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# Functional Diversity of Bacterial and Fungal Endophytes Associated with Mulberry (*Morus* spp.) Cultivated in Southern Karnataka, India

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**ABSTRACT:** Mulberry (*Morus* spp.) cultivation is frequently constrained by both abiotic and biotic stresses, including insect pests and diseases, which adversely affect silkworm health and silk productivity. Endophytes, defined as microorganisms that colonize internal plant tissues without causing visible harm, represent a promising but underexplored biological resource for enhancing plant vigour, stress tolerance and nutritional quality. The present study evaluated the diversity of bacterial and fungal endophytes associated with eight mulberry varieties grown under field conditions in southern Karnataka, India, and assessed their potential implications for mulberry growth and silkworm biology. Endophytic microorganisms were isolated from surface-sterilized leaf and shoot tissues using standard culture-dependent techniques. A total of four dominant endophytic genera were consistently recovered across samples, including *Bacillus* spp. among bacteria and *Aspergillus* spp., *Trichoderma* spp. and *Fusarium* spp. among fungi. The frequency and distribution of these endophytes varied among mulberry varieties and between plant tissues, indicating clear host genotype- and tissue-specific colonization patterns. In general, shoots harboured comparatively higher fungal diversity, while bacterial endophytes, particularly *Bacillus* spp., were more consistently distributed across both tissues. Although quantitative data on isolation frequency and abundance are presented in the results section, the observed patterns indicate differential colonization efficiency among mulberry genotypes. The dominance of *Bacillus* and *Trichoderma* suggests potential plant growth-promoting functions, including improved nutrient availability, enhanced physiological activity and increased stress tolerance of host plants. These microbial interactions are likely to influence mulberry leaf quality, a critical determinant of silkworm growth performance and cocoon traits.

**Keywords:** Sericulture, Microbial diversity, Plant growth promotion, Mulberry.

## 1. INTRODUCTION

Mulberry (*Morus* spp.) forms the backbone of sericulture, as its leaves constitute the sole food source for the silkworm, *Bombyx mori* L. The productivity and profitability of sericulture are therefore intrinsically linked to both the quantity and quality of mulberry leaf yield. Despite its agronomic importance, mulberry cultivation faces serious challenges from abiotic stresses such as drought, soil nutrient depletion and temperature fluctuations, as well as a wide spectrum of biotic agents. More than 300 species of insect and non-insect pests have been reported globally on mulberry, of which over 50 cause significant economic losses by reducing leaf yield, palatability and nutritional value. Furthermore, diseases caused by fungal, bacterial and viral pathogens adversely affect mulberry growth and longevity, thereby indirectly impairing silkworm health, survivability and silk production

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efficiency (Hosamani et al., 2020; Vanitha, 2018). In the context of climate variability and increasing restrictions on chemical inputs, sustainable strategies to enhance mulberry resilience while maintaining leaf nutritional quality have become imperative.

Endophytes are microorganisms that inhabit internal plant tissues for all or part of their life cycle without inducing visible disease symptoms. The term "endophyte" was first introduced by de Bary in 1866 to distinguish internal colonizers from epiphytic microorganisms (Stone et al., 2000). Endophytic communities encompass bacteria, fungi and archaea, many of which establish mutualistic or commensal relationships with their host plants. These microorganisms play critical roles in plant growth promotion, stress mitigation and defense regulation through diverse mechanisms, including the production of phytohormones such as indole-3-acetic acid and gibberellins, solubilization of mineral nutrients, biological nitrogen fixation, synthesis of antimicrobial secondary metabolites and modulation of host defence signalling pathways (Miliute et al., 2015; Malfanova et al., 2013).

In perennial crops such as mulberry, endophytic microorganisms assume greater ecological significance due to long-term host–microbe associations and stable internal niches. Studies have shown that endophytes can enhance host tolerance to drought and nutrient stress by improving water-use efficiency, osmolyte accumulation and antioxidant enzyme activity (Rodriguez et al., 2009; Hardoim et al., 2015). Such stress-alleviating traits are particularly relevant to mulberry cultivation in semi-arid regions, where environmental limitations oftern constrain leaf yield and quality. In addition, endophytes contribute to the biological suppression of plant pathogens through competitive exclusion, antibiosis and the induction of systemic resistance, thereby reducing dependence on chemical pesticides (Harman et al., 2004; Singh et al., 2013).

From a sericultural perspective, the functional role of endophytes extends beyond plant health directly influencing silkworm nutrition and performance. Mulberry leaf biochemical composition particularly protein, carbohydrate, moisture and micronutrient content-is a major determinant of silkworm growth rate, larval duration, survivability and cocoon traits such as cocoon weight, shell weight and filament length (Gunasekhar & Somayaji, 2019; Paul et al., 2005). Endophytes that enhance nutrient assimilation and leaf quality therefore exert an indirect yet profound effect on silkworm biology. Previous studies have reported that mulberry leaves colonized by beneficial endophytes such as *Bacillus* and *Trichoderma* improve larval feeding efficiency, reduce disease incidence and enhance silk yield parameters (Ravikumar et al., 2015; Murugesh et al., 2012).

Despite these potential benefits, systematic information on the diversity, tissue specificity and varietal distribution of endophytic microorganisms in mulberry remains limited, particularly under Indian agro-climatic conditions. Most available studies have focused either on plant growth promotion or disease suppression, with relatively few investigations addressing the integrated mulberry–endophyte–silkworm continuum. Moreover, host genotype plays a crucial role in shaping endophytic community structure, as different mulberry varieties vary in leaf chemistry, phenolic content and defense metabolites, which in turn influence microbial colonization and persistence (Peng et al., 2023; Schulz & Boyle, 2005).

In line with the study titled *"Functional diversity of bacterial and fungal endophytes associated with mulberry (Morus spp.) cultivated in southern Karnataka, India"*, the present investigation was undertaken to isolate and characterize bacterial and fungal endophytic microorganisms from different mulberry varieties grown under rain-fed conditions. The study further aims to elucidate varietal- and tissue-specific patterns of endophytic colonization and to interpret their potential role in influencing mulberry growth performance and the biological responses of silkworms.

## 2. MATERIALS AND METHODS

### 2.1. Study Site and Experimental Material

The present investigation was carried out during 2024–2025 at the "A" Block of the College of Agriculture, Vishweshwaraiah Canal Farm, Mandya, Karnataka, India (12°32′ N latitude, 76°53′ E longitude; 690 m above mean sea level). The experimental location lies within the Southern Dry Zone (Agro-climatic Zone-6) of Karnataka, characterized by semi-arid climatic conditions with distinct monsoonal influence. The region receives an average annual rainfall of approximately 751 mm, of which nearly 70–75% is concentrated during the southwest monsoon period from June to November. Mean annual temperatures range between 21 and 34 °C, with moderate relative humidity during the cropping season, creating favourable conditions for mulberry cultivation and microbial colonization.

Eight mulberry (*Morus* spp.) varieties representing traditional, improved and elite varieties namely Mysore Local, Sahana, S36, DD, AR12, V1, G2 and G4 were selected for the study. These varieties were maintained under

uniform agronomic conditions following the recommended package of practices for rain-fed mulberry cultivation, including spacing, pruning schedule, nutrient management and plant protection measures, as prescribed by Dandin and Giridhar (2014). No chemical fungicides or bactericides were applied during the experimental period to avoid interference with native endophytic microbial populations. Plants selected for sampling were healthy, disease-free and of uniform age, ensuring consistency in endophyte isolation and minimizing environmental and physiological variability.

**2.2. Isolation of Endophytic Microorganisms**

Endophytic microorganisms were isolated from healthy leaf and shoot tissues of each mulberry variety following standard surface sterilization and isolation procedures, as described by Sturz et al. (1999) and Gyaneshwar et al. (2001). The study was designed with a systematic sampling strategy, wherein each mulberry variety was represented by three biological replicates (n = 3) for each tissue type (leaf and shoot). Thus, endophytic populations were independently assessed for leaves and shoots of every variety, ensuring robust comparison across varieties and tissue-specific colonization patterns. All samples were collected from symptom-free, healthy plants and immediately transported to the laboratory in sterile polyethylene bags and processed within 24 h of collection.

Leaf and shoot segments were first washed thoroughly under running tap water to remove adhering soil particles and debris, then rinsed with sterile distilled water. Surface sterilization was carried out in a sequential manner: samples were immersed in 70% ethanol for 1 minute, followed by treatment with 1% sodium hypochlorite (NaOCl) solution for 2–3 minutes and finally rinsed three to four times with sterile distilled water to ensure complete removal of surface sterilants. The effectiveness of surface sterilization was confirmed by plating the final rinse water and performing tissue imprinting on sterile agar plates; the absence of microbial growth after incubation confirmed successful elimination of epiphytic microorganisms and validated the endophytic origin of isolates.

After sterilization, tissues were aseptically blotted dry using sterile filter paper and cut into small segments under laminar airflow conditions. For isolation, leaf and shoot tissues from each replicate were processed separately. Furthermore, bacterial and fungal endophytes were maintained and handled as independent culture sets throughout the study to avoid cross-contamination and ensure accurate characterization of microbial groups. The tissue segments were macerated using a sterile mortar and pestle in sterile phosphate buffer (pH 7.0) to release internal microbial communities.

Appropriate aliquots of the homogenate were inoculated onto specific culture media for isolation. Bacterial endophytes were cultured on Nutrient Agar (NA), while fungal endophytes were isolated on Potato Dextrose Agar (PDA) supplemented with streptomycin (50 mg $L^{-1}$) to suppress bacterial growth. The inoculated plates were incubated at 28 ± 2 °C under controlled laboratory conditions. Bacterial cultures were incubated for 24–48 hours, whereas fungal cultures were incubated for 5–7 days to allow sufficient colony development.

Distinct colonies emerging from internal tissues were periodically observed, and morphologically different bacterial and fungal colonies were sub-cultured separately to obtain pure cultures. These purified isolates were maintained independently: bacterial isolates on Nutrient Agar slants and fungal isolates on PDA slants, both stored at 4 °C for further morphological, biochemical and molecular characterization.

**2.3. Morphological and Biochemical Characterization of Endophytic Isolates**

Bacterial endophytes were characterized based on colony morphology, including size, shape, colour, margin and elevation, as observed on Nutrient Agar plates. Microscopic examination was carried out to determine cell shape and arrangement using light microscopy by Gram staining. Motility was assessed using the hanging drop method, while catalase activity was determined by the evolution of oxygen bubbles upon the addition of 3% hydrogen peroxide, following standard microbiological protocols (Cappuccino & Sherman, 2014). These morphological and biochemical traits were used for preliminary identification of bacterial isolates up to the genus level.

Fungal endophytes were identified based on macroscopic and microscopic characteristics. Colony morphology, including growth pattern, pigmentation, texture and sporulation, was recorded on PDA medium. Microscopic features such as hyphal structure, septation, conidiophore arrangement and spore morphology were examined by mounting fungal structures in lactophenol cotton blue stain and observing them under a compound microscope. Identification was carried out using standard mycological keys and descriptions provided by Barnett and Hunter (1998) and Domsch et al. (2007).

Molecular identification (16S rRNA/ITS sequencing) was not conducted due to scope and resource limitations. All endophytic isolates were tentatively identified to the genus level based on morphological and biochemical characteristics, which is an accepted preliminary approach in endophyte ecology studies where the focus is on community composition and functional relevance rather than molecular taxonomy (Schulz & Boyle, 2005; Hyde & Soytong, 2008).

## 3. RESULTS AND DISCUSSION

### 3.1. Diversity, Abundance and Tissue-Specific Distribution of Endophytes in Mulberry Varieties

The present investigation demonstrated that mulberry plants harbor a stable and functionally significant endophytic microbial community, comprising both bacterial and fungal taxa colonizing internal leaf and shoot tissues without inducing visible disease symptoms. Across the eight mulberry varieties evaluated, four dominant endophytic genera—*Bacillus*, *Aspergillus*, *Trichoderma* and *Fusarium* were consistently isolated (Figure 1). Similar dominance of these genera has been reported in perennial crop systems, where long-lived tissues favour selective microbial associations rather than random colonization (Stone et al., 2000; Malfanova et al., 2013). The persistence of these genera across varieties indicates strong host compatibility and ecological fitness within mulberry tissues.

A pronounced varietal and tissue-specific colonization pattern was evident. Traditional mulberry varieties such as Mysore Local and DD were consistently colonized by *Aspergillus* spp. in both leaf and shoot tissues, suggesting systemic colonization and long-term host adaptation. In contrast, improved mulberry varieties such as Sahana, S36 and V1 predominantly harbored *Bacillus* spp., reflecting the influence of host genotype on microbial recruitment. Host-driven selection of endophytes is well documented and is often mediated through differences in leaf nutrient composition, phenolics and secondary metabolites shaped by breeding practices (Miliute et al., 2015; Peng et al., 2023).

Leaves supported a higher prevalence of growth-promoting fungi such as *Trichoderma*, while shoot tissues favoured stress-tolerant fungi such as *Fusarium*. Such tissue specificity reflects differences in carbon availability, oxygen concentration and defense signalling within plant organs (Schulz & Boyle, 2005). Similar compartmentalization of endophytes has been reported in mulberry and other woody plants, where leaf tissues serve as hotspots for beneficial symbionts due to their metabolic activity (Nataraja et al., 2011; Rekha et al., 2014).

**Table 1.** Occurrence of endophytes in plant tissues of mulberry varieties

| Variety | Endophytes | |
|---|---|---|
| | **Leaf** | **Shoot** |
| Mysore local | *Aspergillus* spp. | *Aspergillus* spp. |
| Sahana | *Bacillus* spp. | *Bacillus* spp. |
| S36 | *Bacillus* spp. | *Bacillus* spp. |
| DD | *Aspergillus* spp. | *Aspergillus* spp. |
| AR12 | *Trichoderma* spp. | *Fusarium* spp. |
| V1 | *Bacillus* spp. | *Bacillus* spp. |
| G2 | *Trichoderma* spp. | *Trichoderma* spp. |
| G4 | *Trichoderma* spp. | *Fusarium* spp. |

### 3.2. Functional Relevance of *Bacillus* spp. as Dominant Bacterial Endophytes

Bacterial endophytes isolated from Sahana, S36 and V1 exhibited rod-shaped, motile, Gram-positive and catalase-positive characteristics, confirming their tentative identification as *Bacillus* spp. The systemic presence of *Bacillus* in both leaf and shoot tissues indicates its ability to colonize vascular and intercellular spaces efficiently, a trait that has been widely reported for *Bacillus* endophytes in crop plants (Gyaneshwar et al., 2001; Singh et al., 2013).

The predominance of *Bacillus* spp. in high-yielding mulberry varieties is agronomically significant, as members of this genus are known to produce phytohormones such as indole-3-acetic acid, gibberellins and cytokinins, which enhance leaf expansion, chlorophyll synthesis and photosynthetic efficiency (Rao and Sivaprasad, 2007; Rekha et al., 2014). Additionally, *Bacillus* spp. solubilize inorganic phosphates and secrete siderophores, thereby improving nitrogen and phosphorus availability within mulberry leaves (Nagaraju & Giridhar, 2017).

Improved mulberry leaf nutritional status directly influences silkworm biology. Gunasekhar and Somayaji (2019) emphasized that silkworm growth, larval duration and cocoon traits are strongly dependent on leaf protein and carbohydrate content. Silkworms reared on *Bacillus*-associated mulberry leaves have been reported to show higher larval weight, improved efficiency of conversion of ingested food (ECI), increased cocoon weight and shell ratio (Ravikumar et al., 2015). The present findings corroborate

these observations, underscoring the pivotal role of *Bacillus* endophytes in mulberry–silkworm interactions.

Moreover, *Bacillus* spp. produce antimicrobial lipopeptides and endospores that suppress foliar pathogens and enhance plant resilience against biotic stress (Ravikumar *et al.*, 2015). Their natural abundance in elite mulberry varieties such as V1 highlights their potential as biological inputs for sustainable sericulture.

### 3.3. Ecological and Physiological Role of Fungal Endophytes in Mulberry

Fungal endophytes isolated in the present study belonged predominantly to *Aspergillus*, *Trichoderma* and *Fusarium*, each exhibiting distinct ecological functions. *Aspergillus* spp., isolated consistently from Mysore Local and DD varieties, exhibited septate hyphae and conidial spores typical of endophytic *Aspergillus*. Several studies have demonstrated that *Aspergillus* endophytes enhance phosphorus solubilization, nitrogen metabolism and secondary metabolite synthesis in host plants (Strobel & Daisy, 2003; Kavitha et al., 2011).

In mulberry, *Aspergillus* endophytes have been associated with increased leaf protein and carbohydrate accumulation, thereby improving the nutritional profile for silkworm feeding (Gowda et al., 2009; Zhang et al., 2010). Silkworms reared on such leaves exhibit faster larval growth, improved silk gland activity and superior cocoon parameters, including shell weight and filament denier (Zhang et al., 2010). These findings indicate that *Aspergillus* functions as a beneficial symbiont in the mulberry–silkworm system under non-pathogenic conditions.

### 3.4. Multifunctional Role of *Trichoderma* spp. in Mulberry–silkworm Systems

*Trichoderma* spp. were predominantly isolated from AR12, G2 and G4 varieties, with consistent colonisation in G2. *Trichoderma* is widely recognized as a multifunctional endophyte with strong biocontrol and growth-promoting capabilities (Harman et al., 2004; Bisset, 1991). Its ability to produce antifungal metabolites, hydrolytic enzymes and elicitors of induced systemic resistance makes it an effective symbiont in mulberry cultivation (Krishnaveni et al., 2014).

Colonization by *Trichoderma* enhances mulberry shoot biomass, leaf area and chlorophyll content, thereby increasing photosynthetic efficiency and leaf yield (Singh et al., 2011). These improvements translate into enhanced silkworm performance, as leaves with higher protein content and reduced anti-nutritional compounds improve digestibility and assimilation (Murugesh et al., 2012). Silkworms fed on Trichoderma-associated leaves show higher larval survival, reduced disease incidence and increased cocoon shell weight and filament length (Murugesh et al., 2012).

The natural presence of *Trichoderma* in elite mulberry varieties underscores its potential as a biological agent to

**Table 2.** Morphological and biochemical characterization of bacterial endophytes

| Variety | Morphological character | | Biochemical character | | Tentative genus |
|---|---|---|---|---|---|
| | Cell shape | Motility | Gram staining | Catalase test | |
| Sahana (Leaf and Shoot) | Rod | Motile | Gram-positive | Positive | *Bacillus* spp. |
| S36 (Leaf and Shoot) | Rod | Motile | Gram-positive | Positive | *Bacillus* spp. |
| V1 (Leaf and Shoot) | Rod | Motile | Gram-positive | Positive | *Bacillus* spp. |

**Table 3.** Characterization of fungal endophytes

| Variety | Hyphal type | Spore type | Tentative genus |
|---|---|---|---|
| Mysore local (Leaf and Shoot) | Septate | Conidial spores | *Aspergillus* spp. |
| DD (Leaf and Shoot) | Septate | Conidial spores | *Aspergillus* spp. |
| AR12 (Leaf) | Septate | Conidia (round) | *Trichoderma* spp. |
| AR12 (Shoot) | Septate | Sickle-shaped | *Fusarium* spp. |
| G2 (Leaf and Shoot) | Septate | Conidia (round) | *Trichoderma* spp. |
| G4 (Leaf) | Septate | Conidia (round) | *Trichoderma* spp. |
| G4 (Shoot) | Septate | Sickle-shaped | *Fusarium* spp. |

improve mulberry productivity and silk yield while reducing reliance on chemical pesticides.

### 3.5. Dualistic Behaviour of *Fusarium* spp. as asymptomatic endophytes

*Fusarium* spp. were isolated from shoot tissues of AR12 and G4 varieties without any visible disease symptoms. Although *Fusarium* is commonly regarded as a plant pathogen, several studies have demonstrated that many *Fusarium* strains behaviour under favourable conditions (Schulz & Boyle, 2005). Such strains may contribute to nutrient cycling and to the mild induction of host defence mechanisms.

In mulberry, endophytic *Fusarium* has been reported to enhance carbohydrate metabolism and nitrogen assimilation, though it may also induce slight increases in phenolic compounds (Murugesh et al., 2012). This dual effect can influence silkworm biology, a marginally prolonged larval duration due to increased phenolic digestion. Nevertheless, cocoon traits generally remain stable or improved, particularly shell weight and filament length (Murugesh et al., 2012).

The restricted distribution of *Fusarium* observed in the present study suggests tight host regulation, preventing

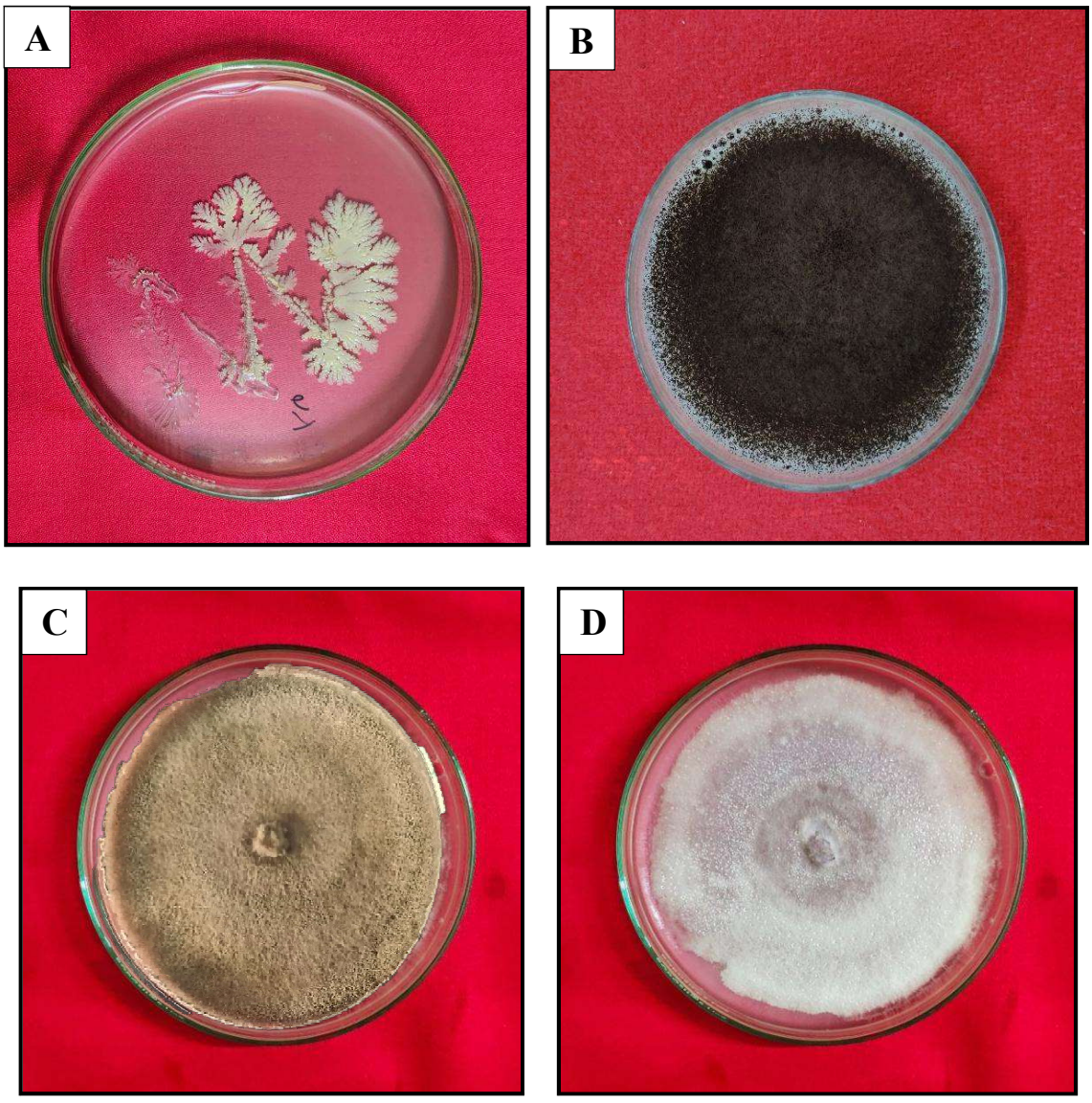


**Figure 1.** Morphology of endophytes:A. *Bacillus* spp., B. *Aspergillus* spp., C. *Trichoderma* spp., D. *Fusarium* spp.

pathogenic expression while allowing potential functional benefits.

Overall, the identification of bacterial and fungal endophytic isolates in the present study was carried out primarily based on morphological and cultural characteristics, including colony morphology, pigmentation, growth pattern and microscopic features using standard taxonomic keys. Molecular identification techniques such as 16S rRNA gene sequencing for bacterial isolates and ITS region sequencing for fungal isolates were not performed in the present investigation due to resource and scope limitations. This represents a methodological limitation of the study and the isolates were therefore characterised only up to the morphological level. This limitation has been duly acknowledged and should be considered when interpreting the taxonomic resolution of the reported endophytic diversity.

### 3.6. Implications for Sustainable Sericulture and Applied Microbiology

The present study clearly demonstrates that endophytic microorganisms play a crucial role in regulating mulberry growth, leaf quality and silkworm biology. Beneficial endophytes such as *Bacillus* and *Trichoderma* enhance mulberry physiology, improve resistance to biotic stress and indirectly promote silkworm growth and silk production. Even fungal endophytes with dual roles, such as *Aspergillus* and *Fusarium*, contribute positively when maintained in a balanced symbiotic state. Harnessing these naturally occurring endophytes represents a promising, eco-friendly strategy for sustainable sericulture. Integration of endophyte-based approaches can reduce dependence on chemical fertilizers and pesticides, enhance leaf quality, and improve economic returns to farmers, aligning with the principles of sustainable agriculture and applied microbiology (Vanitha, 2018; Hosamani et al., 2020).

In addition to endophytic interactions, there is also significant scope to explore the role of phyllosphere-associated microbial communities in shaping mulberry–silkworm performance. The phyllosphere microbiome, residing on the leaf surface, may influence leaf surface chemistry, nutrient dynamics and microbial-mediated modulation of plant metabolites, which directly affect silkworm feeding behaviour and physiological performance. These surface-associated microbial populations may also help maintain foliar health by suppressing opportunistic pathogens, thereby indirectly stabilising leaf quality and the nutritional consistency required for optimal silkworm development. However, the present investigation was limited to endophytic microorganisms, and phyllosphere microbial communities were not included in the analysis. Future integrated studies involving both endophytic and phyllosphere microbiomes, along with silkworm bioassays, would provide a more comprehensive understanding of plant–microbe–insect interactions in mulberry-based sericulture systems.

## 4. CONCLUSION

The present study highlights the ecological and functional significance of endophytic microorganisms in mulberry (*Morus* spp.) and their potential strengthening the mulberry–silkworm production system. The isolation of dominant bacterial and fungal endophytes from the genera Bacillus, Aspergillus, Trichoderma, and Fusarium from multiple mulberry varieties demonstrates that mulberry plants harbour a stable and diverse endophytic community with strong host- and tissue-specificity. The observed variation in endophytic colonization among traditional and improved mulberry varieties underscores the influence of host genotype and internal plant microenvironments in shaping endophyte diversity. The predominance of beneficial endophytes such as *Bacillus* and *Trichoderma*, in high-yielding mulberry varieties suggests their important role in enhancing plant growth, nutrient assimilation and resistance to biotic and abiotic stresses. These improvements in mulberry physiological status and leaf nutritional quality are likely to translate into better silkworm growth, survivability and cocoon traits, thereby reinforcing the close interdependence between plant-associated microbiota and silkworm biology. Even endophytes with dual ecological behaviour, such as *Aspergillus* and *Fusarium*, appear to contribute positively when maintained in a balanced, asymptomatic association within host tissues. Overall, the findings emphasize the potential of exploiting naturally occurring endophytic microorganisms as eco-friendly biological inputs for sustainable mulberry cultivation and sericulture. Integration of endophyte-based strategies can reduce reliance on chemical fertilizers and pesticides, improve leaf quality and enhance silk productivity while maintaining environmental safety. Future studies employing molecular identification, functional assays and silkworm bioassays will further strengthen the understanding of endophyte-mediated mechanisms and facilitate their practical application in sustainable sericulture systems.

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**CRediT authorship contribution statement**

Nitish Kumar, L. S.: Conceptualization, Methodology, Investigation, Data curation, Formal analysis, Visualization, Writing – original draft preparation. G. Sugeetha: Conceptualization, Supervision, Methodology, Validation, Resources, Writing – review and editing.Asha, N. N.: Investigation, Data curation, Validation, Formal analysis, Writing – review and editing.All authors have read and approved the final version of the manuscript and agree to its submission for publication.

**Conflict of interest**

The authors declare no conflicts of interest, either financial or personal, that could have influenced the results or interpretation of this study.

**Declaration of generative AI and AI-assisted technologies in the writing process**

During the preparation of this manuscript, AI-assisted writing tools were used solely for language editing, grammatical refinement, and improvement of sentence structure. The scientific content, data interpretation and conclusions were developed, verified and approved entirely by the authors. The use of AI tools did not involve the generation of scientific data, results or references. The authors take full responsibility for the accuracy and integrity of the content presented in this manuscript.

**Data availability statement**

The data generated and analysed during the current study are included within this manuscript. All datasets supporting the conclusions of this research, including isolation records and observational data on endophytic microbial diversity are available from the corresponding author upon reasonable request. The raw culture isolates are preserved in the laboratory collection and can be made available for further research purposes, subject to institutional guidelines and material transfer conditions.

## REFERENCES

Barnett, H.L., & Hunter, B.B. (1998). *Illustrated genera of imperfect fungi* (4th ed.). APS Press.

Bisset, J. (1991). A revision of the genus *Trichoderma*. I. Section Longibrachiatum sect. nov. *Canadian Journal of Botany, 69*, 2373-2417.

Cappuccino, J.G., & Sherman, N. (2014). *Microbiology: A laboratory manual* (10th ed.). Pearson Education.

Dandin, S.B., & Giridhar, K. (2014). *Handbook of sericulture technologies*. Central Silk Board, Ministry of Textiles, Government of India.

Domsch, K.H., Gams, W., & Anderson, T.H. (2007). *Compendium of soil fungi* (2nd ed.). IHW-Verlag.

Gowda, K.N.N., Rajanna, D., & Ramesh, H.L. (2009). Effect of mulberry leaf quality on economic parameters of silkworm (*Bombyx mori* L.). *Indian Journal of Sericulture, 48*, 12-17.

Gunasekhar, V., & Somayaji, M.R. (2019). Influence of mulberry leaf quality on growth and cocoon traits of *Bombyx mori* L. *Journal of Entomology and Zoology Studies, 7*, 1085-1090.

Gyaneshwar, P., James, E.K., Mathan, N., Reddy, P.M., Reinhold-Hurek, B., & Ladha, J.K. (2001). Endophytic colonization of rice by a diazotrophic strain of *Azoarcus*. *Applied and Environmental Microbiology, 67*, 3328-3337.

Hardoim, P.R., van Overbeek, L.S., & van Elsas, J.D. (2015). Properties of bacterial endophytes and their proposed role in plant growth. *Trends in Microbiology, 23*, 463-471.

Harman, G.E., Howell, C.R., Viterbo, A., Chet, I., & Lorito, M. (2004). *Trichoderma* species—Opportunistic, avirulent plant symbionts. *Nature Reviews Microbiology, 2*, 43-56.

Hosamani, V., Raghavendra, S., & Suresh Kumar, N. (2020). Pests and diseases of mulberry and their management. *International Journal of Chemical Studies, 8*, 2555-2561.

Hyde, K.D., & Soytong, K. (2008). The fungal endophyte dilemma. *Fungal Diversity, 33*, 163-173.

Kavitha, R., Raguchander, T., Samiyappan, R., & Saravanakumar, D. (2011). Endophytic bacteria for plant growth promotion and suppression of bacterial blight of cotton. *African Journal of Biotechnology, 10*, 2380-2386.

Krishnaveni, M., Ramesh, H.L., & Rajanna, D. (2014). Effect of *Trichoderma* spp. on mulberry growth and leaf yield. *Journal of Biopesticides, 7*, 128-133.

Malfanova, N., Franzil, L., Lugtenberg, B., & Chebotar, V. (2013). Endophytic bacteria with plant growth-promoting properties. *Plant and Soil, 362*, 1-12.

Miliutė, I., Buzaitė, O., & Stanys, V. (2015). Bacterial endophytes in agricultural crops and their role in stress tolerance. *Agronomy Research, 13*, 468-478.

Murugesh, K.A., Mahalingam, C.A., & Saravanan, D. (2012). Influence of endophytic fungi on mulberry leaf quality and silkworm performance. *Indian Journal of Sericulture, 51*, 72-78.

Nagaraju, R., & Giridhar, K. (2017). Role of biofertilizers in improving mulberry productivity. *Indian Journal of Agricultural Sciences, 87*, 153-158.

Nataraja, K.N., Reddy, A.R., & Prasad, T.G. (2011). Endophytes in perennial plants: Diversity and functions. *Journal of Plant Biology, 38*, 1-12.

Paul, D.C., Subba Rao, G., & Deb, D.C. (2005). Impact of leaf quality on silkworm growth and cocoon characters. *Journal of Insect Physiology, 51*, 1-7.

Peng, J., Zhang, Y., Li, H., & Chen, X. (2023). Host genotype-driven variation in endophytic microbial communities. *Plant and Soil, 485*, 135-150.

Rao, S.R., & Sivaprasad, V. (2007). Role of plant growth-promoting bacteria in mulberry cultivation. *Indian Journal of Sericulture, 46*, 92-97.

Ravikumar, G., Mahalingam, C.A., & Rajanikanth, K. (2015). Influence of bacterial endophytes on mulberry leaf quality and silkworm performance. *Journal of Applied and Natural Science, 7*, 593-598.

Rekha, P.D., Lai, W.A., Arun, A.B., & Young, C.C. (2014). Effect of free and encapsulated plant growth-promoting bacteria on plant growth. *Journal of Microbiology, 52*, 93-101.

Rodriguez, R.J., White, J.F., Arnold, A.E., & Redman, R.S. (2009). Fungal endophytes: Diversity and functional roles. *New Phytologist, 182*, 314-330.

Schulz, B., & Boyle, C. (2005). The endophytic continuum. *Mycological Research, 109*, 661-686.

Singh, L.P., Gill, S.S., & Tuteja, N. (2011). Unraveling the role of fungal symbionts in plant stress tolerance. *Plant Signaling & Behavior, 6*(2), 175-191.

Singh, R., Singh, S., & Sharma, S. (2013). Endophytic bacteria: Role in plant growth promotion and biocontrol. *Agricultural Reviews, 34*(3), 223-233.

Stone, J.K., Bacon, C.W., & White, J.F. (2000). An overview of endophytic microbes. In C.W. Bacon & J.F. White (Eds.), *Microbial endophytes* (pp. 3-29). Marcel Dekker.

Strobel, G., & Daisy, B. (2003). Bioprospecting for microbial endophytes. *Microbiology and Molecular Biology Reviews, 67*(4), 491-502.

Sturz, A.V., Christie, B.R., & Nowak, J. (1999). Bacterial endophytes: Potential role in developing sustainable systems of crop production. *Critical Reviews in Plant Sciences, 18*(1), 1-30.

Vanitha, S. (2018). Sustainable mulberry cultivation practices for sericulture. *Indian Journal of Ecology, 45*(4), 681-687.

Zhang, Y., Wang, Y., & Li, Z. (2010). Influence of mulberry leaf quality on silkworm growth and silk production. *African Journal of Biotechnology, 9*, 912-916.