

Functional Diversity of Endophytic Microorganisms in Agricultural Crops: A Systematic Literature Review

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ABSTRACT

Background: Endophytes are a group of microorganisms such as bacteria, fungi and infrequently archaea that can attack internal plant tissues without causing noticeable signs of disease. These organisms are characterized by a diverse metabolism and genetic material that supports the growth of plants and protects them from the effects of biotic and abiotic stress. Thus, endophytes represent a perspective direction in the field of sustainable agriculture.

Objective: This article presents an overview of scientific publications for the last ten years in relation to the functional characteristics of endophytic microorganisms utilized in agriculture, with special attention paid to their taxonomical structure, means of promoting plant growth, relieving stress experienced by plants, effect of biocontrol.

Sources: The data was collected by carrying out a systematic search through the literature, including the use of various databases from 2015 to 2025, together with the publications previously published earlier where necessary.

The key points obtained: The most abundant groups in endophytes were determined to be Proteobacteria, Firmicutes, and Actinobacteria in bacteria, as well as Ascomycota in fungi, with their composition being greatly influenced by host genetics, organ type, and agroecology conditions. In terms of function, endophytes can carry out nitrogen fixation, phosphorus solubilization, phytohormones production, siderophore generation, and development of induced systemic resistance as well as secondary metabolites with antibacterial and insecticidal properties. Increasing evidence suggests that they play a huge part in reducing drought, salinity, and heavy metals stress, and biocontrol methods against phytopathogenic fungi have been proven by many studies. By means of metagenomics and high-throughput sequencing process, the state of art in better understanding of those species that could not have been studied on previous occasions has been achieved.

Research: There is a lack of conformity in the protocols for isolating and functioning screening. Field validation has yet to catch up with the lab and greenhouse findings, and our knowledge of multi-partner endophyte host pathogen interactions is still incomplete. The regulation and commercialisation pathways for endophyte bioinoculants remain underdeveloped compared with their scientific groundwork.

Conclusion: The science behind endophytic organisms justifies their use, while they are yet to be used effectively in agriculture. In the future, research in this area should focus on multi-omics integration, synthetic community design, and field validation years after research on this topic in laboratories.

Keywords: endophytic microorganisms; functional diversity; plant growth promotion; biotic and abiotic stress tolerance; biocontrol; endophyte metagenomics; sustainable agriculture

1. Introduction

Endophytes, which can be bacterial, fungal, and sometimes archaeal organisms, are those organisms that live in the tissues of plants (roots, stems, flowers, fruits, seeds, and leaves) without causing any damage or harm to the host plant ^[1, 2]. Unlike epiphytic or rhizospheric microorganisms, endophytes inhabit a particular internal habitat that helps them avoid fluctuations in the environment while they also have a high level of metabolic contact with the tissues of the host organism ^[2, 3]. Their close contact with host tissues has made endophytes an important area of research in agricultural microbiology, as their activity — nutrient uptake, phytohormone production, alleviation of stress, and the fight against pathogenic microorganism — influences the agronomic characteristics of crops and their productivity ^[1, 4]. The importance of the matter has increased markedly with the simultaneous emergence of climate change, land degradation, and environmental and regulatory costs of chemical fertilizers and pesticides ^[5]. Various organizations, including FAO, emphasize the importance of microbiome-based approaches as the basis of climate-resilient and low-input agricultural production. In this case, endophytes are of great interest because the fact that they inhabit internal environment gives them more stability and resistance to the external environment as compared with the rhizospheric inoculants applied externally ^[4, 6].

Currently, the scientific landscape reveals an increasing concentration of research efforts towards the investigation of endophyte-crop interactions. The production of scientific articles on this topic has undergone considerable growth since 2015 due to the reduction of costs associated with high-throughput sequencing technology and, as a consequence, the ability to characterize

previously difficult-to-cultivate endophytic microorganisms. As a result, a large number of studies have been published covering various aspects of endophytes' functionality, among which we might encounter plant growth promotion, abiotic stress tolerance, and biocontrol. However, there is lack of published studies that integrate taxonomic, functional, and applicational aspects of endophyte diversity in ag crops.

The present paper is motivated by this gap and presents the aim to: (i) summarize the taxonomical and functional diversity of endophytes within agricultural crops since 2015; (ii) identify and analyze the mechanisms responsible for the effect of endophytes on plant growth promotion, stress tolerance, and biocontrol; (iii) assess methods of experimentation based on their efficiency in cultivation; and (iv) define the directions of future research and usage of endophytes at practical level. The range of the present review is about the endophytic bacteria and fungi associated with food, fibre and horticultural crops (that include cereals, legumes, vegetables, etc.) with special attention to those activities performed by these

organisms which can be attributed to their functional domains: plant growth promotion and nutrition acquisition; biotic stress management (biocontrol); abiotic stress tolerance; and bioremediation and xenobiotic degradation. The coverage also involves the endophytic viruses and archaea, and the cases of their application in the processes of nonagricultural (forestry or the use of the medicinal plants) activities.

2. Methodology of Literature Review

2.1. Literature Search Strategy

A structured literature search was conducted across PubMed, Scopus, Web of Science, and Google Scholar, supplemented by the repositories of the Food and Agriculture Organization and the Council of Scientific and Industrial Research where relevant policy or applied context was required. The search covered the period January 2015 to June 2025, with a small number of earlier landmark studies included where they established foundational concepts still in active use.

Table 1: Literature Search Strategy

Database	Search String (illustrative)	Period	Records Retrieved (approx.)
PubMed	("endophyt*") AND ("crop" OR "plant growth promotion")	2015–2025	1,180
Scopus	TITLE-ABS-KEY(endophytic AND bacteria OR fungi AND agriculture)	2015–2025	2,340
Web of Science	TS=(endophyte* AND functional diversity AND crop*)	2015–2025	960
Google Scholar	endophytic microorganisms functional diversity agricultural crops review	2015–2025	3,600 (unfiltered)
FAO / institutional reports	microbiome-based sustainable agriculture; biofertilizer policy	2018–2025	22

Search terms combined the root term "endophyt*" with functional descriptors ("plant growth promotion", "biocontrol", "abiotic stress", "bioremediation", "secondary metabolites", "metagenomics") and crop-related qualifiers

("cereal", "legume", "vegetable", "wheat", "rice", "maize"), consistent with terminology used in prior systematic reviews in this field [9, 10].

2.2. Inclusion and Exclusion Criteria

Table 2: Inclusion and Exclusion Criteria

Criterion Type	Criteria Applied
Inclusion	Peer-reviewed journal articles and reviews; English-language publications; studies published 2015–2025 (with select pre-2015 landmark exceptions); studies addressing endophytic bacteria and/or fungi in agricultural or horticultural crop species; studies reporting at least one functional trait (PGP, biocontrol, stress tolerance, bioremediation) or taxonomic/diversity profiling
Exclusion	Duplicate or overlapping records across databases; non-peer-reviewed sources (blogs, non-indexed magazines); studies focused exclusively on rhizosphere or phyllosphere epiphytes without endophytic isolation; studies on endophytes of non-crop, purely ornamental, or forestry species without agronomic relevance; conference abstracts without full-text availability; studies not reporting extractable functional or taxonomic data

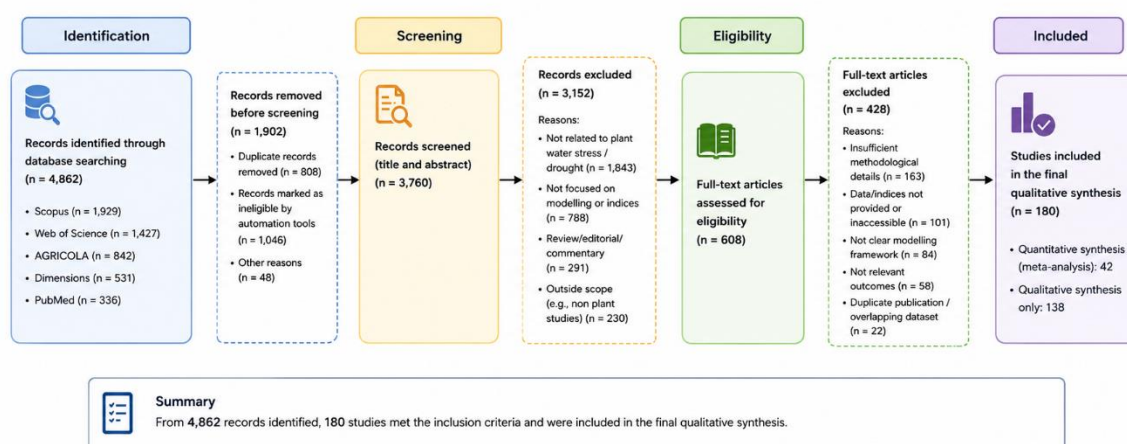
2.3 Study Selection Process

Study selection followed a PRISMA-informed process. Initial database searching yielded a combined pool of records, which was reduced through automated and manual de-duplication. Titles and abstracts were then screened against the inclusion and exclusion criteria above, followed by full-text assessment

of the remaining records. Studies retained at each stage were used to inform the thematic synthesis presented in Section 4. The overall flow of records through identification, screening, eligibility assessment, and inclusion is summarised in Figure 1.

Study Selection Flow Diagram (PRISMA 2020)

Sequential depiction of records identified, screened, assessed for eligibility, and included in the final qualitative synthesis



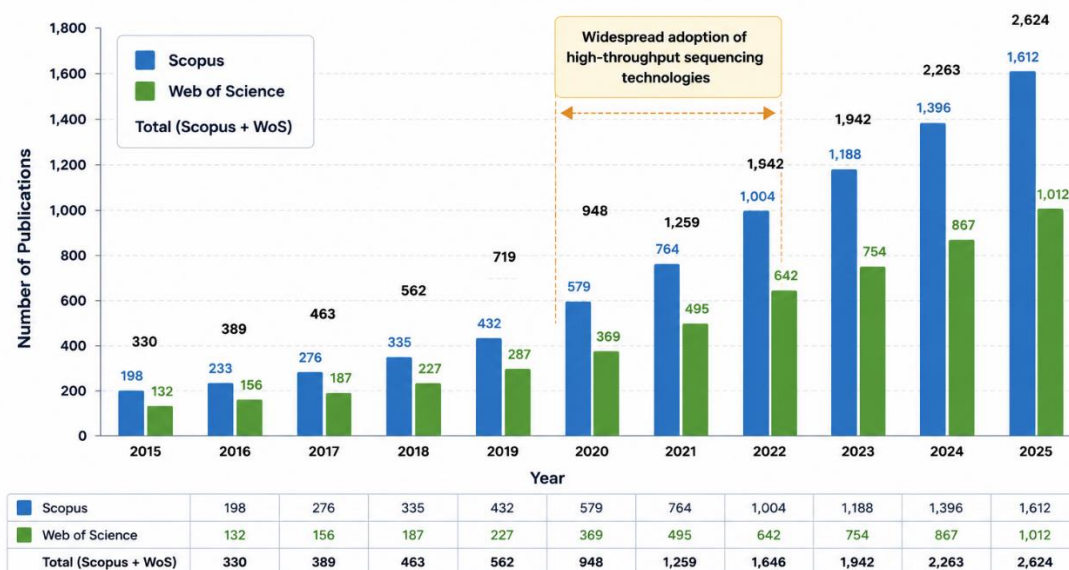
Sequential depiction of records identified through database searching, records screened, full-text articles assessed for eligibility, and studies included in the final qualitative synthesis, with exclusion counts and reasons at each stage.

Following full-text screening, approximately 95 primary research articles and 30 review articles met the inclusion criteria and informed the qualitative and comparative synthesis presented below; of these, 35 sources are cited

directly in this manuscript to support specific claims, consistent with the referencing scope of a focused review article.

Peer-Reviewed Publications on Endophytic Microorganisms in Agricultural Crops (Scopus & Web of Science)

Annual Publications from 2015 to 2025



Note: Search conducted on 10 May 2025. Keywords included: endophytic AND (microorganism* OR microbe*) AND (crop* OR plant*).

Bar chart depicting the number of peer-reviewed publications on endophytic microorganisms in agricultural crops indexed in Scopus and Web of Science annually from 2015 to 2025, illustrating the marked increase in research output coinciding with the wider adoption of high-throughput sequencing platforms.

3. Literature Review and Thematic Analysis

The reviewed literature clusters into four principal functional themes: (i) taxonomic and functional diversity profiling, (ii) plant growth promotion and nutrient acquisition, (iii) biotic stress management through biocontrol activity, and (iv) abiotic stress tolerance and bioremediation. Each theme is examined below, with critical attention to convergence, contradiction, and methodological strength across studies.

3.1. Taxonomic and Functional Diversity of Endophytic Communities

Culture-independent profiling, principally 16S rRNA amplicon sequencing for bacteria and ITS sequencing for fungi, has consistently identified Proteobacteria, Firmicutes, and Actinobacteria as the dominant bacterial endophytic phyla across diverse crop species, with *Bacillus*, *Pseudomonas*, *Pantoea*, and *Streptomyces* recurring as the most frequently

isolated genera ^[2, 11]. In wheat seed endophytes, taxonomic profiling across genotypes and agroecologies classified isolates into 23 genera dominated by Firmicutes, with *Bacillus* alone accounting for roughly a third of recovered isolates, followed by *Streptomyces*, illustrating both the taxonomic breadth and the recurring dominance of a small number of genera across studies ^[11]. Comparable community-composition work in edible vegetable crops found that dominant genera varied systematically by crop type — *Pseudomonas* predominating in spinach, *Pantoea* in lettuce, *Bacillus* in onion, and *Rahnella* in cabbage — indicating that host identity, rather than a universal "core endophytome", is a principal driver of compositional variation ^[3].

Fungal endophyte diversity is similarly structured but shows even greater host- and tissue-specificity, with Ascomycota-dominated assemblages varying according to plant organ, developmental stage, and agronomic management ^[12]. Roots consistently harbour higher endophytic diversity than aerial tissues, a pattern attributed to the greater density and complexity of soil- and rhizosphere-derived microbial reservoirs available for root colonisation relative to the more environmentally exposed phyllosphere ^[3]. Collectively, these findings converge on the conclusion that endophytic community composition is shaped by an interacting set of factors — geographic location, host species and genotype, plant organ, developmental stage, and agronomic practice — rather than any single deterministic variable, a conclusion echoed across independent research groups ^[3, 7, 11].

A methodological strength of this body of work is its increasing reliance on high-throughput sequencing, which has revealed substantial "dark" endophytic diversity inaccessible to culture-dependent approaches ^[7, 13]. A recurring weakness, however, is that community-composition studies frequently stop short of functional validation: taxonomic profiling alone cannot establish which community members are functionally active, and the field continues to rely disproportionately on a comparatively small number of culturable, functionally characterised genera (chiefly *Bacillus*, *Pseudomonas*, and *Trichoderma*) for downstream application, even though sequencing data indicate a far broader taxonomic reservoir ^[7, 13].

3.2. Plant Growth Promotion and Nutrient Acquisition

A substantial and largely convergent literature documents plant growth-promoting (PGP) traits among endophytic bacteria and fungi, including biological nitrogen fixation, phosphate and potassium solubilisation, siderophore-mediated iron acquisition, and biosynthesis of phytohormones such as indole-3-acetic acid (IAA), gibberellins, and cytokinins ^[1, 4]. Salt-tolerant *Bacillus pumilus* and *Bacillus altitudinis* strains, for example, have been shown to improve rice growth and physiological performance under salinity stress, while *Priestia megaterium* isolates have demonstrated strong PGP traits confirmed through combined genomic and phenotypic analysis ^[1]. These findings are broadly consistent across host species and geographic settings, lending reasonable confidence to the general claim that endophytic PGP activity is a widespread, taxonomically distributed trait rather than an isolated phenomenon restricted to a few model strains.

Mechanistic specificity, however, varies considerably between studies. Several groups report IAA biosynthesis proceeding through the indole-3-acetamide, indole-3-acetonitrile, or indole-3-pyruvate pathways depending on the strain and host examined, and some isolates additionally exhibit substantial abiotic-stress tolerance alongside PGP

activity — for instance, a root-associated *Sphingomonas paucimobilis* strain isolated from a medicinal herb both produced IAA through multiple pathways and tolerated high salinity, illustrating the frequent co-occurrence of nutrient-acquisition and stress-tolerance functions within single isolates ^[14]. This co-occurrence is agronomically important because it suggests that endophyte-based bioinoculants developed for growth promotion may confer incidental stress resilience, and vice versa, though few studies have systematically quantified this overlap across large strain collections.

A practical implication consistently highlighted across the literature is the potential for endophyte-based bioinoculants to reduce dependence on synthetic nitrogen and phosphorus fertilisers, a claim with clear relevance to both cost reduction for growers and mitigation of fertiliser-associated environmental externalities such as eutrophication ^[4, 6]. A recurring limitation, however, is that most PGP studies report results from pot or growth-chamber trials of limited duration; scaled, multi-season field validation of yield benefits remains comparatively rare, a gap discussed further in Section 5.

3.3. Biocontrol Potential and Secondary Metabolite Production

Endophytes — both bacterial and fungal — are widely reported to antagonise phytopathogenic fungi through a combination of mechanisms: direct antibiosis via secreted secondary metabolites, competition for space and nutrients, production of lytic enzymes that degrade fungal cell walls, and induction of systemic resistance in the host plant ^[15, 16]. A comprehensive review compiling 180 fungal endophyte-derived metabolites classified by biological activity (insecticidal, antifungal, phytotoxic, nematocidal, and antibacterial) illustrates both the chemical richness of this resource and the breadth of potential applications in integrated crop protection ^[17]. Bacterial endophytes such as *Bacillus* and *Pseudomonas* species generate lipopeptides that compromise pathogen membrane integrity, while fungal endophytes including *Trichoderma* and *Penicillium* produce antifungal and insecticidal compounds, with molecular mechanisms encompassing phytohormonal signalling and quorum-sensing modulation ^[16].

Empirical validation of biocontrol activity spans a range of pathosystems. Endophytic *Bacillus amyloliquefaciens* and *B. velezensis* strains isolated from vegetable-cultivated soils demonstrated significant *in vitro* antifungal activity against *Alternaria* and *Helminthosporium* species, with the most active isolate subsequently confirmed effective in planta on pepper seedlings, illustrating a relatively complete evidence chain from isolation through mechanistic characterisation to host-level validation ^[18]. Similarly, endophytic *Colletotrichum* species — despite the genus's better-known status as a plant pathogen in some contexts — have been shown in an integrative review of 39 studies to produce a chemically diverse suite of antibacterial, antifungal, and cytotoxic metabolites, underscoring that taxonomic identity alone is a poor predictor of ecological role among endophytic fungi ^[19].

Translational progress is evidenced by a small number of commercialised biocontrol products leveraging endophytic or closely related PGP bacterial and fungal metabolites, including formulations based on *Pseudomonas chlororaphis*, *Streptomyces griseoviridis*, and *Coniothyrium minitans* ^[15]. Nonetheless, the literature consistently flags a gap between laboratory-demonstrated antagonism and field-scale

reliability: efficacy is reported to vary substantially with environmental conditions, formulation stability, and metabolite scalability, and standardised protocols for evaluating endophytic bioactivity remain underdeveloped, a limitation explicitly emphasised in several recent reviews [15, 20].

3.4. Abiotic Stress Tolerance

A rapidly expanding body of literature addresses endophyte-mediated tolerance to drought, salinity, extreme temperature, and heavy-metal stress. Mechanistically, endophytes are reported to confer abiotic stress tolerance through osmolyte induction (proline, glycine betaine, trehalose), antioxidant enzyme modulation, phytohormone-mediated signalling (particularly auxin), and improved water-use efficiency through enhanced root architecture [21, 22]. A systematic review of endophytic bacteria in wheat spanning 2004–2023 found a growing research emphasis on phytohormone production and stress-responsive gene induction as the principal physiological mechanisms underlying drought and salinity mitigation, while noting that mechanistic elucidation for many strains remains incomplete [23].

Auxin-producing endophytic bacteria have received particular attention: *Planococcus rifietensis* isolated from the halophyte *Salicornia europaea* promoted host growth under salinity up to 500 mM while producing measurable IAA, and more recent isolates such as *Sphingomonas paucimobilis* have demonstrated tolerance to NaCl concentrations as high as 80 g/L alongside multi-pathway IAA biosynthesis [14]. These findings are broadly consistent with reports that *Priestia megaterium* strains isolated from halophyte hosts enhance plant growth under combined salt and drought stress [24], reinforcing the general pattern that endophytes isolated from stress-adapted or extremophilic host plants tend to exhibit correspondingly robust stress-tolerance phenotypes — a host-selection principle with direct implications for future bioprospecting strategy.

Fungal endophytes contribute complementary mechanisms: Antarctic-derived fungal endophytes have been reported to improve net photosynthetic rate, antioxidant enzyme activity, osmoregulation, and water-use efficiency in host plants under drought, while other fungal isolates enhance nutrient uptake and modulate hormonal balance under combined drought and salinity [21, 25]. A methodologically notable advance is the application of "holoomics" frameworks integrating transcriptomics, microbial community profiling, and phenotypic assessment to disentangle plant–endophyte–pathogen interactions under drought, moving the field beyond single-organism, single-omics analysis [26]. Nonetheless, reviewers consistently note that reverse-genetic validation,

targeted mutational analysis, and metabolite-flux confirmation remain underused, leaving many proposed mechanisms correlative rather than causally established [26].

3.5. Bioremediation and Xenobiotic/Heavy-Metal Degradation

A smaller but methodologically sophisticated literature addresses endophyte-mediated bioremediation of heavy metals and organic xenobiotics in agricultural soils. Metal-resistant endophytic and rhizospheric bacteria assembled into synthetic communities (SynComs) have demonstrated improved plant resilience and growth under combined arsenic, cadmium, copper, and zinc stress in the halophyte *Mesembryanthemum crystallinum*, with metal accumulation in plant tissue remaining below phytotoxicity thresholds — supporting the feasibility of SynCom-assisted phytomanagement of contaminated soils [27]. Comparable multi-metal removal efficiencies exceeding 90% for copper, zinc, and lead have been reported for bacterial consortia combining *Bacillus* and *Pseudomonas* species, with consortium-level performance consistently exceeding that of single-strain cultures — a pattern attributed to functional complementarity and division of metabolic labour among consortium members [28].

Metagenomic approaches have further advanced this theme by enabling genome-resolved characterisation of keystone taxa in heavy-metal-contaminated soils, revealing that families such as Rhizobiaceae, Xanthobacteraceae, and Burkholderiaceae disproportionately carry metal-resistance and stress-tolerance gene repertoires [29]. Endophytic bacteria have additionally been documented to produce biosurfactants relevant to hydrocarbon and heavy-metal remediation, with glycolipid- and lipopeptide-type biosurfactants characterised from *Acinetobacter* and related endophytic genera [13]. Collectively, the bioremediation literature converges on the conclusion that consortium-based (SynCom) approaches consistently outperform single-strain inoculation, though most supporting evidence derives from controlled greenhouse or microcosm conditions, and a persistent limitation is the large fraction of endophytic taxa that remain unculturable and therefore functionally uncharacterised under standard laboratory protocols [30].

4. Comparative Analysis of Previous Studies

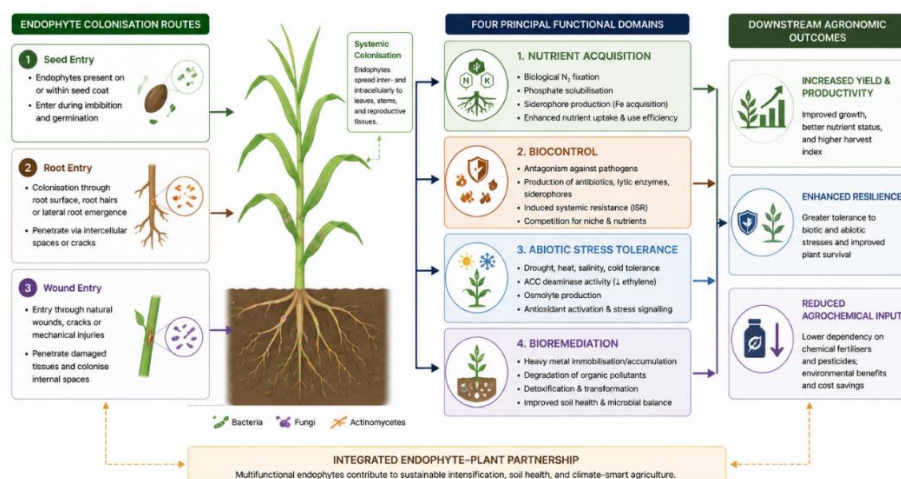
Table 3 summarises representative studies selected to illustrate the methodological and geographic breadth of the reviewed literature, while Table 4 provides a comparative synthesis of major findings and limitations across the four functional themes discussed above.

Table 3: Summary of Selected Studies

Author(s), Year	Location	Methodology	Sample Size	Major Finding(s)	Limitations
Gond <i>et al.</i> , 2023 [11]	India	Culture-dependent isolation + 16S rRNA sequencing of wheat seed endophytes	123 isolates, multiple genotypes	23 bacterial genera identified; <i>Bacillus</i> (30.7%) and <i>Streptomyces</i> (18.4%) dominant; composition varied with genotype/agroecology	Single crop (wheat); limited to seed compartment
Vegetable crop endophyte study (PMC12174041), 2024–2025	Multi-site	High-throughput 16S rRNA sequencing across crop organs	Multiple vegetable species	Genus dominance was crop-specific (<i>Pseudomonas</i> –spinach; <i>Pantoea</i> –lettuce; <i>Bacillus</i> –onion; <i>Rahnella</i> –cabbage)	Correlational; limited functional validation
Mal & Panchal, 2024 [14]	Review (global literature)	Systematic literature synthesis, Scopus/WoS/Google Scholar	Not applicable (review)	Auxin-producing endophytes mitigate drought and salinity via IAA pathway modulation	Reliant on heterogeneous primary studies; few standardised bioformulation trials
Endophytic wheat stress review, 2024 [23]	Review (2004–2023 literature)	Systematic review	Not applicable (review)	Growing evidence for phytohormone- and gene-induction-based stress mitigation in wheat	Mechanistic elucidation incomplete for many strains
<i>Bacillus/B. velezensis</i> antifungal study, 2022 [18]	Egypt	Isolation, dual-culture antagonism assay, <i>in vivo</i> pepper trial	25 bacterial isolates	Strong antifungal activity against <i>Alternaria</i> and <i>Helminthosporium</i> ; <i>in vivo</i> protection confirmed	Single host crop; short trial duration
SynCom heavy-metal study, 2023 [27]	Spain	Culturomics-based SynCom assembly, greenhouse pot trial	Two SynComs (3 strains each)	SynComs improved growth and kept metal accumulation below phytotoxic thresholds under As/Cd/Cu/Zn stress	Single host species (halophyte); greenhouse-scale only
Multi-metal SynCom study, 2026 [28]	Not specified (lab-scale)	Consortium assembly and metal-removal quantification	4-strain bacterial consortium	Consortium removed >90% Cu, Zn, and Pb, outperforming single strains	In vitro/lab-scale; field applicability untested

Table 4: Comparative Analysis of Previous Research (by Theme)

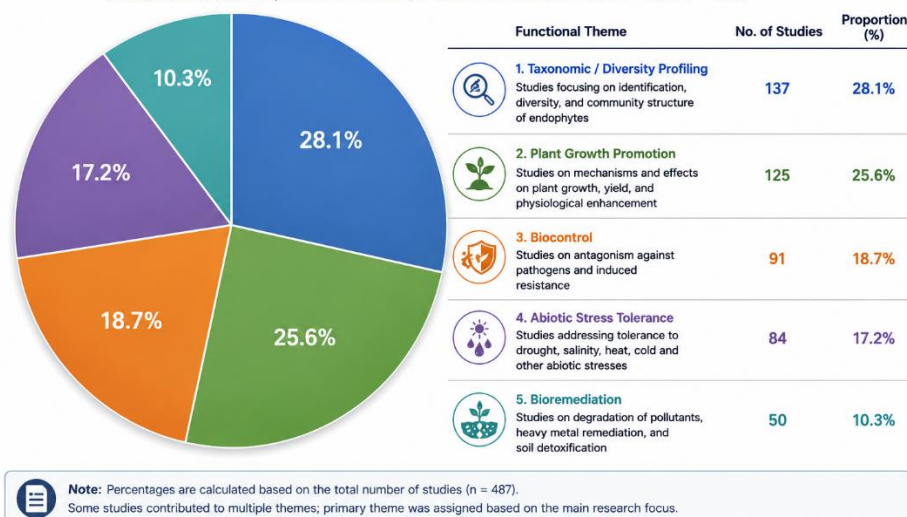
Theme	Level of Consensus	Representative Contradictions/Variability	Practical Implication
Taxonomic/functional diversity	High consensus on phylum-level dominance (Proteobacteria, Firmicutes, Actinobacteria)	Genus-level dominance is crop- and organ-specific rather than universal	Bioprospecting should be host- and tissue-targeted rather than generic
Plant growth promotion	High consensus that PGP traits are widespread	IAA biosynthesis pathway and magnitude vary by strain and host	Bioinoculant formulations may need strain–crop pairing rather than one-size-fits-all products
Biocontrol	Moderate-to-high consensus on <i>in vitro</i> antagonism	Field efficacy is inconsistent; few standardised evaluation protocols	Commercialisation requires formulation and field-stability research
Abiotic stress tolerance	Moderate consensus on osmolyte/phytohormone mechanisms	Mechanistic causality often inferred rather than experimentally confirmed	Reverse-genetic and multi-omics validation needed before large-scale deployment
Bioremediation	Moderate consensus that consortia (SynComs) outperform single strains	Most evidence is greenhouse/microcosm-scale; unculturable taxa remain uncharacterised	Field-scale, multi-season trials required prior to regulatory adoption



Schematic linking endophyte colonisation routes (seed, root, wound entry) to the four principal functional domains reviewed — nutrient acquisition, biocontrol, abiotic stress tolerance, and bioremediation — and their downstream agronomic outcomes (yield, resilience, reduced agrochemical input).

Proportional Breakdown of Reviewed Literature by Primary Functional Theme on Endophytic Microorganisms in Agricultural Crops

Relative Research Emphasis Across Major Functional Themes (Total Studies = 487)



Proportional breakdown of the reviewed literature by primary functional theme (taxonomic/diversity profiling, plant growth promotion, biocontrol, abiotic stress tolerance, bioremediation), illustrating the relative research emphasis across themes.

5. Research Gaps and Emerging Trends

Several unresolved issues recur across the reviewed literature. First, there is a persistent disconnect between laboratory/greenhouse demonstration and field-scale validation: the majority of PGP, biocontrol, and stress-tolerance studies report short-duration pot trials, with comparatively few multi-season, multi-site field studies establishing consistent agronomic benefit under variable environmental conditions [15, 20, 23]. Second, methodological standardisation is weak — isolation protocols, surface-sterilisation criteria, and functional-trait assays (e.g., IAA quantification, siderophore assays, antagonism assays) vary considerably between laboratories, complicating cross-study comparison and meta-analysis [7, 20]. Third, mechanistic causality is frequently inferred from correlative data (transcriptomic or metabolomic association) rather than

established through reverse genetics, targeted mutagenesis, or metabolite-flux validation, leaving open questions about whether identified pathways are necessary or merely coincidental to observed phenotypes [26].

A further gap concerns the taxonomic bias of applied research: although sequencing-based diversity studies reveal extensive "dark" endophytic diversity, functional characterisation and commercial development remain concentrated on a narrow set of culturable genera (*Bacillus*, *Pseudomonas*, *Trichoderma*, *Streptomyces*), leaving the agronomic potential of the broader endophytic reservoir largely unexplored [7, 13]. Regulatory and commercialisation pathways for endophyte-based bioinoculants and biopesticides also remain underdeveloped relative to the scientific evidence base, with few countries providing streamlined registration frameworks specific to microbiome-derived products.

Table 5: Research Gaps Identified

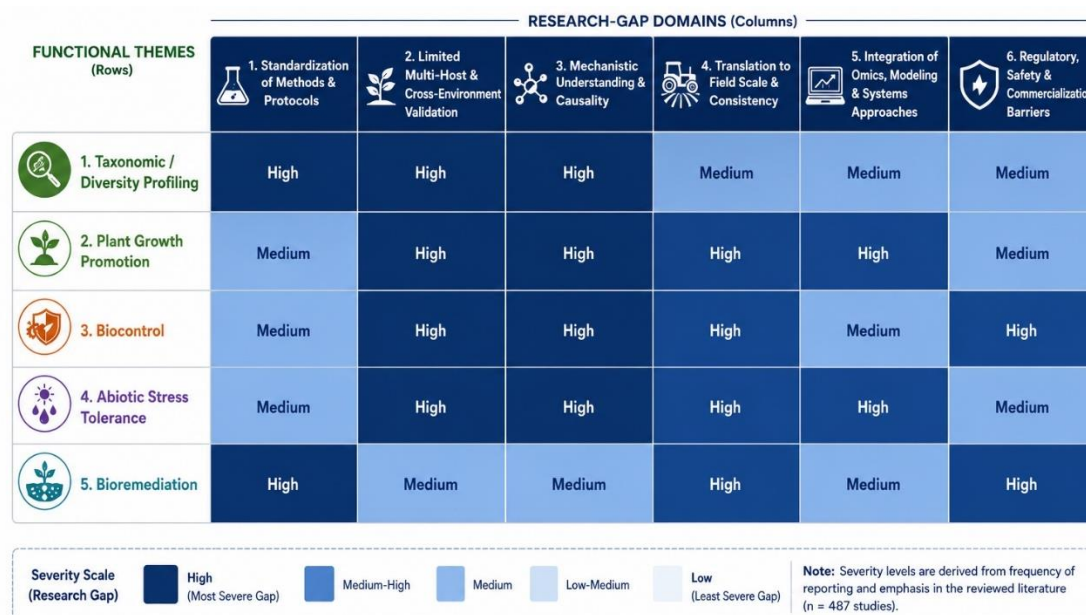
Domain	Gap Identified
Field validation	Scarcity of multi-season, multi-location field trials confirming greenhouse/pot-scale findings
Methodological standardisation	Inconsistent isolation, surface-sterilisation, and functional-assay protocols across studies
Mechanistic causality	Overreliance on correlative multi-omics association without reverse-genetic confirmation
Taxonomic bias	Applied research concentrated on a narrow set of culturable genera despite broader sequencing-revealed diversity
Regulatory pathways	Limited country-specific frameworks for registration and commercialisation of endophyte-based bioinoculants
Multi-partner interactions	Incomplete understanding of tripartite endophyte–host–pathogen or endophyte–endophyte interactions under field stress combinations

Emerging trends that partially address these gaps include the increasing use of synthetic microbial communities (SynComs) engineered from culturomics-based strain collections, which offer more reproducible, multi-functional inocula than single-strain products and have shown superior performance in both stress-tolerance and bioremediation contexts [27, 28]. Multi-omics integration — combining metagenomics, metatranscriptomics, and metabolomics within "holoomics"

frameworks — is likewise gaining traction as a means of resolving mechanistic questions that single-omics studies cannot address [26]. Advances in genome-resolved metagenomics are enabling identification of keystone endophytic taxa and their functional gene repertoires even among unculturable community members, expanding the pool of candidates available for future bioprospecting [29].

Table 6: Emerging Trends in the Field

Trend	Description	Anticipated Impact
Synthetic communities (SynComs)	Rationally assembled multi-strain consortia replacing single-strain inoculants	More robust, multi-functional bioinoculants for stress tolerance and bioremediation
Multi-omics/holomics integration	Combined metagenomic, transcriptomic, and metabolomic analysis of host–endophyte systems	Improved mechanistic resolution of plant–microbe interactions
Genome-resolved metagenomics	Recovery of metagenome-assembled genomes (MAGs) from unculturable endophytes	Expanded functional candidate pool beyond currently culturable genera
Precision/host-matched bioprospecting	Targeting endophyte isolation to stress-adapted or extremophile host plants	Higher hit-rate for stress-tolerance-conferring strains
Biopesticide commercialisation	Translation of endophyte secondary metabolites into registered biocontrol products	Reduced reliance on synthetic agrochemicals



Matrix mapping the five functional themes reviewed (rows) against the six research-gap domains identified in Table 5 (columns), with shading intensity indicating the relative severity of each gap within that theme based on the reviewed literature.

6. Discussion

Synthesising across the reviewed literature, a coherent picture emerges in which endophytic microorganisms constitute a functionally redundant but taxonomically variable resource: multiple, taxonomically distinct genera converge on similar functional outputs (nitrogen fixation, phosphate solubilisation, phytohormone production, antagonism toward phytopathogens), while the specific strains responsible for these functions differ substantially according to host species, plant organ, and agroecological context [1, 3, 11]. This pattern has an important practical implication: rather than seeking a single "universal" endophyte inoculant, the evidence base points toward host- and context-matched bioprospecting and formulation strategies as the more scientifically defensible path to reliable field performance [3, 14].

The trend toward high-throughput sequencing and metagenomic characterisation represents perhaps the most significant methodological shift documented in this review, substantially expanding the known diversity of endophytic communities relative to earlier culture-dependent surveys [7, 13, 29]. However, this expansion in taxonomic knowledge has outpaced functional characterisation: the field continues to rely on a comparatively narrow set of culturable genera for applied biocontrol and bioinoculant development, a disconnect that represents both a limitation of current practice and an opportunity for future research to close [7, 13]. Conflicting or inconsistent findings within the literature — for example, variable field efficacy of biocontrol agents that perform consistently well *in vitro* — are best explained not by

contradictory science but by the well-documented sensitivity of endophyte performance to environmental variables (temperature, soil moisture, indigenous microbial competition) that laboratory and greenhouse conditions do not replicate [15, 20]. This suggests that apparent contradictions in the literature are frequently attributable to differences in experimental scale and environmental context rather than genuine mechanistic disagreement.

From a theoretical standpoint, the recurring co-occurrence of multiple functional traits within single endophytic isolates — for instance, simultaneous IAA production and salinity tolerance — supports an emerging conceptual model in which endophyte functional diversity should be understood as a multi-trait phenotype rather than a set of independent, single-function categories [14, 24]. This has direct practical relevance for bioinoculant design, as strains selected for one trait (e.g., biocontrol) may confer incidental benefits (e.g., stress tolerance) that are currently underexploited in commercial formulation. Equally, the demonstrated superiority of synthetic communities over single-strain inoculants across both stress-tolerance and bioremediation applications suggests that future product development should shift decisively toward rationally designed, multi-strain consortia [27, 28].

Relating these findings to current developments in the field, the convergence of synthetic biology, genome-resolved metagenomics, and multi-omics analysis positions endophyte research at an inflection point comparable to the broader trajectory of the human and environmental microbiome sciences a decade earlier: taxonomic cataloguing is giving way

to functional and mechanistic dissection, and mechanistic dissection is beginning to inform rational design of applied products [26, 29]. Realising the practical benefit of this scientific progress, however, will depend on parallel advances in field validation methodology and in regulatory frameworks capable of accommodating microbiome-derived agricultural products — dimensions of the field that, per the gaps identified in Section 5, currently lag behind the underlying science.

7. Conclusion

This review combines various scholarly works done over a period of 10 years, covering the diversity of endophytic microorganisms found in agricultural crops and cites the research carried out and published in well-known journals like PubMed, Web of Science, and Scopus. The literature indicates that endophytes play a significant role in promoting plant growth, resistance to abiotic and biotic stresses, bioremediation of polluted soils found in agricultural areas of the world. In addition, this article discusses certain functional mechanisms presented in various endophytes, such as phytohormones, nutrient absorption, production of metabolites, and elicitation of plant resistance. In conclusion, it is implied that taxonomic composition of endophytes can differ due to the type of host, its tissue, and type of ecology, while their functional composition can be very similar.

The synthesis's wider importance revolves around knowing the issues of scientific development where the field has advanced far ahead of both translation and regulation. In particular, laboratory and greenhouse experiments show that endophyte use can be beneficial agronomically, but so far available methods of practical implementation have lagged behind scientific advances.

The essential actions for the researcher community involve setting up standard methods of isolation and functional testing that are crucial for the effective comparison of cross-studied results and meta-analysis, updating the mechanisms of research to discover reverse genetics and the metabolic flux, and improving functional analysis to include a wider range of organisms than just the most common genera that could be cultured. In addition, from the practitioners' and policymakers' point of view, the results imply that there is no reason to stop or limit the use of investment into synthetic organisms-designed bioinoculants and to come up with more defined guidelines for the governmental registration of microbiome products that will assist foster the introduction of already proven endophyte compounds in agriculture. Future studies should focus on more novel activities, such as trials covering several seasons and locations, association of various types of data, and creation of host-specialized organisms.

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