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Review article

Bacterial Endophytes: A Versatile Factory for Producing Indole-3-acetic Acid, Recent Advances and Development

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Abstract

The growing scientific interest and exploration of endophytes from plants have shown vital plant health promotion, and are attracting scientific interest. The endophytes, including bacteria, significantly strengthen the host plants' growth and resilience, fortifying the plants' ability to combat pathogens and adapt to environmental stresses. Previous studies have investigated the pivotal role of endophytic bacteria in modulating the synthesis of secondary metabolites with medicinal properties and diverse biological effects. Endophytic bacteria are well-known sources of metabolites with notable medicinal potential and ability to boost plant growth, fortifying invulnerability to abiotic stress and biotic stress on plants. The catalog of primary and secondary metabolites that are produced by different endophytes indole-3-acetic acid (IAA) is an eminent constituent of the auxin in the indole derivatives family. IAA governs nearly every facet of botanical growth and progression, making it among the most significant phytohormones for plants. Notably, the endophyte bacteria deliver IAA which holds significance in growth and progression interactions with plants. Delving into the mechanisms underlying the biological synthesis and functions of IAA in endophytic bacteria can boost the production and application of IAA in agriculture and allied sectors. This review unifies recent research advancements in the production of IAA from bacterial endophytes and explains the pathway analysis for the biological synthesis of IAA.

Keywords: endophytes; metabolite; bacteria sustainability; indole-3- acetic acid; microbial diversity

1. Introduction

The beneficial association between microorganisms and plants in the macro or the micro-environment inside the plant has been explored in-depth for their augmenting effects on plant progression and metabolite production. Many metabolites, especially secondary metabolites including mechanisms to withstand abiotic and biotic stresses are essential for plants to thrive in their natural environments (Vardharajula et al., 2011). The association of microorganisms with plants is pivotal on account of the con-commitment effect of such organisms on plant growth and therapeutic metabolite production (Santoyo et al.,

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2016). These beneficial bacteria also provide a comprehensive scope of assets to their host plants, assisting them in dealing with various biotic and abiotic environmental challenges (Miliute et al., 2015). They coexist asymptomatically within the plant's cellular surroundings and carry out symbiotic roles such as supplying signaling molecules or secondary metabolites. These substances act as exogenous and endogenous influences that are crucial for the mutualistic relationship between the plant and endophytic bacteria (Eid et al., 2021). Medicinal plants exhibit a targeted approach in selecting endophytes, often impacted by the supply of secondary metabolites and the ingredients of root exudates. Consequently, microbial communities within these plants vary according to their nutritional demands, environmental conditions, and soil type (Wu et al., 2021). Secondary metabolites also find applications in the pharmaceuticals, cosmetics, and agriculture industries (Daud et al., 2019; Aswani et al., 2020; Yeshi et al., 2022). There is a belief that plant phytochemical composition is linked, whether directly or indirectly, to endophytic bacteria and the way the bacteria engage with host plants (Qi et al., 2012). Moreover, in addition to separately synthesizing secondary metabolites, endophytes develop symbiotic relationships with plants, consequently augmenting the biosynthesis of biologically active compounds produced by the host plants. Researchers have explored the symbiotic effects of medicinal plants and endophytic bacteria, evaluating them as a significant root of components with enhanced medicinal potential compared to plants functioning solo (Strobel, 2003; Heinig et al., 2013; Hardoim et al., 2015). Isolated endophytic bacteria affiliated with medicinal plants exhibit a broader array of secondary metabolites compared to those metabolites produced by plants alone. Hence, plants can serve as readily accessible reservoirs of microorganisms with significant biotechnological potential. The growing global population has led to rapid urbanization and industrialization, which is in turn leading to considerable pressure on cultivated land for increased crop production. To meet demand, there has been a widespread adoption of herbicides, agrochemicals like fertilizers, and fungicides. However, their excessive and indiscriminate use has had detrimental effects on various aspects of the ecosystem. It has led to polluted groundwater and aquifer-polluted soil (Singh et al., 2022). Hence, there is a critical demand for sustainable approaches to preserve the properties of soil and water that are essential for sustaining crop production and ecological balance. Rhizospheric and endophytic bacteria produce significant quantities of plant growth-progression substances, which directly or indirectly influence the advancement of medicinal plants (Sharma et al., 2020). Endophyte bacteria improve phyto development via various approaches including nutrient scavenging, biocontrol of plant pathogens, and enhancing sufferance to environmental challenges (Berg et al., 2014). Various phytohormones have been reported for the physiological function of plants including jasmonic acid, ethylene, gibberellin, cytokinin, and auxin; among these, auxin is considered a crucial aggregate of molecules present not only by plants but also by microorganisms such as fungi and bacteria. The foremost vital and ubiquitous auxin in plants is IAA (Teale et al., 2006). IAA influence extends far beyond the mere regulation of plant growth, it also impacts quorum sensing, bacterial cellular function, and the environment. As described by Paque and Weijers (2016), IAA is a chemical species that can "influence almost anything." The prime pathways extensively studied for the biological synthesis of IAA include the indole-3-pyruvic acid (IPA) pathway, the indole-3-acetonitrile (IAN)/indole-3-acetaldoxime (IAOx) pathway, and the indole-3-acetamide (IAM) pathway. This review seeks to enhance our current comprehension of the production of IAA in endophyte bacteria.

2. Heterogeneity of Endophyte Bacteria in Medicinal Plant

The biotic association between microorganisms found in different microenvironments and plants have been reported to show intriguing association in three major ways, *viz.,* on the surface (epiphytic), inside the plant tissues (endophytic), and around the roots (rhizospheric). Endophytic microbes are sourced from diverse origins and hold potential applications as biofertilizers and biopesticides, contributing to sustainable agricultural practices. Multifarious endophytic microorganisms, spanning cyanobacteria, bacteria, archaea, and fungi, have been utilized in various applications. These microbes hold promise for applications as biofertilizers and biopesticides, facilitating the development of agricultural continuity (Hussain et al., 2015; Mehmood et al., 2020; Rana et al., 2020). Endophytic microorganisms have been noted to inhabit diverse plant regions, including, seeds, leaves, roots, fruits, stems, and flowers (Kiani et al., 2019). Medicinal plants select endophytes by the supply of secondary metabolites and the ingredients of root secretions. This selection process is driven by factors like the plant's nutritional offerings, ecological conditions, and soil type, bringing about the diversification of microbial communities within them (Abbamondi et al., 2016). According to a previous study described by Yang et al. (2020), the bacterium *Bacillus velezensis* was isolated from the seeds of the medicinal plant *Zea mays* L. Yin et al. (2019) stated that *Bacillus subtilis* was isolated from the medicinal plant *Ligusticum chuanxiong*. Ghiasvand et al. (2020) conducted a study of *Kytococcus schroeteri* and *Paenibacillus Polymyxa* isolated from the medicinal plant *Ephedra foliate*. Li et al. (2021) examined the microbial diversity associated with perennial ryegrass seeds. In a similar investigation, *Pseudomonas frideriksbergensis* was isolated from the medicinal plant *Arnebia euchroma* (Jain et al., 2021*)*. Sharma et al. (2021) isolated 15 genera of bacteria from roots of *R. Officinalis: Lactobacillus*, *Serratia, Bacillus*, *Pseudomonas, Beijerinckia*, *Ensifer, Enterobacter, Cedecea, Kosakonia*, *Paenibacillus*, *Lysobacter, Aneurinibacillus*, *Oxynema*, *Pantoea*, and *Pseudoxanthomnas.* A similar study conducted by Shurigin et al. (2022) isolated endophytic bacteria from the roots and leaves of the medicinal plant yellow iris and these endophytic bacteria were classified within the genera *Streptomyces, Xanthomonas translucens, Staphylococcus, Bacillus, Janthinobacterium, Agrobacterium, Pantoea, Paenibacillus, Enterobacter, Pseudomonas, Brevibacterium, Rhizobium*, and *Variovorax.* In a separate study, endophyte bacteria isolated from *Endostemon obtusifolius* were reported (Ogbe et al., 2023). In another investigation, *Bacillus siamensis* was isolated from *Coriandrum sativum* (Ibrahim et al., 2019). Figure 1 represents the diversity of endophyte bacteria isolated from medicinal plants.

3. Biosynthesis of IAA Engages in Bacteria

The exploration of bacterial species has uncovered diverse pathways for IAA synthesis. Notably, these pathways bear a striking resemblance to those present in plants, underscoring a close similarity between bacterial and plant mechanisms for IAA biosynthesis (Spaepen et al., 2007). The characterization of IAA biosynthetic pathways might be achieved using genetic approaches, such as developing strains deficient or overproducing in IAA, or through biochemical approaches, involving the seclusion and assessment of enzymes involved in catalyzing IAA biological synthesis. Biosynthesis of IAA via bacteria can occur in the existence or nonexistence of tryptophan. While the enzymes and genes accountable for the tryptophan-independent pathway have not been

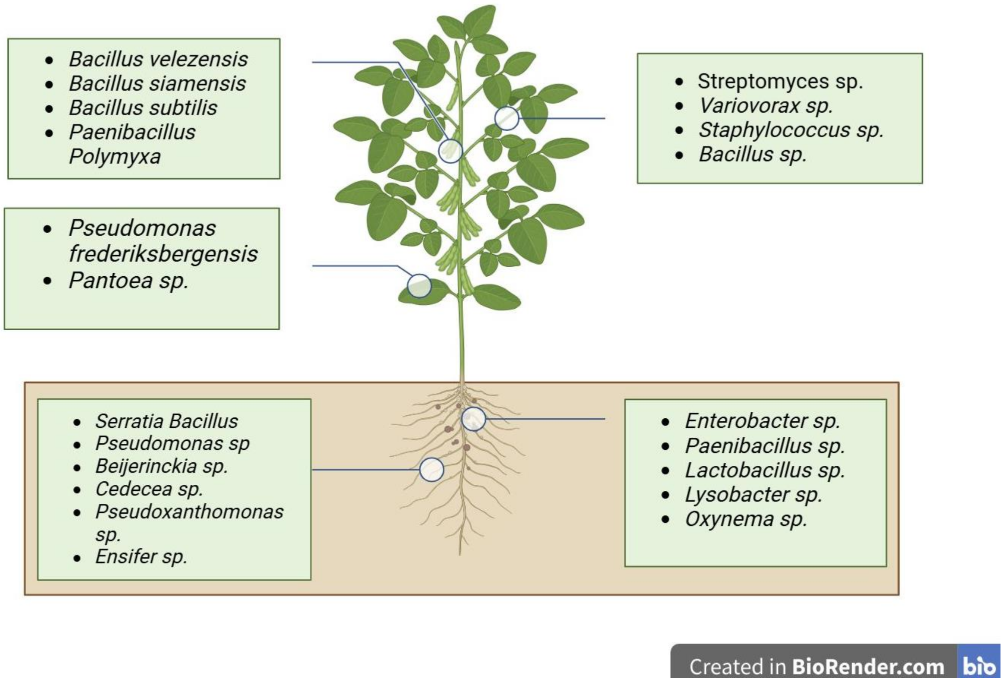

Figure 1. Diversity of endophyte bacteria from a medicinal plant

known so far, a range of co-factors, enzymes, and genes engaged in the tryptophan-dependent pathways were studied extensively by Patten et al. (2013). Tryptophan production is highly energy-demanding for bacteria, making it a costly process for the cell. Consequently, cells maintain low levels of endogenous tryptophan. Elevated levels of the IAA type of chemical species, which belong to auxin, are only generated when there is an excess of externally supplied tryptophan. However, cells may produce lower levels of IAA from their tryptophan reserves, but only if this does not disrupt protein translation (Ibrahim et al., 2019). The comprehensively investigated pathways for IAA biosynthesis are the indole-3-acetamide (IAM) pathway, the indole-3-acetonitrile (IAN)/indole-3-acetaldoxime (IAOx) pathway, and the indole-3-pyruvic acid (IPA) pathway. Figure 2 represents a brief overview of diverse pathways involved in the biosynthesis of IAA reported in bacteria.

3.1 IAM pathway engages in bacteria

The IAM pathway is the comprehensively investigated pathway found in bacteria. There are two stages in this pathway. In the first stage with the help of the enzyme tryptophan-2-monooxygenase (IaaM) transcribed from the iaaM gene, tryptophan is altered into IAM. Subsequently, in the second stage, with the help of IAM hydrolase (IaaH) transcribed from iaaH gene, IAM is transformed into IAA. The genes iaaM and iaaH have been detected and delineated in diverse genera of bacteria, including *Pantoea agglomerans, Pseudomonas syringae, Rhizobium, Bradyrhizobium* and *Agrobacterium tumefaciens* (Sekine et al., 1989; Clark, 1993; Morris, 1995; Theunis et al., 2004). Recent studies have demonstrated that the IAM pathway is present in the majority of bacterial species (Tang et al., 2023).

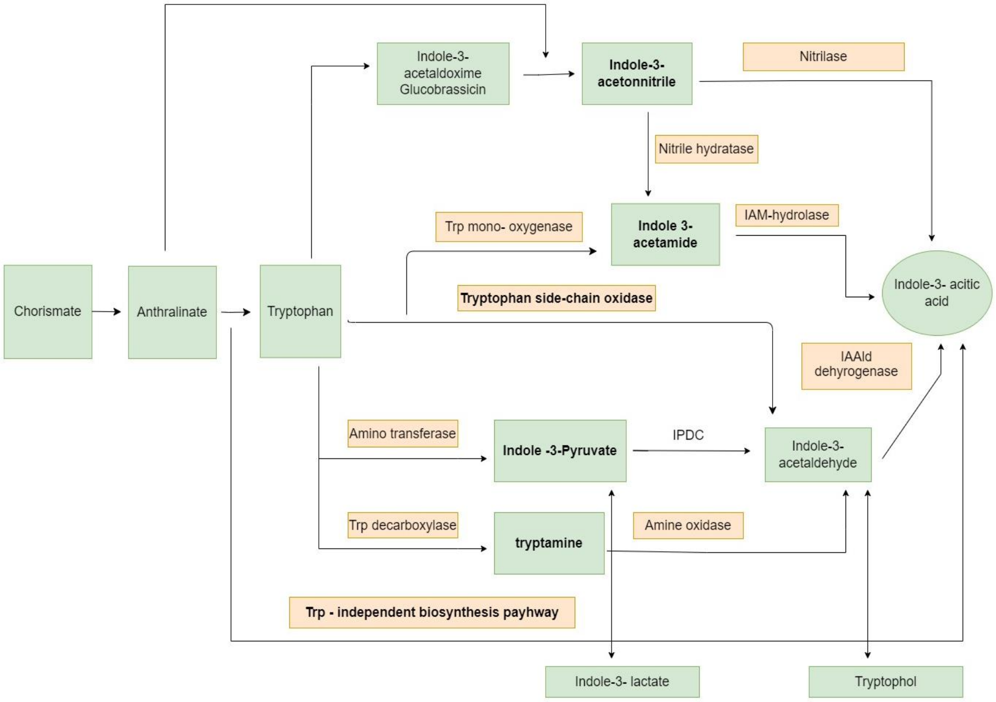

Figure 2. Brief overview of diverse pathways involved in the biosynthesis of IAA reported in bacteria

3.2 IPA pathway

The IPA pathway is a prominent route for the biological synthesis of IAA in plants, serving as a vital hormone. Despite its importance, the precise genes or enzymes governing this pathway remain elusive. Conversely, in a diverse array of bacteria,iIncluding the pathogenic cyanobacteria *Pantoea agglomerans*, and valuable species like *Rhizobium, Enterobacter cloacae, Azospirillum,* and *Bradyrhizobium,* IAA fabrication through the IPyA pathway has been extensively studied and documented (Spaepen et al., 2007). This pathway first involves the transamination of tryptophan to indole-3-pyruvate (IPyA) by an aminotransferase. IPyA undergoes decarboxylation to form indole-3-acetaldehyde (IAAld) catalyzed by indole-3-pyruvate decarboxylase (IPDC) by following the rate-limiting steps. Finally, IAAld is oxidized to supply IAA, executing the pathway. The confirmation and assessment of the gene responsible for encoding the crucial enzyme indole-3-pyruvate decarboxylase (IPDC) were achieved across several bacterial species such as *Enterobacter cloacae, Azospirillum brasilense Pseudomonas* sp., *Paenibacillus agglomerans* and *Enterobacter* sp. This breakthrough has notably advanced our knowledge of the IPyA pathway and its significance in the formation of IAA among diverse bacterial groups (Koga et al., 1991; Costacurta et al., 1994; Brandl & Lindow, 1996; Patten & Glick, 2002; Zhang et al., 2021).

3.3 Tryptamine pathway (TAM) engages in bacteria

The TAM pathway is among the four tryptophan-dependent mechanisms for IAA biosynthesis in plants and has also been reported in microorganisms (Tang et al., 2023). In a particular study on *Bacillus cereus*, confirmation came through the detection of tryptophan decarboxylase activity (Perley & Stowe, 1966). Furthermore, the pathway was identified by observing the changes of externally supplied tryptamine into IAA (Hartmann et al., 1983). The presence in plants of intrinsically produced tryptamine was confirmed, and genes deciphering tryptophan decarboxylases, which facilitate the transforming of tryptophan to tryptamine, were reported across various plant species. This suggested that plants had a pathway for synthesizing IAA using tryptamine. The critical step occurred in this pathway is presumably facilitated through a flavin monooxygenase, which is likely to be a protein referred to as YUCCA, which catalyzes the transition of tryptamine to N-hydroxytryptamine. However, further investigation is necessary to validate the existence of transitional compounds following N-hydroxyl-tryptamine in the pathway, such as indole-3-acetaldehyde and indole-3-acetaldoxime. In bacteria, the ultimate phase of the tryptamine (TAM) pathway differs from that in plants. In bacteria, it occurs with the help of an amine oxidase enzyme, which immediately converts TAM to indole-3-acetaldehyde (IAAld). This distinct enzymatic reaction distinguishes the bacterial pathway from the corresponding pathway in plants (Hartmann et al., 1983).

3.4 Tryptophan side-chain oxidase (TSO) pathway engages in bacteria

The role of TSO pathway in *Pseudomonas fluorescens* CHA0 has been extensively reviewed. In this pathway, the amino acid tryptophan undergoes direct conversion to indole-3-acetaldehyde (IAAld), with sidestepping of the intermediate indole-3-pyruvate (IPyA). Subsequently, IAAld is further oxidized to yield IAA. This distinctive mechanism underscores a departure from the conventional IPyA pathway for IAA biological synthesis in bacteria (Spaepen et al., 2007; Tang et al., 2023).

3.5 Tryptophan-independent pathway engages in bacteria

An investigation into gene-deletion mutants of *Arabidopsis thaliana*, specifically those deficient in genes related to tryptophan synthesis, with a particular focus on the genes encoding tryptophan synthase alpha and beta revealed elevated amounts of IAA derivatives. This finding triggered the proposition of a parallel pathway not reliant on tryptophan for the synthesis of IAA (Last et al., 1991; Normanly et al., 1993). The tryptophan-independent pathway is thought to originate from either indole-3-glycerolphosphate or indole. However, the enzymes responsible for this pathway remain unidentified. There is uncertainty about the importance and even the existence of this pathway (Müller & Weiler, 2000). Studies of *Azospirillum brasilense* utilizing an isotopically labeled compound revealed the presence of a tryptophan-independent pathway. This pathway becomes dominant when tryptophan is absent from the medium, with approximately 90% of IAA synthesized via this pathway, while only 0.1% is generated through the IAM pathway (Prinsen, 1993). However, pathways associated with enzymes have yet to be recognized, and there is ongoing scrutiny regarding their existence and importance. Indeed, some bacteria exhibit multiple pathways for IAA biosynthesis. For instance, in *Paenibacillus agglomerans*, genes associated with both the indole-3-pyruvate (IPyA) and indole-3-acetamide (IAM) pathways have been identified. This versatility suggests that bacteria may employ distinct pathways depending on environmental circumstances or metabolic requirements (Manulis et al., 1998). Researcher's understanding of bacterial IAA biosynthesis extends back to the late 20th century, as evident from the cited references. Advancements in analytical methods for detecting and measuring intermediates, coupled with the swift advancements in functional genomics, promise to furnish a more comprehensive understanding of the various pathways engaged in IAA biological synthesis in bacteria (Jahn et al., 2021).

3.6 Indole-3-acetonitrile pathway

Recent research has thoroughly investigated the biological synthesis of IAA via the IAN pathway in plants. In the concluding stage of this pathway, with the help of the action of a nitrilase enzyme, identified IAN is converted into IAA (Bartling et al., 1992). Recently, two pathways have been proposed for this process of conversion: one via indolic glucosinolates involving indole-3-acetaldoxime, and another via glucobrassicin (Bak et al., 2001; Zhao et al., 2001). Nitrilases that exhibit specificity for indole-3-acetonitrile have been identified in bacteria like *Alcaligenes faecalis* (Nagasawa et al., 1990; Kobayashi et al., 1993). Furthermore, in *Rhizobium* sp. and *Agrobacterium tumefaciens*, engagements of amidase and nitrile hydratase have been detected. This suggests the potential conversion of IAN to IAM, which could then be further transformed into IAA (Kobayashi et al., 1993).

4. IAA-producing Endophyte Bacteria from Various Medicinal Plant

IAA-producing endophyte bacteria recently isolated from medicinal plants are described in Table 1. IAA stands out as the most potent auxin in plants, driving a wide range of vital biological processes. It serves as a fundamental metabolite, prompting growth activities like callus generation, cell proliferation, elongation, and specialization towards environmental cues. Additionally, it contributes to tropic responses, flowering regulation, and the occurrence of parthenocarpy. Its influence extends to maintaining apical dominance, thwarting cell aging, and fostering the development of both root and fruit systems. Furthermore, auxins exhibit a protective role, impeding the premature shedding of fruits, leaves, and flowers (Duca et al., 2014). Numerous bacterial species possess the capability to synthesize IAA, including those found in soil, epiphytic environments, endophytes, marine habitats, methylotrophs, and cyanobacteria (Duca et al., 2014). Regulating the IAA in plants represents a significant mechanism through which endophytic bacteria can boost plant development. By producing IAA these bacteria can enhance the root biomass and surface area of plants, as well as stimulate the generation of lateral roots. This ultimately leads to an overall improvement in the progress of host plants (Afzal et al., 2019). In another investigation, Tao et al. (2022) isolated *Lelliottia amnigena, Achromobacter marplatensis, Alcaligenes* sp., *Klebsiella aerogene,* and *Bacillus megaterium* from *Pairs polyphylla* var. *yunnanensis* (*Paris* L.). All of the isolated endophytes produced IAA, which acted as a huge responsibility in plant progress. *Bacillus vallismortis* was isolated from *Brassica napus* L and demonstrated IAA production (Nagah et al., 2024). The endophytic bacteria *Pseudomonas frideriksbergensis* and *Pseudomonas* sp. ALB20, originating from the threatened medicinal herb *Arnebia euchroma,* were discovered to significantly improve plant growth. This enhancement was linked to their capacity to synthesize IAA (Jain et al., 2021). Sharma et al. (2021) isolated endophyte bacteria *Pseudomonas mediterranea*, *Bacillus subtilis, Bacillus flexux, Bacillus simplex,*

Table 1. Reported IAA-producing endophytic bacteria isolated from each medicinal plant

Name of Medicinal Plants	Endophytic Bacteria	References
Arnebia euchroma	• *Pseudomonas frideriksbergensis* • *Pseudomonas* sp. ALB20	(Jain et al., 2021)
Rosmarinus officinalis	• *Bacillus subtilis* KU21 • *Pseudomona japonensis* KU13 • *Bacillus simplex* KA2 • *Pseudomona putida* KU2 • *Pseudomonas mediterranea* KA7 • *Cedecea lapagei* KU14 • *Pseudomona aeruginosa* SI12 • *Pseudomona koreensis* KA11 • *Pseudomonas oryzihabitans* KU5 • *Bacillus flexux* KA10 • *Pseudomona agglomerans* KA14	(Sharma et al., 2021)
Iris pseudacorus L	• *Bacillus cereus* HRT1 • *Bacillus toyonensis* HRT5 • *Agrobacterium tumefaciens* HRT9 • *Rhizobium galegae* HRT12 • *Agrobacterium vitis* HRT14 • *Pseudomonas gessardii* HRT18 • *Staphylococcus succinus* HST1 • *Brevibacterium frigoritolerans* HST10 • *Paenibacillus lautus* HST12 • *Bacillus megaterium* HST16 • *Paenibacillus xylanexedens* HST18 • *Bacillus aryabhattai* HSN1	(Shurigin et al., 2022)
Endostemon obtusifolius	• *Paenibacillus polymyxa*	(Ogbe et al., 2023)
Pairs polyphylla var. *yunnanensis* (Paris L.)	• *Lelliottia amnigena* • *Achromobacter marplatensis* • *Alcaligenes* sp. • *Klebsiella aerogenes* • *Bacillus megaterium*	(Tao et al., 2022)
Brassica napus L	• *Bacillus vallismortis* • *Bacillus tequilensis*	(Nagah et al., 2024)
Aconitum carmichaelii Debx	• *Pseudomonas* sp. • *Sphingobacterium* sp. • *Xanthomonas* sp. • *Enterobacter* sp. • *Microbacterium* sp. • *Agrobacterium* sp. • *Pantoea* sp. • *Rummeliibacillus* sp. • *Bacillus* sp. • *Klebsiella* sp.	(Dal'Rio et al., 2024)

Table 1. Reported IAA-producing endophytic bacteria isolated from each medicinal plant (continued)

Name of Medicinal Plants	Endophytic Bacteria	References
Asphodelaceae	• *Pantoea cypripedii* • *Paraburkholderia* sp. • *Bacillus megaterium* • *Enterobacter tabaci* • *Brevibacillus agri* • *Chryseobacterium taiwanense* • *Enterobacter ludwigii* • *Lysinibacillus macrolides* • *Microbacterium aerolatum* • *Lysinibacillus macrolides* • *Enterobacter asburiae* • *Enterobacter* sp.	(Silva et al., 2020)
Lycoris radiata	• *Pantoea* sp. • *Rosenbergiella* sp. • *Stenotrophomonas* sp. • *Enterobacter* sp.	(Liu et al., 2020)
Platycodon grandiflorum	• *Rhizobium* sp. BF-E16 • *Xenophilus azovorans* BF-E21 • *Rhizobium azooxidifex* BF E17, • *Rhizobium* sp. BF-E15, • *Microbacterium* sp. BF-E14, • *Rhizobium* sp. BF-E15, • *Rhizobium* sp. BF-E18,	(Huang et al., 2019)
Arctium lappa L.	• *Pantoea* sp. • *Pseudomonas* sp.	(Liu et al., 2022)
Pulicaria incisa	• *Burkholderia cepacia* • *Brevibacillus brevis* • *Paenibacillus* • *Bacillus cereus* • *Barengoltzii* • *Acinetobacter radioresistant* • *Bacillus subtilis* • *Agrobacterium fabrum*	(Fouda et al., 2021)

Pseudomonas oryzihabitans, Pseudomona putida, Cedecea lapagei, Bacillus tequilensis, Pseudomona koreensis, Pseudomona agglomerans, Pseudomona aeruginosa, and *Pseudomonas japonensis* from *Rosmarinus officinalis*, all of which were capable of IAA production. In a report by Shurigin et al. (2022), 12 endophyte bacteria *Agrobacterium tumefaciens* HRT9, *Rhizobium galegae* HRT12, *Agrobacterium vitis* HRT14, *Pseudomonas gessardii* HRT18, *Staphylococcus succinus* HST1, *Brevibacterium frigoritolerans* HST10, *Paenibacillus lautus* HST12, *Bacillus megaterium* HST16, *Paenibacillus xylanexedens* HST18 and *Bacillus aryabhattai* HSN1were isolated from the roots and leaves of *Iris pseudacorus* L and tested for IAA production. *Asphodelaceae* is universally acknowledged for its time-honored medicine-related substantial commercial relevance globally (Ogbe et al., 2023). The analysis by Dal'Rio et al. (2024) revealed that *Bacillus thuringiensis* and *Paenibacillus polymyxa*, isolated from the medicinal plant *Tropaeolum majus* L, synthesized IAA. *In vivo* trials showed that seeds treated with these bacteria displayed enhanced seed growth, with a 20.3% elevated seed growth compared to unrefined seeds. In another investigation by Silva et al. (2020), different genera of IAA-producing endophyte bacteria *Pantoea cypripedii, Enterobacter asburiae, Enterobacter ludwigi, Paraburkholderia* sp., *Bacillus megaterium, Chryseobacterium taiwanense, Brevibacillus agri, Enterobacter tabaci, Lysinibacillus macrolides, Enterobacter* sp., *Microbacterium aerolatum,* and *Paraburkholderia* sp. were isolated. *Paraburkholderia* sp., produced the highest amount of IAA among the isolated endophytes.

5. Conclusion and Future Prospective

Endophyte bacteria play crucial roles in medicinal plants, offering significant benefits such as managing plant diseases, fostering plant development, diminishing phytopathogens, and influencing the chemical composition within the host. The catalogs of existing studies have shown that the endophyte bacteria discovered within medicinal plants excel at producing secondary metabolites and growth-promoting compounds, such as IAA, which could boost plant progression. The studies hold special intriguing interest for medicinal plants for the diverse phytohormones present in them, often associated with medicinal properties. Substituting pesticides or chemical fertilizers with endophytes is fascinating since it promotes the use of medicinal plants in both consumer and agriculture sectors, while eliminating synthetic chemical residue. Hence, endophyte bacteria could serve as significant facilitators in eliminating artificial chemical compounds. Consequently, there is a growing imperative to extract endophyte bacteria obtained from medicinal plants for research as plant-proliferation promoters, offering an eco-friendly alternative to synthetic chemicals and contributing to environmental conservation efforts. Moreover, there is an increasing demand for research emphasizing on the isolation of endophyte bacteria from medicinal plants and investigating their potential as enhancers that stimulate medicinal plant progress. The endophyte bacteria derived from medicinal plants acquire the innate ability to fabricate IAA, thus enabling the biotechnological sector to carry out extensive fermentation of this compound on a large scale, independent of the need to cultivate medicinal plants. Exploring and focusing on the cell-to-cell communications between host medicinal plants and endophytic bacteria are crucial, and this will involve the utilization of evolving tools including next-generation sequencing, metabolomics, and proteomics. These advanced tools are essential for understanding the significant mechanisms in the production of IAA and also can significantly enhance our ability to optimize its production. Consequently, these endophytic bacteria may emerge as viable commercial biofertilizers for diverse crops in the foreseeable future, contributing to the sustenance of sustainable agricultural practices.

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7. Authors' Contributions

Sohail Khan; Literature Search, Writing—original draft and Editing. Ashwani Mathur; Conceptualization, Supervision, Writing—review and Editing.

8. Conflicts of Interest

The authors state that they do not have any contradictions of interest.

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