

A Short Review on Different Bacteria Types Molecularly Isolated from Different Plant Sources

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ABSTRACT

This review highlights the different methods used for characterizing and identifying bacteria from different plant sources using molecular techniques, with the aim of emphasizing the importance of these tools in advancing microbial research. Traditional culture-based methods, though still valuable, often lack the precision, discriminatory power, and speed required for accurate bacterial identification, particularly when dealing with closely related or slow-growing organisms. In contrast, molecular approaches such as 16S rRNA gene sequencing, PCR-based assays, and protein-profiling techniques have significantly enhanced taxonomic resolution and provided deeper insights into the complexity of bacterial diversity within rhizospheric soils and plant tissues. Across a range of plant systems, including *citrus sinensis*, *lycopersicon esculentum*, and *centella asiatica*, molecularly identified bacterial isolates have demonstrated traits of considerable agronomic and biotechnological relevance. These include plant growth-promoting properties, nutrient solubilization, stress tolerance, and antimicrobial activity, all of which contribute to plant health and sustainable crop improvement. Importantly, the detection and molecular characterization of previously unreported endophytic bacterial species from various geographical regions further underscore the influence of environmental and ecological factors on microbial distribution and diversity.

Keywords: Bacteria, molecular identification, characterization, PCR-based assays, plant sources.

1.0 INTRODUCTION

Bacterial identification plays a vital role in microbiology and clinical diagnostics, as accurate detection of bacterial pathogens supports appropriate treatment decisions and helps limit the spread of infectious diseases (Sengupta *et al.*, 2020). Conventional culture-based approaches, although widely used, often lack the speed and precision needed for timely and reliable identification, which may contribute to treatment delays or suboptimal therapeutic outcomes. In contrast, molecular methods offer faster and more dependable results. These techniques rely on analyzing genetic material, with polymerase chain reaction (PCR) being one of the most common tools. PCR targets and amplifies defined DNA regions to enable identification, often in combination with sequencing or hybridization procedures (Van Belkum *et al.*, 2020). DNA sequencing, in particular, can directly determine bacterial species by matching obtained sequences with established reference databases (Ackerman *et al.*, 2021). Another advanced technique, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), rapidly distinguishes bacteria by assessing the mass-to-charge profiles of their protein constituents (Angeletti, 2019). Additionally, fluorescence in situ hybridization (FISH) employs fluorescently labeled DNA probes that bind to specific genetic targets within bacterial cells, enabling

precise visualization and identification (Harmsen *et al.*, 2021). This review was intended to highlight current research on characterization and isolation of bacteria from different plant sources through molecular methods.

2.0 BACTERIA FROM THE ROOT OF CITRUS FRUIT TREE (CITRUS SINENSIS L.)

Citrus fruits (*Citrus sinensis* L.), members of the *Rutaceae* family, are widely cultivated across tropical and subtropical regions of the world (Khan *et al.*, 2021). Their origin is traced to the southern Himalayan region, encompassing northeastern India and parts of China, the latter being the leading global producer of citrus (Rao *et al.*, 2020). Nutritionally, citrus fruits are highly valuable, containing sugars, organic and amino acids, vitamin C, and essential minerals like calcium and magnesium. These attributes make them significant contributors to human diets, whether consumed fresh or processed (Olahan *et al.*, 2023). The rhizosphere, the soil zone surrounding plant roots enriched by root exudates and microbial activity, is highly responsive to environmental conditions and therefore serves as a reliable indicator of soil quality and health (Fierer *et al.*, 2021).

A diverse soil microbiome is essential for sustaining the growth and productivity of terrestrial plants, including citrus species. Numerous soil microorganisms support

plant development by regulating hormonal balance, improving tolerance to stress, and contributing to stable yields (Dukare *et al.*, 2022). Bacteria, a key component of these microbial communities, play major roles in nutrient cycling, decomposition of organic matter, improving soil fertility, and preventing the spread of plant diseases (Dai *et al.*, 2021). The structure of bacterial communities within soil is closely linked to soil ecological integrity and has a notable impact on crop performance (Hermans *et al.*, 2020). Several factors shape bacterial diversity in soils, including parent material and pH (Jin *et al.*, 2022), temperature (Gao *et al.*, 2022), fertilization methods (Wan *et al.*, 2021), irrigation water quality (Gao *et al.*, 2022), and the use of copper-based fungicides (Huang *et al.*, 2021).

3.0 ENDOPHYTIC BACTERIA FROM TOMATO (*LYCOPERSICON ESCULENTUM* MILL.)

Tomato (*Lycopersicon esculentum* Mill.) is one of India's most significant vegetable crops and serves as a rich source of vitamins, minerals, organic acids, essential amino acids, and dietary fiber. Major tomato-producing countries include the United States, several European nations, China, and Japan. In India, tomato cultivation covers approximately 193.7 million hectares, with leading production coming from Andhra Pradesh (27.93 mt), followed by Madhya Pradesh (24.60 mt), Karnataka (18.37 mt), Gujarat (14.25 mt), Odisha (13.12 mt), West Bengal (12.65 mt), and Telangana (8.91 mt). Within Telangana specifically, tomatoes are grown on about 0.7 million hectares, yielding roughly 19.37 million tons annually, with a productivity rate of 28.1 MT/ha (Indian Horticulture Database, 2021). The major tomato-producing districts in the state include Ranga Reddy, Medak, Khammam, Adilabad, and Mahaboobnagar.

Endophytic bacteria are microorganisms that reside within the internal tissues of healthy plants without inducing disease symptoms or harming the host (Compant *et al.*, 2021). They have been isolated from a wide range of plant species, including trees, fodder plants, vegetables, fruits, cereals, and other crops (Al-Kaabi *et al.*, 2020). Once inside the plant, these prokaryotes may remain confined to the initial entry point or move throughout the plant system (White *et al.*, 2019). Endophytes are known to produce various bioactive metabolites such as alkaloids, steroids, terpenoids, peptides, polyketones, flavonoids, quinols, and phenols, all of which contribute to enhanced plant growth and improved resistance to pathogens (Santoyo *et al.*, 2020).

Given their ecological compatibility with plant pathogens, endophytic bacteria represent a promising alternative source of biocontrol agents for plant disease

management (Carrión *et al.*, 2019; Moronta-Barrios *et al.*, 2021). Endophytes associated with *Lycopersicon esculentum* Mill have been shown to exhibit several beneficial traits that may outperform conventional fungicides. These bacteria produce growth promoting substances such as indole-3-acetic acid (IAA), ammonia, hydrogen cyanide (HCN), and siderophores, all of which support both growth enhancement and disease suppression.

4.0 BACTERIAL ENDOPHYTES FROM *CENTELLA ASIATICA* LEAVES

Centella asiatica (L.) Urban (*Apiaceae*) is a valuable perennial herb widely found in both temperate and tropical wetland environments (Biswas *et al.*, 2021). Commonly referred to as pennywort or gotu kola, it thrives in warm, humid regions and is native to tropical wetland habitats. Its distribution spans the subtropical and tropical areas of India, parts of Venezuela, Madagascar, China, Mexico, South Africa, South America, and several Southeast Asian countries (Bahmani *et al.*, 2021; Wijayanto *et al.*, 2020). For centuries, plant extracts from this species have been used in traditional medicine to treat skin ailments including eczema, leprosy, varicose ulcers, psoriasis, and lupus as well as disorders affecting the female genitourinary system (Kumari *et al.*, 2019; Prakash *et al.*, 2020).

Endophytic bacteria have been isolated from various tissues of medicinal plants, including leaves, stems, roots, and fruits. Numerous studies have documented these endophytes using diverse microscopic and molecular approaches (Nongkhlaw & Joshi, 2021; Dong *et al.*, 2020). Research on endophytes associated with *C. asiatica* leaves has largely centered on fungal species such as *Aspergillus sp.*, *Ceratobasidium sp.*, *Fusarium sp.*, *Phialemoniopsis sp.*, *Colletotrichum sp.*, *Glomerella sp.*, *Guignardia sp.*, *Nigrospora sp.*, *Curvularia sp.*, and *Colletotrichum sp.* (Radiastuti *et al.*, 2019; Manandhar *et al.*, 2022). Although both fungal and some bacterial endophytes have been isolated, identified, and characterized, information specifically addressing bacterial endophytes in *C. asiatica* remains limited. Most existing studies on *C. asiatica* endophytes emphasize fungal communities, with relatively little attention paid to the bacterial counterparts.

5.0 CONCLUSION

This short review was able to highlight different types of bacteria that were previously isolated through molecular techniques with a view of deepening our understanding of bacterial communities associated with different plant species. The review has further shown how identified microorganisms, including species from genera such as

Bacillus, *Lysinibacillus*, *Leucobacter*, and *Alcaligenes*, exhibit functional attributes that are beneficial to plant health, potential as biological inoculants in enhancing crop productivity and soil health. Furthermore, the isolation of unique endophytic bacteria from *Centella asiatica* in distinct ecological regions reinforces the influence of geography on microbial diversity and the need for continued exploration. As molecular approaches continue to advance, they hold promise for expanding biotechnological applications, improving sustainable agricultural practices, and fostering the development of novel bioactive compounds.

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