Therefore, understanding their sources and mechanisms is vital to ensure the success of food fermentation processes. LAB can be naturally found on various plant, animal skin surfaces, as well as animal gut intestine. The type of LAB present is distinct for each microbiota but a comprehensive overview that describes the source of raw food microbiota has remained missing. Hence, the microbiota and distribution of LAB at various plant, terrestrial livestock and aquatic sources will be reviewed according to the phylum dominance and the genus of LAB detected across different host. Finally, the relationship between the LAB detected from and the fermented food is also reviewed.

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1. Introduction

Lactic acid bacteria (LAB) are a group of phylogenetically related microorganisms that are Gram positive, catalase negative, non-sporulating, non-motile, produce lactic acid as one of their main products, low G+C content and contain small genomes of 2 to 3 Mb (Mazzoli et al., 2014). Some common LAB belong to the genera Lactococcus, Streptococcus, Lactobacillus, Leuconostoc, Pediococcus, Weissella and Bifidobacterium (Zapaśnik et al., 2022). However, it is important to note that the genus Lactobacillus was reclassified to 25 different genera in 2020 (Zheng et al., 2020). LAB are used extensively in food biotechnology for fermentation and preservation purposes. LAB excrete organic acids, especially lactic acid, to acidify food products and produce other metabolites to achieve the desired organoleptic properties and quality of the foods produced (de Souza et al., 2023). Thus, understanding their metabolic activity and their roles in these processes simplifies the management and improvement of such industrial applications. In a human context, probiotics that mainly comprises LAB provide health benefits to humans and, to a certain extent, possess therapeutic properties (Tang et al., 2023). LAB are generally nutritionally fastidious and require various sugars, vitamins, minerals and peptides to support their continuous growth. Therefore, it is not surprising that traces of LAB can be found on plant phyllospheres, fermented food as well as human and animal guts because these nutrient rich habitats are able to sustain the growth of these microorganisms (Amenu & Bacha, 2023; Sirisopapong et al., 2023; Tang et al., 2023; Zhou et al., 2024). However, a comprehensive review about the dominating LAB from various parts of plant, terrestrial animals, aquatic products that can be used to produce fermented food is missing. Therefore, this review addressed the tools used for the identification of LAB and relating the dominant phylum with the presence of LAB in different microbiota.

2. Tools for the Identification of Lactic Acid Bacteria

Technological advancements and the usefulness of lactic acid bacteria, especially as probiotics have urged an immediate need on identification and classification of these bacteria prior to subsequent tests. Traditionally, identification of a potential probiotic was carried out by biochemical/phenotypic methods which include carbohydrate fermentation, their ability to grow at varying temperatures and salt concentrations in conjunction with their morphology and Gram staining characteristics (Donelli et al., 2013). However, the genotypic methods are currently more commonly used to identify LAB. Table 1 outlines the common methods used to detect and identify LAB from the host. The choice of method largely depends on the type of sample used, the purpose of application that is whether to examine the presence of LAB or whether isolation is required; and the desired level of specificity from genus and species identification to high-resolution strain typing. The methods used can be further divided into genotypic and phenotypic methods, but genotypic methods are more reliable in identifying the species of the microorganisms detected (Moraes et al., 2013).

Since the discovery of polymerase chain reaction (PCR) technique to amplify DNA, bacterial identification has become relatively easy and offers higher precision than the conventional phenotypic identification method. LAB are relatively easy to be identified genotypically as there are various methods that allow complete identification from food. The Food and Agriculture Organization of the United Nations (FAO) and the World Health Organization (WHO) recommended the 16S rRNA sequencing method and the randomly amplified polymorphic DNA (RAPD) method to identify lactic acid bacteria, especially those carrying beneficial properties, at the strain level (FAO/WHO, 2002). Consequently, most LAB isolated from plants, animal and food utilized this method as a definitive identification method (Ma et al., 2023; Rahman et al., 2026). The process of isolation requires a suitable culture medium such as Man Rogosa Sharpe (MRS) and the medium needs to be incubated at a suitable temperature, normally around 37oC (Martín-Miguélez et al., 2025).

The target bacterial colonies will be selected for DNA extraction and subsequently subjected to 16S rRNA sequencing for identification. Then, if strain differentiation is required, randomly amplified polymorphic DNA (RAPD) can be an easy an cheap alternative while Whole Genome Sequencing (WGS) can be used for precise strain differentiation (Sharma et al., 2020; Yadav & Shukla, 2017). Conversely, if a particular LAB is targeted in a particular microbiota, then the Quantitative PCR (qPCR) can be used to quantify the number of LAB in the sample (Sarun, 2026).

Table 1. The application and methodologies for the identification of lactic acid bacteria

Method	Principle	Discriminatory Power	Application	Limitation in Detecting LAB	Advantages in detecting LAB
Genotypic methods					
16-23S rRNA sequencing	Amplify corresponding DNA with specific primers targeting specific regions follow by determination of gene nucleotide sequences *(Singh et al.*, 2009)	Species	Identification of unknown LAB isolates	Cannot distinguish closely related LAB species (Olivier *et al.*, 2023)	General method used to identify newly isolated LAB, a method required to deposit gene sequences to NCBI gene bank

Method	Principle	Discriminatory Power	Application	Limitation in Detecting LAB	Advantages in detecting LAB
Genotypic methods					
Quantitative Real time PCR (qPCR)	Amplify DNA in real-time by using fluorescent dyes or sequence-specific probes that allow quantification of target DNA (Sarun, 2026)	Species	Quantitative detection of LAB from a particular matrix (Sarun, 2026)	Unable to distinguish viable and dead cells. Specific primer need to be designed to quantify specific LAB (Dreier *et al.*, 2022; Guo *et al.*, 2024a)	Sensitive and able to quantify specific LAB from a pool of LAB strains without culturing the LAB (Zamanpour *et al.*, 2025)
Multi-locus sequencing typing (MLST)	Characterizes bacterial strain by their unique allelic profiles by measuring the variations in housekeeping genes (Khanal *et al.*, 2022)	Strain	To differentiate strains of LAB in a particular microbiota	No standardized genes for analysis (Skotniczny & Satora, 2023)	Able to discriminate closely related LAB (Sharma *et al.*, 2020)
Randomly amplified polymorphic DNA (RAPD)	Utilizes short primers which anneals to multiple random target sequences and generate fingerprints of DNA bands that differs between bacterial species (Yadav & Shukla, 2017)	Strain	To create fingerprint database of LAB isolated from a particular microbiota, hence differentiating the strains of the isolated LAB (Ben Amor *et al.*, 2007)	Poor reproducibility of LAB strains. (Sharma *et al.*, 2020)	Good discriminary power and it can be enhanced by increasing number of primers(Sharma *et al.*, 2020)
Denaturing gradient gel electrophoresis (DGGE)	Amplify 16S rRNA region with primers, follow by separation of DNA fragments based on the decreased electrophoretic mobility of PCR amplified in polyacrylamide gels. (Bagheripoor-Fallah *et al.*, 2015)	Species	Determine the changes of LAB communities in a particular microbiota by determining the DNA band changes in the microbiota without undergoing bacteria colony isolation process	Poor detection of when number of LAB is low that causes incorrect estimation of LAB diversity in the food. (Sharma *et al.,* 2020*)*	No cultivation of LAB required from the food. (Sharma *et al.*, 2020)

Method	Principle	Discriminatory Power	Application	Limitation in Detecting LAB	Advantages in detecting LAB
Genotypic methods					
Repetitive element sequence-based PCR (Rep-PCR)	Use primers to amplify repetitive regions of the genome and the resulting DNA fingerprint patterns are compared after performing a standard gel electrophoresis (Bagheripoor-Fallah *et al*., 2015)	Strain	To further differentiate the strains of microorganism in the microbiota	Sensitive to DNA quality and electrophoresis conditions that causes reproducibility problem (Skotniczny & Satora, 2023)	With suitable primer, it can discriminate all types of LAB that contain only small amount of DNA. (Sharma *et al*., 2020)
Pulse field gel electrophoresis (PFGE)	Digest the DNA by restriction enzyme follow by subjecting the DNA fragments to an electric field with periodic reorientation in polarity (Yadav & Shukla, 2017)	Strain	Differentiate changes of specific strain over time, and also differentiate LAB in a sample (Ben Amor *et al*., 2007)	Labour intensive and takes 3-4 days to complete (Sharma *et al*., 2020)	Good ability to discriminate different LAB strains with high reproducibility(Sharma *et al*., 2020)
Next Generation Sequencing (NGS)	Directly sequence the bacterial RNA or DNA simultaneously (Wensel *et al*., 2022)	Species	Directly determine the microbial composition of specific microbiota.	Time consuming and expensive to generate all the information required (Skotniczny & Satora, 2023)	Generate vast amount of molecular data about identity and metabolism responses that allow highest discrimination power of LAB (Skotniczny & Satora, 2023)
Whole-genome sequencing (WGS)	Analyzes complete microbial DNA sequences by comparing target genomes to references using single nucleotide polymorphism (SNP) or gene-by-gene approaches to identify nucleotide differences, deducing evolutionary relationships and genetic functions (Sharma *et al*., 2020)	Strain	To deduce evolutionary and divergence relationships among LAB strains, characterize metabolic functions of the isolated LAB (El-Hosseny *et al*., 2025; Sharma *et al*., 2020)	Very expensive and requires highly qualified personal (Sharma *et al*., 2020)	Highly precise and reproducable data to distingush closely related strains (Sharma *et al*., 2020)

Method	Principle	Discriminatory Power	Application	Limitation in Detecting LAB	Advantages in detecting LAB
Chemotaxonomic Methods					
Matrix-Assisted Laser Desorption Ionization—Time of Flight Mass Spectrometry (MALDI-TOF MS)	Analyze composite fingerprints from both metabolic products and proteomic features then compare with records in database (Zhao & Liu, 2026)	Strain	As a powerful complementary tool of 16s rRNA Sequencing methods to identify lactic acid bacteria	Cannot identify a novel LAB	A reliable, fast and simple method with low chemical reagent cost (Oğuz & Andiç, 2024)
Phenotypic					
API system	Identify fermentation pattern of bacteria (Moraes *et al*., 2013)	Species	Phenotypic identication of microorganisms. Used as the second line of identification	Misidentifications due to different fermentation patterns. Cannot be relied as primary identification method	Shows fermentability of sugars and easy to perform
Biolog	Identify fermentation pattern of bacteria (Moraes *et al*., 2013)	Species	Phenotypic identication of microorganisms. Used as the second line of identification	Misidentifications due to different fermentation patterns. Cannot be relied as primary identification method	Shows fermentability of various carbon sources, easy to perform

3. Lactic Acid Bacteria in Terrestrial Food Animals

All animals carry microorganisms. These microorganisms, regardless of whether they are beneficial or harmful to the host, are found mainly in the gastrointestinal tract. Their populations often outnumber the total host cells, where animals are estimated to contain about 108 bacteria per g dry weight in ileal, and up to 1012 bacteria colonizing the colon (Canny & McCormick, 2008). This large number of microorganisms in mammalian gastrointestinal tract comprises 500 to 1000 bacterial species that constantly interact with the host and other members of the microbial community (Kim & Isaacson, 2015). In addition, the dominant phyla were reported to be Bacteroidetes and Firmicutes, which account for approximately 98% of total mammalian gut bacteria known to date (Yoon et al., 2015). Firmicutes are Gram-positive bacteria that might able to produce endospores, which enhances their ability to withstand the harsh gastrointestinal conditions of animals. The Firmicutes will work together with other microorganisms such as Bacteroidetes to break down complex carbohydrates and aid in nutrient absorption (Dias et al., 2025). Bacteroidetes on the other hand are Gram-negative bacteria that normally carries genes encoding carbohydrate-active enzymes, allowing them to assist animals, particularly mammals to digest complex carbohydrates from plants (Cerqueira et al., 2020). Nevertheless, it is well known that animal microbiota are prone to change, with shifts in microbial density and composition influenced by age, diet, environment, and other factors. Moreover, variations in microbiome composition have also been detected in each animal, which further complicates the situation (Jiang et al., 2020). Although it is impossible to provide a definitive description of the microbiota of a particular animal, efforts have been made to provide a general overview of the microbial community of all animal species. LABs can be generally found in intestine, fecals, oral cavity, reproductive

tract, teat canal and milk of mammals (Figure 1). Owing to this review focus on microbiota from food and food sources, the microbiota and LAB from a few common and important livestock are discussed here.

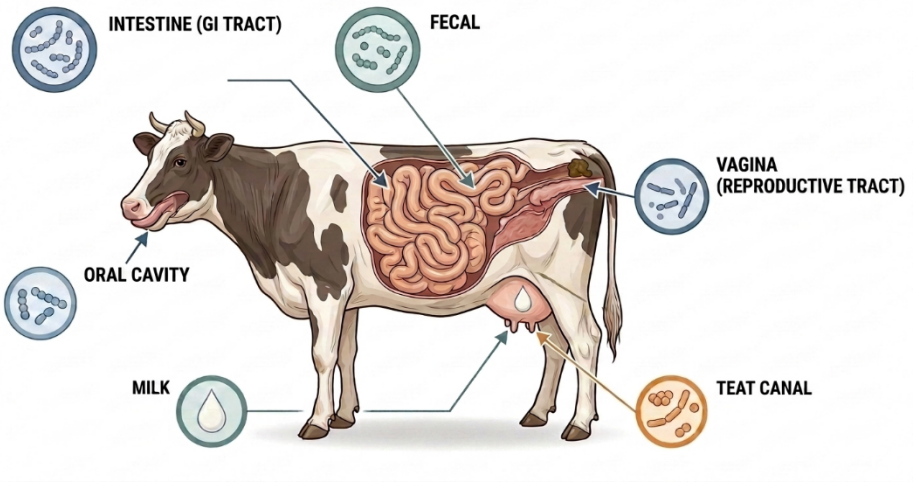


Figure 1. The general location of LAB identified from cattle and mammals

The domesticated broiler chicken is one of the most important food and protein sources in the world. The chickens have a very complex intestinal environment which comprises highly diversified microorganisms with more than 900 bacterial species (Sztandarski et al., 2022). The microbial community of the chicken gastrointestinal tract starts to develop immediately after hatching. However, unlike mammals that give birth, these newly hatched chickens have little maternally derived bacteria and are exposed to bacterial communities on the egg surface as well as the nest environment (Stanley et al., 2013). The chicken gut comprises three upper gut segments, namely the crop, gizzard and stomach. Consequently, each segment exhibits different biological functions and microbiota. Similar to most other animals, Firmicutes (80.62%) was the most abundant phylum across all chicken gut segments, followed by Proteobacteria (7.89%), Bacteroidetes (5.91%), of total microorganisms respectively. Upon further investigation, the same study mentioned that Lactobacillaceae family, which is part of the LAB is the most dominant genus accounting for 16.4% of total read abundance (Burrows et al., 2025). Similarly, Firmicutes was also the dominant phylum in ilea and caeca of chicken and Lactobacillales was predominant, accounting for 30% of total ilea population (Mohd Shaufi et al., 2015). Some of the main Lactic acid bacteria identified were Limosilactobacillus vaginalis, Limosilactobacillus reuteri, Ligilactobacillus salivarius, Ligilactobacillus saerimneri, Lactiplantibacillus plantarum, L. crispatus, and L. gallinarum (Ma et al., 2023; Rios-Galicia et al., 2024). Apart from Lactobacillaceae, Bifidobacterium is another dominant lactic LAB in chicken intestine, such as Bifidobacterium pseudolongum subsp. pseudolongum and subsp. globosum, B. pullorum, B. animalis subsp. lactis, B. boum, B. thermacidophilum subsp. thermacidophilum and B. thermophilum (Grande et al., 2024). Crucially, because Lactobacillaceae, Lactobacillales, and other LABs belong to Firmicutes phylum (Table 2), these studies provided an insight that LABs dominate chicken intestinal tracts regardless of their intestinal segments. LAB improve immune systems and inhibit growth of harmful pathogens in the chicken intestine, hence improve the overall health of chickens (Halder et al., 2024). Owing to this, poultry farmers supplemented chickens with LAB as probiotics to improve growth performance (Idowu et al., 2025).

Cows are herbivores, thus their digestive tracts are theoretically different from chickens that have been discussed previously. The ingested plant materials reside in the foregut while the rumen is inhabited by high density of microbiota to digest the plant materials. Therefore, understanding the microbiota of cows is particularly important as it affects the quality and composition of the meat and milk produced. Cows harbour complex microbiota with approximately 1010 bacteria and Firmicutes was found to be the most abundant phylum (47.9%), followed by Proteobacteria (8.6%) (Deusch et al., 2015; Paul et al., 2025). Hence, the Firmicutes mainly helps in breaking down carbohydrates of grasses ingested by cows (Dias et al., 2025). Similar to the chickens, LAB significantly contributes to the total intestinal community comprising numerous genera including various reclassified Lactobacillaceae, Lactococcus, Pediococcus, and Streptococcus (Marshall et al., 2022). There is a great difference among the microbiota of ruminal and fecal

with the milk, which is widely consumed by humans ($p<0.001$). Despite as mentioned in Figure 1 that LAB can be found in various parts of the cow, the study found extensive amount of Streptococcus, along with Lactobacillaceae, Lactococcus and Propionibacterium in milk, which Streptococcus, was not found to be abundant at other parts of cow (Guo et al., 2024b; Williamson et al., 2022). Variation of dominating LAB especially between milk, teat and intestine can be due to different microenvironment, as cattle intestines are more anaerobic and nutrients are mainly from fibrous grasses. However, the milk is a nutritionally dense liquid that might lead to favour facultative anaerobic Streptococcus. Therefore, the microbiota and LAB composition of milk is especially important when milk is used for food fermentation, and to determine the safety of the milk for human consumption.

Table 2. The dominant phylum and lactic acid bacteria across different microbiota

Matrix Type	**Isolation site**	**Dominant Phylum**	**Genus of Lactic acid bacteria found**
Terrestial food animal			
Chicken	Upper gut	Firmicutes (Burrows *et al.*, 2025)	*Limosilactobacillus* (Rios-Galicia *et al.*, 2024)
	Lower gut (ilea and caeca)	Firmicutes (Mohd Shaufi *et al.*, 2015)	*Ligalactobacillus*, *Limosilactobacillus, Lactiplantibacillus*, *Weissella*, *Bifidobacterium* (Grande *et al.*, 2024; Ma *et al.*, 2023; Rios-Galicia *et al.*, 2024; Wang *et al.*, 2023)
Cow	Gut	Firmicutes (Paul *et al.*, 2025)	*Lactobacillus acetotolerans*, *Lentilactobacillus*, *Ligilactobacillus*, *Paucilactobacillus*, *Lacticaseibacillus*, *Limosilactobacillus*, *Lactococcus*, *Pediococcus*, *Streptococcus* (Han *et al.*, 2014; Williamson *et al.*, 2022)
	Milk	Proteobacteria, Firmicutes (Salman *et al.*, 2023)	*Lactococcus, Propionibacterium*, *Streptococcus, Leuconostocs, Pediococcus, Entrococcus, Lacticaseibacillus, Lactobacillus delbrueckii, Lactiplantibacillus, Limosilactobacillus, Weissella* (Franciosi *et al.*, 2009; Zhang *et al.*, 2022)
Aquatic			
Fish	Skin	Proteobacteria, Gammaproteobacteria (Bell *et al.*, 2024)	*Lactobacillaceae*, *Lactococcus, Leuconostoc, Enterococcus* (El-Jeni *et al.*, 2019; Kato *et al.*, 2016)
	Gill	Proteobacteria (Wu *et al.*, 2021)	*Lactiplantibacillus, Enterococcus, Leuconostoc,* (El-Jeni *et al.*, 2019; Vargas-González *et al.*, 2024)

Matrix Type	Isolation site	Dominant Phylum	Genus of Lactic acid bacteria found
Aquatic			
Fish	Mouth	Pseudomonadota, Proteobacteria (Huavas *et al*., 2024; Ruiz *et al*., 2025)	*Lactiplantibacillus, Streptococcus* (Huavas *et al*., 2024; Vargas-González *et al*., 2024)
	Intestine	Proteobacteria (Xu *et al*., 2024)	*Lactococcus, Pseudolactococcus, Lactiplantibacillus*, *Enterococcus*, *Weissella*, *Lactobacillus, Leuconostocs* (Hossain *et al.,* 2026; Iorizzo *et al.,* 2021; Vargas-González *et al.,* 2024)
Crab	Shell	Proteobacteria, Bacteroidetes (Kraemer *et al*., 2020)	Not available
	Intestine	Firmicutes (Jiang et al., 2023; Liu et al., 2023a)	*Streptococcus*, *Ligilactobacillus*, *Lactiplantibacillus, Lacticaseibacillus, Weissella, Lactococcus, Vagococcus, Enterococcus, Pediococcus* (Lambuk *et al.,* 2022)
Prawn	Intestine	Proteobacteria (Zeng *et al*., 2017)	*Streptococcus*, *Enterococcus*, *Lactiplantibacillus, Liquorilactobacillus, Lactococcus, Pediococcus* (Lambuk *et al.,* 2022)
Plants			
Vegetable	Leaves	Proteobacteria (Capparotto *et al*., 2026)	*Lactiplantibacillus, Weissella, Enterococcus, Pediococcus, Leuconostoc, Lactococcus* (Presutto *et al.,* 2026)
Sweet potato	Tuberous roots	Proteobacteria, Firmicutes (Pepe-Ranney *et al*., 2020)	*Limosilactobacillus, Enterococcus* (Pepe-Ranney *et al.,* 2020)
Olive tree	Rhizophere	Proteobacteria, Actinobacteria (Wentzien *et al.,* 2023)	*Enterococcus, Lactococcus, Weissella, Leuconostoc, Pediococcus, Latilactobacillus, Lactiplantibacillus* (Fhoula *et al.,* 2013)
Foods			
Sauerkraut	Fermented cabbage	Firmicutes (Liu *et al*., 2023c)	*Latilactobacillus, Loigolactobacillus, Lactiplantibacillus, Levilactobacillus Pediococcus, Leuconostoc (Gaudioso et al*., 2022; Zhang *et al*., 2023)
Kimchi	Fermented cabbage	Firmicutes (Lee *et al.,* 2022)	*Leuconostoc, Weissella, Latilactobacillus, Lactococcus, Lactiplantibacillus* (Ko *et al.,* 2023; Lee *et al.,* 2022)

Matrix Type Foods	Isolation site	Dominant Phylum	Genus of Lactic acid bacteria found
Tempeh	soy bean	Firmicutes, Proteobacteria (Yarlina *et al*., 2022)	*Pediococcus, Lacticaseibacillus, Limosilactobacillus, Enterococcus* (Magdalena *et al.,* 2024; Yarlina *et al.,* 2022)
Soy sauce	Fermented soy bean	Firmicutes (Liu *et al*., 2023b)	*Weissella, Leuconostoc, Limosilactobacillus, Streptococcus, Enterococcus, Pediococcus, Lactiplantibacillus, Leuconostoc* (Liu *et al*., 2023b)
Sucuk	Fermented goat meat	Firmicutes (Bilecen Şen *et al*., 2026)	*Levilactobacillus, Lactiplantibacillus, Lacticaseibacillus* (Bilecen Şen *et al.,* 2026)
Kefir	Fermented milk	Firmicutes (Ströher *et al*., 2025)	*Lentilactobacillus, Lactobacillus, Leuconostoc, Lactococcus, Lactiplantibacillus, Ligilactobacillus, Limosilactobacillus, Bifidobacterium, Enterobacter, Streptococcus* (Ströher *et al.,* 2025)
Pla-ra	Fermented fish	Firmicutes (Rodpai *et al*., 2021)	*Loigolactobacillus, Ligilactobacillus, Weissella, Latilactobacillus, Lactiplantibacillus, Acetilactobacillus, Companilactobacillus, Lactococcus, Lacticaseibacillus, Bifidobacterium, Limosilactobacillus* (Rodpai *et al*., 2021)

4. Lactic Acid Bacteria in Aquatic Products

Freshwater and marine fish are an important food source in the human diet. Similar to animals, the fish, crustaceans and molluscs from both freshwater and marine environments contain large numbers of microorganisms residing on various parts of the skin, shells and gut (Figure 2). The composition of the microbiota in fish, crustaceans and molluscs largely depends on the species, environmental conditions, temperature and even water contamination (Cortés-Sánchez et al., 2024). In the context of fish microbiota, it has been generalized that the microbiota of marine fish from temperate waters comprises the genera Pseudomonas, Shewanella, Acinetobacter, Aeromonas, Vibrio, Moraxella, Psychrobacter, Photobacterium, Micrococcus, Corynebacterium, Bacillus, lactobacilli and Clostridium (Françoise, 2010). To withstand environmental pathogens, the fish skin is coated in a dense mucus layer that facilitates microbial adhesion, forming a protective biological barrier.(Nakatani et al., 2025). Consequently, a high density of bacteria resides within the outermost skin layer of fish. Meta-analysis from previous studies found that among 98 different fish species examined, the phylum Proteobacteria and Gammaproteobacteria were the dominant on the fish skins (Bell et al., 2024). In the context of LAB, some attempts of isolating and identifying the LAB species from the skin were unsuccessful despite 600 cfu/g of Lactobacillaceae and 280 cfu/g of Lactococcus spp were detected from Pebbly fish skin of Lake Albert (Kato et al., 2016; Vargas-González et al., 2024).

Mechanistically, isolation of LAB is mostly performed by using fish intestine, partially due to the fish skin is not anaerobic that facilitate the growth of LAB and the constant shear stress of water pressure around the fish may be unfavourable for the growth of LAB on the skin. However, Principal Coordinate Analyses (PCoA) demonstrated that surrounding water microbiota clustered more closely with skin microbiota than with gill microbiota, indicating that the ambient water column influences the fish skin microbiota more directly than it does internal respiratory surfaces (Rosado et al., 2021). Similar to the skins, other fish components such as the gill, mouth and swim bladder also contain relatively lesser LAB as these environments are unfavourable to colonization of LAB. The attempts of isolating lactic acid bacteria from mouth, swim bladder and gill mucus were also being conducted on Salmonoids, which Lactiplantibacillus sp. were mainly isolated from mouth and gill mucus while Leuconostoc mesenteroides were mainly isolated from the swim bladder (Vargas-González et al., 2024).

The intestines of fish harbour the highest abundance of microorganisms compared to other anatomical region. It was estimated that around 108 bacterial cells were residing at the fish gut, comprises mainly aerobes or facultative anaerobes (Talwar et al., 2018). The microbiota of the fish gut is greatly influenced by season, as the intestinal microorganisms react differently when there is a change in water temperature, and the feeding pattern is different due to differences in food availability between hot summer and cold winter seasons. Therefore, the dominant phyla are Proteobacteria (38%), Fusobacteria (38%) and Firmicutes (9%) during summer. However, when the climate turns to winter, Firmicutes increased to 19% while Fusobacteria decreased to 17% (Xu et al., 2024). Furthermore, the amount of baseline LAB populations within the fish intestine varies across species and habitat, where Cyprinus carpio was reported to carry around 2600 cfu/g of LAB, while Pebbly fish intestine carries 300 cfu/g of LAB (Al-Noor et al., 2023; Kato et al., 2016). Some of the LAB species isolated from fish gut were Lactococcus lactis, L. garvieae, L. formosensis, Lactiplantibacillus plantarum, Enterococcus faecalis, Weissella paramesenteroides, and Lactobacillus acidophilus (Hossain et al., 2026; Iorizzo et al., 2021). These indigenous LAB in fish functions similarly as the LAB from terrestrial food animals to enchance overal health benefits of fish by modulating host immunity, optimizing nutrient assimilation, and competitively excluding opportunistic aquatic pathogens. pathogens.

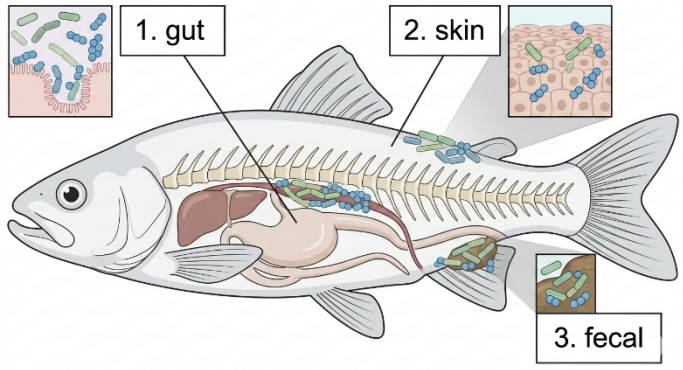


Figure 2. The general location of LAB identified from aquatic fish

Unlike animal or fish skins that are relatively soft surfaces that harbour microorganisms, it is interesting to note that the hard crustacean shells also carry considerable amounts of microorganisms. The shells from brown crab Cancer pagurus were mainly dominated by Proteobacteria (34% to 52%), Bacteroidetes (31% to 45%) and Actinobacteria (7% to 19%) (Kraemer et al., 2020). Shrimps, which represent another key group of crustaceans, are also reported to harbor a higher amount of Proteobacteria than other phyla (Cornejo-Granados et al., 2018). Although there are slight variations between different crustaceans, studies commonly showed Firmicutes, which is the dominant phylum of lactic acid bacteria, is not dominating the shell. Therefore, no studies have successfully isolated lactic acid bacteria from the crab

or prawn shells to date. This might be due to lactic acid bacteria are fastidious bacteria that require more nutrient dense habitat than the crab shell. Currently, most of the literature detected or isolated lactic acid bacteria from the intestine of crustaceans, because the environment is nutrient-dense and suitable to the survival of facultative anaerobes. The genera of LAB that proliferate at the intestines of crustaceans are mainly lactobacilli, Lactococcus, Leuconostoc, Enterococcus, Streptococcus, Carnobacterium, Pediococcus, and Weissella (Ringø et al., 2020). Several species of LAB were successfully isolated from the crab and shrimp intestines, such as Enterococcus faecalis, E. faecium, E. pseudovium, E. raffinosus, Lactiplantibacillus plantarum, L. salivarius, L. rhamnosus, L. pentosus,Weissella confusa, W. cibaria, Lactococcus garvieae, Streptococcus parauberis and Pediococcus pentosaceus (Lambuk et al., 2022; Migaou et al., 2024).

5. Lactic Acid Bacteria on Plants

Plants are essential for sustaining life on Earth, acting as attractive hosts for colonization of diverse microorganisms. Humans consume plants as part of their daily diet and utilize them as vital source of various micro and macro-nutrients. Microorganisms colonize three distinct locations of the plant, the first location is the phyllosphere, which includes the surfaces of leaves, stems, flowers and fruits; the second location is the rhizosphere, which comprises the roots; and also colonize the endophytes, inhabiting inside the plant cells (Figure 3) (Santoyo, 2025). The plant surface, namely the phyllosphere, is considered a hostile environment for microorganisms, because it is exposed to the intense heat and irradiation from the sun in addition to the limited availability of nutrients to support their normal growth (Berlec, 2012). Fresh vegetables are widely consumed by humans. They can be consumed either raw, or heat treated via boiling or frying and consumed as a delicacy. In this context, vegetable microbiota are particularly important, because they directly contribute to the subsequent fermentation processes. Despite the harsh conditions on the phyllosphere, the leaf of lettuce was found to contain mainly Proteobacteria (71.3%), followed by Bacteroidota (8.4%) and 7% of Firmicutes (Capparotto et al., 2026).

Although Firmicutes, which is the phylum for most lactic acid bacteria, is not the most dominant phylum on leaf surfaces, lactic acid bacteria still harbour up to 1 x 105 CFU/g of leaf surface population (Zwielehner et al., 2008). However, phylum composition depends on the species of vegetable tested, temperature and amount of rainfall. For example, it was mentioned that reduced air temperature may weaken the plant cells that causes the leaves to be susceptible to rainfall, thereby releasing nutrients to the leaf surface for bacterial growth. Although Firmicutes populations were relatively stable without significant variations at different seasons, the amount of most dominant Proteobacteria fluctuated throughout different seasons (Lopez-Velasco et al., 2011). Hence, the proportion of Firmicutes that contain LAB on the leaf fluctuates across seasons as well. Lactiplantibacillus pentosus, Weissella soli, Pediococcus pentosaceus, and Leuconostoc mesenteroides were part of the lactic acid bacteria identified on lettuce leaves (Presutto et al., 2026). These LAB might help maintain plant health by preventing invasion of pathogenic bacteria into the plant cells as they exhibit antimicrobial activity against common pathogens such as Listeria monocytogenes on lettuce (Park et al., 2025).

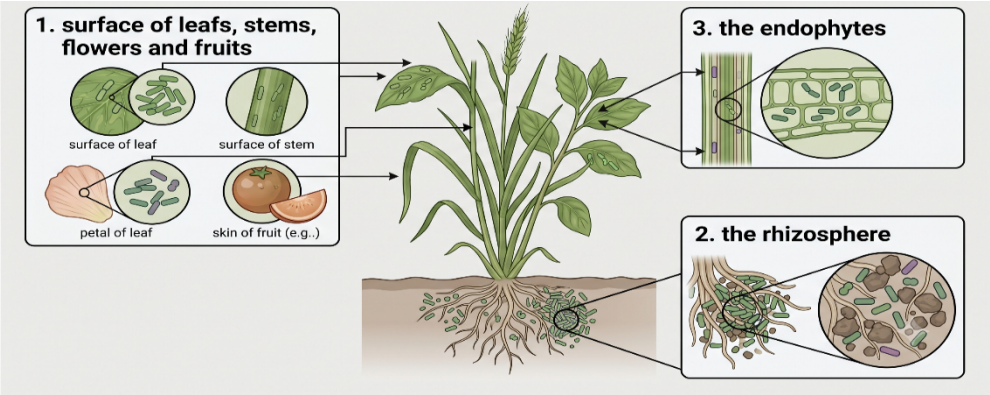


Figure 3. The general location of lactic acid bacteria identified from plants

It is well established that considerable numbers of bacteria are present in soil and efforts to examine soil microbiota are ongoing (Hebbar et al., 2025). Therefore, considering the plant roots are constantly in contact with the soil, the rhizosphere harbours a dense and complex microbiota. The rhizosphere microbiota are similar to other plant microbial communities, with variations detected across species, and they are largely influenced by different soil types, moisture, root lysates, secretions or exudates (Ramírez-Puebla et al., 2013). Plants that contain tuberous roots were dominated by Proteobacteria and Firmicutes. The root tubers of sweet potato activity modifies physiochemical attributes of the soil by releasing plant exudates, and exerts selective pressure on microbes that can colonize rhizome tissues by using immune systems (Pepe-Ranney et al., 2020). Therefore, the microbiota of soil will be slightly different from the roots. For example, Acidobacteria will be in abundance at the soil surrounding the sweet potato compared with the sweet potato root tubers (Mwazembe et al., 2025).

Lactic acid bacteria are relatively less in root tubers of common food with bacterial identification in Cilembu sweet potato yielding Klebsiella, Enterobacter, Pseudomonas, Chryseobacterium, Sphingomonas, Micrococcus, Kocuria, Microbacterium, Sphinghobacterium, Exiguobacterium, Bacillus, Streptomyces, Paracoccus, Staphylococcus, Methylobacterium, Arthrobacter and Serratia but no lactic acid bacteria was found dominant (Tangapo et al., 2018). However, the LAB Limosilactobacillus fermentum and Enterococcus faecalis can be found on sweet potato which Limosilactobacillus fermentum were specifically mentioned being detected 14 times in one sample of sweet potato, out of 19544 total observations from that sample (Pepe-Ranney et al., 2020). Other types of roots, such as olive tree rhizophere have reported presence of Latilactobacillus, Enterococcus, Pediococcus, Lactococcus, Weissella and Leuconostoc (Fhoula et al., 2013). Therefore, plant roots generally carry some LAB which can contribute to the microbiota of spontaneous fermentation of root products, that eventually provide another delicacy.

6. Lactic Acid Bacteria in Fermented Food

Fermentation of food can be categorised into submerged fermentation which used liquid substrates, or the solid-state fermentation, performed at solid substrates to increase nutrient efficiency. (Siddiqui et al., 2023). Most fermentations were originally spontaneous, that is, selectively utilizing the original microbiota from the raw materials to initiate fermentation. Over time, humans were able to control fermentation outcomes by introducing the back-slopping method and starter cultures (Sionek et al., 2023). Depending on the materials and final products desired, food fermentation can be carried out by either bacteria, yeast or mould. Meat, seafoods, milk, vegetables and fruits are being used as food matrices for lactic acid fermentation. Production of fermented food, such as fermented vegetables and fruits takes advantage of the plant microbiota, especially lactic acid bacteria that flourish on the plant (Peres et al., 2012). As mentioned previously in this review, large numbers of microorganisms colonized the plant surface, meat and fish skins. Among them, LAB played significant role in food fermentation to produce the desired organoleptic properties of the fermented food (Sionek et al., 2023).

LAB ensured the success of fermentation by excreting lactic acid and other organic acids to reduce the pH of the food matrix, which in turn suppresses the growth of spoilage microorganisms (Pragalaki et al., 2013). In addition, they synthesise a wide variety of other primary and secondary metabolites such as bacteriocins to enhance the antagonistic effect against spoilage bacteria (Tian et al., 2026). The number of lactic acid bacteria varies at different fermentation stages, hence prolonged fermentation might result in decreased total viable bacteria in the food (Demarigny, 2012). In this context, lactic acid fermentation has emerged as an important fermentation process in food production.

Firmicutes is the predominant phylum in most of fermented plant products, such as sauerkraut, kimchi, soy sauce and tempeh (Table 2). However, there are differences in the species of LAB detected in each fermented food product. For example, genus Latilactobacillus, Loigolactobacillus, Lactiplantibacillus, Levilactobacillus, Pediococcus, Leuconostoc were found in fermented cabbage of sauerkraut; while Pediococcus, Lacticaseibacillus, Limosilactobacillus, Enterococcus, were found in tempeh which is produced by solid-state fermentation (Gaudioso et al., 2022; Magdalena et al., 2024; Yarlina et al., 2022; Zhang et al., 2023). The LAB that colonized phyllosphere of the cabbage mostly contributes to the spontaneous fermentation of sauerkraut, while the LAB isolated from tempeh can originate from the surface of soy bean

used. Nevertheless, if starter cultures were used to initiate the fermentation such as fermentation of sauerkraut, the diversity of LAB will be lower than spontaneously fermented sauerkraut, but contain richer volatile flavour compounds because the starter cultures were specifically selected that is able to produce more esters and alcohol compounds than other LAB (Liu et al., 2023c).

Similar to vegetable and fruit fermentation, numerous meat and aquatic products were also fermented by LAB. Fermented meat and aquatic products are best represented by fermented sausages and Asian fermented shrimp cincalok (Murwani et al., 2024; Yang et al., 2022). These LAB played the same role as in plant fermentation to produce desirable organoleptic properties in the final products. Although it is presumed that these LAB originates from the meat and their microenvironment, LAB mostly colonize the guts of these animals and marine organisms. Nevertheless, numerous reports have confirmed the occurrence of LAB in raw meats, and they have been considered as spoilage bacteria in meat manufacturing industries because they lower meat pH and produce undesirable flavours (Doulgeraki et al., 2012; Rahkila et al., 2015). In this context, Pothakos et al. (2015) stated that LAB contamination occurs during handling, transportation and manufacturing of raw meat, while the source of LAB might be from the abiotic surfaces and food processing plants, as well as the surface of animal skins. Consequently, this indicates the possible origin of these LAB in meat fermentation.

In cincalok (fermented shrimp), out of 8 main bacteria isolated, 4 were found to be LAB, namely the Tetragenococcus halophilus, Enterococcus faecalis, Pisciglobus halotolerans and Levilactobacillus brevis (Murwani et al., 2024). The Tetragenococcus and Pisciglobus are not the typical LAB found in shrimp intestines or exoskeleton (Lambuk et al., 2022). They might be present at levels below the detection limit of the molecular methods used, or introduced by handlers during preparation of cincalok. Consequently, LAB isolated from Italian fermented sausage salani were mainly Latilactobacillus sakei, Latilactobacillus curvatus and Leuconostoc mesenteroides; while the LAB isolated from Turkish fermented sausage sucuk were mainly Lactiplantibacillus plantarum, Pediococcus acidilactici, Lactiplantibacillus pentosus, Weissella hellenica and Latilactobacillus sakei (Kamiloğlu, 2022; Nikodinoska et al., 2023). Despite the huge diversity in the LAB species involved in meat fermentation, it is presumed that fermentation is largely affected by the preparation method, surrounding environment and fermentation conditions.

Fermented dairy products appeared to be one of the most widely consumed fermented food. Traditional fermented foods range from beverages such as sour milk, fermented milk, and kefir; coagulated milk such as cheeses; to desserts such as yogurt (Shiby & Mishra, 2013). Fermentation of dairy products is relatively similar to other types of fermented food, as it can be done spontaneous practices, back sloping method or through the use of starter cultures. The presence of LAB in raw milk was discussed in this review previously, hence showing the reason of possible fermentation by LAB through spontaneous fermentation. A recent study identified nine different fermented dairy products, namely ayran, kefir, khurunga, shubat, two cottage cheeses, bryndza, khuruud and suluguni-like cheese; all of which were dominated by very distinct LAB. For example, Lactobacillus delbrueckii and Streptococcus thermophilus dominated kefir and aryan; while Lentilactobacillus kefiri, Lb. kefiranofaciens, Bifidobacterium mongoliense, Lactiplantibacillus plantarum and Lb. helveticus dominated shubat (Elcheninov et al., 2024). Therefore, the differences in microbiota contribute to the distinct organoleptic properties among fermented dairy products.

7. Conclusion

Lactic acid bacteria form an important part of microbiota in various parts of the plant, animal and humans. Their presence in these habitats may occur as a minority population or may dominate among the total microorganisms that colonize the habitat. They can be symbiotic, which the host provide nutrient to support growth, while the LAB improve the health of the host. LAB are also useful in various lactic acid fermentation of food to produce lactic acid to lower the pH of the food and ensure the success of the fermentation. However, the dominant LAB in the raw material used might be slightly different from the LAB isolated from the fermented food products. The LAB and overall microbiota of the fermented food is also affected by the use of starter cultures, as well as introduction of bacteria during handling and preparation of the fermented food. In future research, understanding the transition of LAB from natural reservoirs to the fermented food requires more advanced multi-omics integration. Combining shotgun metagenomics with transcriptomics,

proteomics, and metabolomics will enable researchers to determine the changes in LAB across different environments, how LAB respond to food fermentation process in genetic and proteomic perspectives and the outcome of the fermentation. The matching genes from DNA of different environments can be determined to understand the transfer of LAB to food, hence understand further about their mechanism of colonization and survival in fermented foods. These advanced bio-engineering strategies are able to assist in further constructing an in-depth knowledge of fermented food, optimize fermentation processes and increase the safety of the fermented products.

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The authors declare no conflicts of interest.

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The authors declared Gemini Pro was used to generate Figures 1, 2, 3. The authors reviewed and edited the content of generated Figure as needed.

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