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RESEARCH PAPER

Screening of entomopathogenic and endophytic fungi from various landscapes and evaluation of their antagonistic activity against *Fusarium* sp.

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ABSTRACT

Forestry research is increasingly focused on exploring microbial resources, including entomopathogenic endophytic fungi (EEFs), as potential biological control agent. This study aimed to explore and characterize fungal isolates obtained from different landscapes and biological sources in South Sulawesi and to evaluate the antagonistic activity of selected isolates against *Fusarium* sp. Sampling was conducted from May to July 2025 in a national park, forestry plant nursery, silkworm rearing centers, natural forests, plantation forests, community forests, and agroforestry systems. Insects, soil, and plant tissues were used as fungal isolation sources. Fungal isolates were characterized based on their morphological features and classified as entomopathogenic (EP), entomopathogenic endophytic (EEF), or endophytic (END) fungi according to their respective sources and observed characteristics. Three selected isolates were evaluated for antagonistic activity against *Fusarium* sp. using a dual-culture assay, and the data were analyzed using one-way analysis of variance (ANOVA) followed by Tukey's HSD test. A total of 72 fungal isolates representing nine fungal taxa were recovered from the different sampling sources. The isolates included *Aspergillus* sp., *Simplicillium subtropicum*, *Penicillium* sp., *Fusarium* sp., *Cladosporium oxysporum*, *Trichoderma* sp., *Cordyceps* sp., *Gibellula* sp., and the microsporidian pathogen *Nosema bombycis.* Among the selected isolates, *S. subtropicum* sp. KuBi1, *B. bassiana,* BGRSP, and *C. oxysporum* KeTi1 significantly inhibited the radial growth of *Fusarium* sp. compared with the untreated control ($P < 0.05$), with the highest percentage inhibition of radial growth reaching 56% for KeTi1. These findings indicate that the selected entomopathogenic fungi have potential as biological control candidates against *Fusarium* sp.; however, further greenhouse and field studies are required to validate their efficacy and assess their suitability for development as microbial biopesticides.

Keywords: Antagonistic activity, *Beauveria* sp., entomopathogenic endophytic fungi, *Fusarium* sp., *C. oxysporum, S. subtropicum*

INTRODUCTION

South Sulawesi is characterized by diverse ecosystems and landscapes, ranging from natural and disturbed forests to agricultural areas. These different environments may harbor diverse communities of microorganisms, including fungi with potential applications in biological control. Among them, entomopathogenic endophytic fungi (EEFs) are particularly promising because of their ability to establish associations with plants while retaining their biological activities against insect pests and, in some cases, plant pathogens. However, the diversity and biological potential of EEFs associated with different landscapes in South Sulawesi remain insufficiently explored.

Biological control has emerged as an important and environmentally sustainable alternative to the intensive use of synthetic pesticides, which may cause environmental contamination, pesticide residues, adverse effects on non-target organisms, and the development of resistance in target pests. This approach utilizes beneficial organisms, including microorganisms such as bacteria, nematodes, and fungi, to suppress pest populations and plant disease development (Bamisile et al., 2021). Compared with conventional chemical pesticides, biological control agents may pose lower risks to non-target organisms, including beneficial predators and parasitoids (Quesada-Moraga et al., 2022), and microbial biological control agents often employ multiple mechanisms of action that may reduce selection pressure for the development of resistance in

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target organisms (Zhao et al., 2023). In addition, some microorganisms may contribute to the degradation of pesticide residues, providing further environmental benefits (Swathy et al., 2024). Among these biological control agents, entomopathogenic fungi are particularly important because of their ability to infect and kill insect pests. For example, *Beauveria bassiana* infects susceptible insects through direct contact, in which fungal spores adhere to the insect cuticle, germinate, penetrate the integument, proliferate within the host, and eventually cause insect mortality (Erdiansyah & Fauziah, 2024).

Beyond their role as insect pathogens, some entomopathogenic fungi can colonize internal plant tissues without causing apparent harm to their hosts, functioning as endophytes and representing a multifunctional group with potential applications in sustainable crop protection (Quesada-Moraga, 2020; Hu & Bidochka, 2021). As endophytes, these fungi can promote plant growth, enhance plant tolerance to environmental stresses, and protect plants against insect pests and plant pathogens through direct and indirect mechanisms (Quesada-Moraga, 2020; Mantzoukas & Eliopoulos, 2020; Ahsan et al., 2024; Benito-Delgado et al., 2025). Endophytic fungi may also produce bioactive secondary metabolites with toxic or antifeedant properties that contribute to plant defense. They can inhabit various plant tissues, including roots, stems, leaves, flowers, fruits, and seeds, although they are generally more frequently detected in roots, stems, and leaves than in reproductive tissues (Verma et al., 2021; Wen et al., 2022). Their ability to establish within plant tissues may provide an ecological advantage by protecting the fungi from unfavorable external conditions, including ultraviolet radiation, high temperatures, and drought, while potentially enabling more persistent protection of the host plant (Aravinthraju et al., 2024).

The biological activities of EEFs are not limited to their entomopathogenic properties. Several species may also suppress plant pathogens through mechanisms such as competition for nutrients and space, mycoparasitism, and the production of antimicrobial secondary metabolites. This multifunctionality makes EEFs particularly attractive as candidates for integrated pest and disease management. Their potential to provide simultaneous protection against insect pests and phytopathogens could reduce dependence on synthetic pesticides and support the development of more sustainable agricultural production systems.

The composition and diversity of entomopathogenic fungi can vary considerably among ecosystems. Previous studies have reported the occurrence of genera such as *Metarhizium* and *Beauveria* in different habitats, including forests and grasslands (Masoudi et al., 2020). Geographic location, vegetation type, land-use change, environmental disturbance, and other ecological factors may influence the distribution and diversity of these fungi. Therefore, exploring EEFs across different landscapes is important for identifying locally adapted isolates with potentially superior biological activities.

Despite the growing interest in EEFs, their diversity and potential biological functions remain poorly understood in many regions of Indonesia, including South Sulawesi. Furthermore, relatively limited information is available regarding the antagonistic potential of locally isolated EEFs against important fungal plant pathogens. Species of *Fusarium* are among the most important groups of phytopathogenic fungi, causing various diseases and substantial losses in numerous agricultural and forestry crops. The identification of EEFs isolates capable of suppressing *Fusarium* growth could therefore provide valuable candidates for the development of environmentally friendly biological control agents.

Accordingly, this study aimed to screen and characterize entomopathogenic endophytic fungi isolated from different landscapes in South Sulawesi and evaluate their antagonistic activity against *Fusarium* sp. pathogens. The study is expected to provide information on the diversity and distribution of locally occurring EEFs and identify potential fungal isolates with multifunctional biological control properties. The findings may serve as a basis for the future development of locally adapted biocontrol agents for sustainable management of insect pests and fungal plant diseases.

MATERIALS AND METHODS

Research Site. This study was conducted from May to July 2025. Samples of fungus-infected insects were collected from butterfly breeding facilities around Bantimurung Bulusaraung National Park, a forestry plant nursery in Samangki Village, Maros Regency, South Sulawesi Province, the Silkworm Breeding Centre at the Social Forestry Center in Gowa Regency, Gowa Regency, South Sulawesi Province, and community silkworm-rearing centers in Tottong Village, Soppeng Regency, South Sulawesi Province. In addition, soil and plant samples were collected from the Makassar Urban Forest, the Hasanuddin University Educational Forest, natural forests, plantation forests,

community forests, and agroforestry systems in Maros Regency (Figure 1).

Soil samples were collected from selected forest and agroforestry sites, whereas plant samples were obtained from healthy plants in the surveyed locations. Fungal isolation, morphological identification, and antagonistic assays were conducted at the Forest Protection and Insect Laboratory, Faculty of Forestry, Hasanuddin University.

Fungal Isolation. Entomopathogenic fungi were isolated from dead insects showing visible signs or symptoms of mycosis were selected for fungal isolation, including pupae and adult butterflies from breeding facilities, insects collected from plant nurseries, and dead silkworm larvae obtained from rearing centers. Dead insects were individually placed in sterile sample containers or Petri dishes lined with moist sterile tissue paper and incubated for 3–7 days to promote the emergence of fungal mycelia. Fungal hyphae or mycelia growing on the surface of insect cadavers were aseptically transferred to Potato Dextrose Agar (PDA) and incubated at 25 ± 2 ºC for 7 days. Individual fungal colonies were subsequently subcultured to obtain pure isolates.

Fungi were also isolated from healthy plant tissues, including leaves and roots. Plant samples were surface sterilized by sequential immersion in 70% ethanol for 1 min, 5.25% sodium hypochlorite (NaOCl) for 3 min, and 70% ethanol for 30 s. The samples were subsequently processed according to the laboratory isolation procedure and placed on PDA for fungal growth and isolation.

Soil samples were collected from four positions beneath the canopy of selected trees, representing the east, north, west, and south directions, and were subsequently homogenized. Soil samples were collected from beneath *Diospyros celebica, Swietenia mahagoni, Aleurites moluccanus, Vitex cofassus, Pinus merkusii,* and *Tectona grandis* trees.

Fungi from soil samples were isolated using two methods. The first method involved an insect-bait technique, in which one portion of each homogenized soil sample was exposed to *Dorcus* sp. larvae to recover insect-pathogenic fungi. Larvae showing fungal infection symptoms were subsequently collected, and the fungi emerging from the cadavers were isolated on PDA. The second portion of each soil sample was used for fungal isolation using the serial dilution method. A 10^{-1} dilution was carried out by adding 1 g of soil to 9 ml of distilled water. Soil suspensions were serially diluted up to 10^{-5}, and aliquots from the selected dilutions were

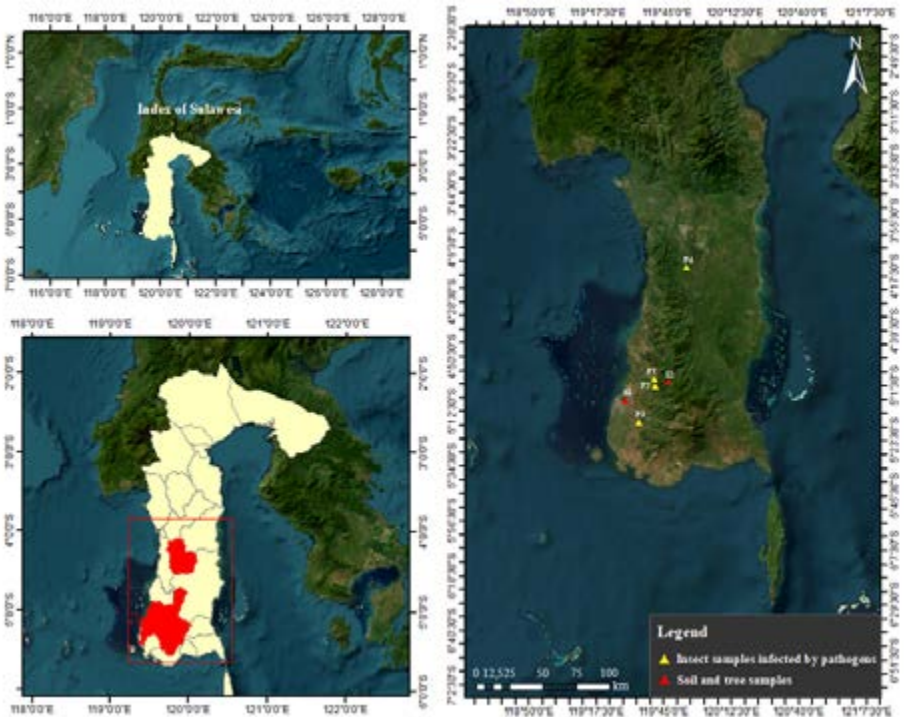


Figure 1. Map showing the sampling locations of fungal isolates in South Sulawesi, Indonesia. Insect samples infected with fungal pathogens were collected from four locations: P1 (119.6785° E, 4.9856° S), P2 (119.6839° E, 5.0330° S), P3 (119.5701° E, 5.2758° S), and P4 (119.8920° E, 4.2385° S). Soil and tree samples were collected from two locations: S1 (119.4838° E, 5.1303° S) and S2 (119.7673° E, 5.0052° S).

spread onto PDA plates for fungal isolation (Jangid & Ojha, 2025). The exact soil-to-water ratio and volume plated should correspond to the procedure used during the experiment.

Fungal Identification. Fungal isolates were identified based on their macroscopic and microscopic characteristics. Macroscopic observations included colony color, colony morphology, mycelial texture, and surface appearance. Microscopic identification included observations of hyphal morphology, spore or conidial characteristics, and the presence of septa. For microscopic examination, a small portion of a pure fungal culture was transferred onto a microscope slide using a sterile inoculating needle. A drop of lactophenol cotton blue was added to the sample, which was then covered with a coverslip. Fungal structures were observed under a light microscope at 400× magnification. The obtained fungi were purified and subsequently identified using identification keys from various literature sources, primarily Lacey (1997) and Kuephadungphan et al. (2022). Isolates exhibiting good growth were selected for use in antagonism assays and further identified via DNA sequencing (sequencing data not shown).

Antagonistic Activity Against *Fusarium* sp. The antagonistic activity of fungal isolates against *Fusarium* sp. was evaluated using a dual-culture assay on PDA. In the control treatment, a plug of *Fusarium* sp. was placed at a distance of 2 cm from the edge of the Petri dish, and its radial growth was recorded as R1. In the dual-culture treatment, *Fusarium* sp. and a fungal isolate were inoculated on the same PDA plate at opposite positions, each at an equal distance of 2 cm from the edge of the Petri dish. The radial growth of *Fusarium* sp. in the presence of the antagonist was recorded as R2 (Figure 2).

Antagonistic activity was assessed based on the reduction in the radial growth of *Fusarium* sp. and the presence of an inhibition zone between the two fungal colonies (Zhang et al., 2025). The percentage inhibition of radial growth (PIRG) was calculated using the following equation (Rosdee et al., 2025):

$$PIRG = \frac{(R1 - R2)}{R1} \times 100\%$$

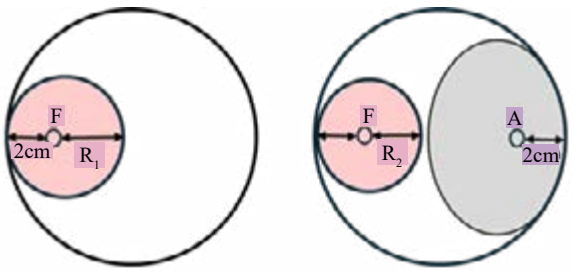
PIRG = Percentage Inhibition of Radial Growth;
R1 = Radial growth of the *Fusarium* sp. colony in the control treatment (mm);
R2 = Radial growth of the *Fusarium* sp. colony in the presence of the antagonistic fungal isolate (mm).

Each fungal isolate was tested in five replicates.

Data Analysis. The isolated fungi were organized according to sample type, collection location, fungal genus, and functional category, including endophytic fungi (END), entomopathogenic fungi (EP), and entomopathogenic endophytic fungi (EEFs).

For the antagonism assay against *Fusarium* sp., the experiment was arranged in a completely randomized design, with fungal isolate as the treatment factor and five replicates for each treatment. The radial growth values of *Fusarium* sp. in the control (R1) and dual-culture treatment (R2) were used to calculate PIRG.

Before statistical analysis, PIRG data were tested for normality using the Shapiro–Wilk test. When the assumptions for parametric analysis were met, the data were subjected to analysis of variance (ANOVA). Significant differences among treatments were determined at $p < 0.05$ and further analyzed using Tukey's honestly significant difference (HSD) test to compare the inhibitory activity among fungal isolates. All statistical analyses were conducted using Microsoft Excel and IBM SPSS Statistics version 26.0.



Control Treatment

Figure 2. Pathogen culture medium (control); dual-culture medium (treatment). Measurement of the radial growth of *Fusarium* sp. (F) mycelia placed at a distance of 2 cm from the edge. R1, radius of the F colony. R2, radius of the F colony in a dual-culture antagonistic to the EEFs isolate A (A on the treatment Petri dish).

RESULTS AND DISCUSSION

Diversity of Fungal Isolates from Different Sources. Isolation of fungi from various sample sources resulted in a diverse composition of endophytic and entomopathogenic fungi (Table 1), originating from insects, soil, leaves, and roots. *Aspergillus* sp. was among the most frequently recovered fungi from insect- and soil-associated samples. Although species of *Aspergillus* are commonly recognized as saprophytic or opportunistic fungi, some isolates have also been reported to possess entomopathogenic activity. For example, *Aspergillus* spp. have previously been evaluated as entomopathogenic fungi, and their sporulation and viability have been shown to be influenced by culture media (Fitriana et al., 2018). *Aspergillus* sp. was the most frequently recovered taxon from insect associated and soil samples. *Aspergillus* sp., *S. subtropicum, C. oxysporum*, and *Metarhizium* sp. were recovered from several insect-associated samples, particularly *Troides helena* and *Bombyx mori*. However, some fungal taxa were less frequently encountered, including *Cordyceps* sp. (isolate PuAl1), which was recovered from a *T. helena* pupa, and *Nosema bombycis*, a microsporidian pathogen associated with silkworm larvae (Figure 3). Unlike the fungal taxa, *N. bombycis* is a microsporidian pathogen and should not be classified as a true fungus. *Gibellula* sp. was also recovered from *T. helena* (isolate TNHe3), silkworm larvae (isolate PBE1), and *Dorcus* sp. (isolate PengBa2). Soil samples yielded additional fungal taxa that were not recorded from the insect samples, including *Trichoderma* sp., *Penicillium* sp., and *Verticillium* sp.

Samples obtained from *B. mori* yielded the highest number of fungal and microsporidian isolates, including *B. bassiana*, *Aspergillus* sp., *Penicillium* sp., *Metarhizium* sp., and *N. bombycis*. Infection by *B. bassiana* in silkworms is associated with white muscardine disease, whereas *Metarhizium* sp. is associated with green muscardine disease. *N. bombycis* is the causal agent of pebrine disease. Silkworm breeding facilities and farmer-managed rearing systems therefore provide opportunities for recovering microorganisms associated with diseased or dead larvae. During rearing, larval mortality may result from multiple microbial agents, allowing different fungal taxa to be recovered from the same production environment. In the present study, *Aspergillus* sp. was the most frequently recovered fungal taxon, represented by nine isolates, whereas *N. bombycis* represented a distinct group of obligate microsporidian pathogens of silkworms. The *B. bassiana* isolates recovered from silkworm-rearing systems represent potential entomopathogenic fungi and may warrant further evaluation for their biological control properties.

Fungi recovered from soil, roots, and leaves represented another component of the fungal diversity. Isolates from soil beneath *D. celebica* and *A. moluccana*, including EboSTB3 and TaKeUt, included *Trichoderma* sp., a genus commonly associated with soil and plant-associated environments. In contrast, isolates obtained from roots and leaves of *A. moluccana*, *S. mahagoni*, and *V. cofassus* could not be identified to a specific taxonomic group because they did not produce diagnostic reproductive structures under the culture conditions used. These isolates were therefore classified as unidentified endophytic fungi based on their recovery from surface-sterilized plant tissues. Endophytic fungi represent an important reservoir of microbial diversity with potential applications in biological control, plant health, and the production of bioactive compounds. Aravinthraju et al. (2024) highlighted the substantial diversity and biotechnological potential of endophytic microorganisms, including their potential for producing antibiotics and other useful metabolites.

The fungal assemblage recovered in this study originated from several ecological compartments, including insect hosts, soil, and plant tissues. Entomopathogenic fungi should be distinguished from endophytic fungi based on their demonstrated biological characteristics rather than solely on the source from which they were isolated. The occurrence of *S. subtropicum, B. bassiana, Metarhizium* sp., *C. oxysporum* and *Gibellula* sp. in insect associated samples is consistent with previous reports identifying

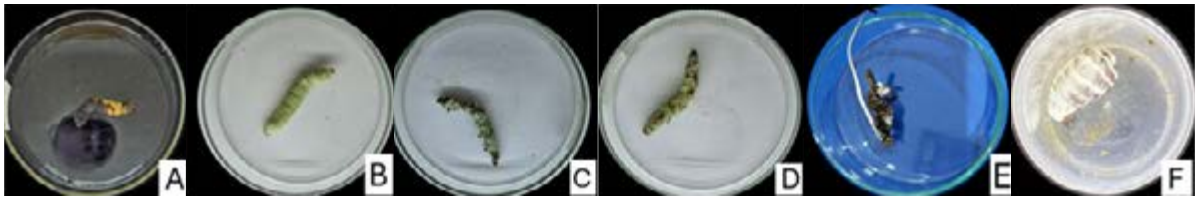


Figure 3. Insect samples serving as sources of fungal isolates. A. Silkworm infected with *N. bombycis*; B. Silkworm infected with *Aspergillus* sp.; C. Silkworms infected with *Beauveria* sp.; D. Silkworms infected with *Metarhizium* sp.; E. *T. helena* pupae infected with *Cordyceps* sp.; F. Pupa infected with *B. bassiana*.

Table 1. Entomopathogenic and entomopathogenic endophytic fungal isolates obtained from different sources and selected isolates tested against *Fusarium* sp.

Isolate	Sample	Vegetation	Fungal taxon	Location							
				PKM	PKTN	HK	HS	PPM	SBC	SRC	Classification
PuAl1	*Troides helena*	-	*Cordyceps* sp.	✓							EP
KuBi1*	*Rhizoecus sp.*	-	*S. subtropicum*					✓			EEF
TNKP2	*T. helena*	-	*Aspergillus* sp.		✓						EP
TNKP3	*T. helena*	-	*Beauveria* sp.		✓						EEF
TNHe1	*T. helena*	-	*Aspergillus* sp.		✓						EP
TNHe2	*T. helena*	-	*Beauveria* sp.		✓						EEF
TNHe3	*T. helena*	-	*Gibellula* sp.		✓						EEF
BN161	*Bombyx mori*	-	*Beauveria* sp.						✓		EEF
BN162	*B. mori*	-	*Aspergillus* sp.						✓		EP
BN163	*B. mori*	-	*Nosema bombycis*						✓		EP
BN164	*B. mori*	-	*Aspergillus* sp.						✓		EP
BN6×16	*B. mori*	-	*Penicillium* sp.						✓		EP
PK01×67	*B. mori*	-	*Aspergillus* sp.						✓		EP
PK01×1671	*B. mori*	-	*Aspergillus* sp.						✓		EP
PK01×1672	*B. mori*	-	*N. bombycis*						✓		EP
PK01×1673	*B. mori*	-	*Aspergillus* sp.						✓		EP
C01BN1671	*B. mori*	-	*Aspergillus* sp.						✓		EP
C01BN1672	*B. mori*	-	*Metarhizium* sp.						✓		EEF
C01BN1673	*B. mori*	-	*Aspergillus* sp.						✓		EP
C01BN1674	*B. mori*	-	*Aspergillus* sp.						✓		EP
PBE1	*B. mori*	-	*Gibellula* sp.						✓		EP
PBE2	*B. mori*	-	*N. bombycis*						✓		EP
PBE3	*B. mori*	-	*N. bombycis*								EP
SRMa	*Dolichoderus* sp.	-	*Aspergillus* sp.						✓		EP
BGRSP*	*B. mori*	-	*B. bassiana*							✓	EP

Table 1. Continued. Entomopathogenic and entomopathogenic endophytic fungal isolates obtained from different sources and selected isolates tested against *Fusarium* sp.

Isolate	Sample	Vegetation	Fungi	Location							
				PKM	PKTN	HK	HS	PPM	SBC	SRC	Classification
KtDu*	*Pseudococcus* sp.	*Durio zibethinus*	*Fusarium* sp.					✓			EP
MetC3	*Troides* sp.	-	*Metarhizium* sp.		✓						EEF
MetC1	*Troides* sp.	-	*Aspergillus* sp.		✓						EP
MetC2	*Troides* sp.	-	*Aspergillus* sp.		✓						EP
MetC4	*Troides* sp.	-	*Aspergillus* sp.		✓						EP
BeanC1	*Troides* sp.	-	*Aspergillus* sp.		✓						EP
BeanC2	*Troides* sp.	-	*Aspergillus* sp.		✓						EP
PengBa1	*Dorcus* sp.	*Diospyros celebica*	*Beauveria* sp.			✓					EEF
PengBa2	*Dorcus* sp.	*D. celebica*	*Gibellula* sp.			✓					EP
EboSTS1	soil	*D. celebica*	*Aspergillus* sp.			✓					EP
EboSTS2	soil	*D. celebica*	*Aspergillus* sp.			✓					EP
EboSTB3	soil	*D. celebica*	*Trichoderma* sp.			✓					EEF
TaKeUt	soil	*Aleurites moluccana*	*Trichoderma* sp.				✓				EEF
TaKeTi*	soil	*A. moluccana*	*C. oxsysporum*				✓				EEF
TaKeSe1	soil	*A. moluccana*	*Penicillium* sp.				✓				EP
TaKeSe2	soil	*A. moluccana*	*Verticillium* sp.				✓				EP
TaKeBa	soil	*A. moluccana*	*Aspergillus* sp.				✓				EP
AKeUt	root	*A. moluccana*	UI				✓				END
AKeBa1	root	*A. moluccana*	UI				✓				END
AKeBa2	root	*A. moluccana*	UI				✓				END
AkKeTi	root	*A. moluccana*	UI				✓				END
AkKeSe	root	*A. moluccana*	UI				✓				END
AMaBa	root	*Swietenia mahagoni*	UI				✓				END

Table 1. Continued. Entomopathogenic and entomopathogenic endophytic fungal isolates obtained from different sources and selected isolates tested against *Fusarium* sp.

Isolates	Samples	Vegetation	Fungi	Location							
				PKM	PKTN	HK	HS	PPM	SBC	SRC	Classification
AMaTi	root	*S. mahagoni*	UI				✓				END
AMaSe	root	*S. mahagoni*	UI				✓				END
AMaUt	root	*S. mahagoni*	UI				✓				END
KePuc	leaf	*A. moluccana*	UI				✓				END
DaKeBa	leaf	*A. moluccana*	UI				✓				END
DaKeTe	leaf	*A. moluccana*	UI				✓				END
DaKeA	leaf	*A. moluccana*	UI				✓				END
DaMaPu	leaf	*S. mahagoni*	UI				✓				END
DaMaBa	leaf	*S. mahagoni*	UI				✓				END
DaMaTe	leaf	*S. mahagoni*	UI				✓				END
Dabi1	leaf	*Vitex cofassus*	UI				✓				END
Dabi2	leaf	*V. cofassus*	UI				✓				END
Dabi3	leaf	*V. cofassus*	UI				✓				END
JaTa1	soil	*Tectona grandis*	UI				✓				END
JaTa2	soil	*T. grandis*	UI				✓				END
PiTa1	soil	*Pinus merkusii*	UI				✓				END
PiTa2	soil	*P. merkusii*	UI				✓				END

PKM = Community Butterfly Breeding; PKTN = Babul National Park Butterfly Breeding; HK = Urban Forest; HS = Secondary Forest; PPM = Tree Nursery (Maros Regency); SBC = Silkworm Breeding Centre (Gowa Regency); SRC = Silkworm Breeding Centers (Soppeng Regency); UI = Unidentified, based only on mycelial characteristics; EP: Entomopathogenic fungi; EEFs: Entomopathogenic endophytic fungi; END = Endophytic. Asterisks indicate isolates tested for antagonistic activity against *Fusarium* sp.

these genera as important insect associated fungi. The KuBi1 isolate, identified as *S. subtropicum* and isolated from the mealybug *Rhizoecus* sp. in Vitex cofassus shows as a potential entomopathogen. Research by Mariappan et al. (2024) indicates that *S. subtropicum* can control *Aphis gossypii*, a pest of cotton plants. In Indonesia, Fitriana et al. (2021) also reported the occurrence of entomopathogenic fungi associated with insect hosts, highlighting the potential of insect associated environments as sources of locally adapted fungal isolates. Panwar & Szczepaniec (2024) emphasized the diversity and biological control potential of entomopathogenic fungi occurring as endophytes. Studies by Reyes-Haro et al. (2024) showed that *B. bassiana* has a broad host range that includes Coleoptera, Lepidoptera, Homoptera, and Hemiptera. The occurrence of *Metarhizium* sp. in *Troides* spp. and *B. mori* is also consistent with the findings of Vivekanandhan et al. (2024), who reported the frequent occurrence of *Metarhizium* associated with soil-dwelling insects.

The diversity of microorganisms recovered from silkworm larvae also reflects the complexity of microbial interactions within rearing environments. The occurrence of *N. bombycis* in several silkworm samples is consistent with Nuraeni et al. (2024), who identified this microsporidian as an important pathogen in sericulture. Infection by *N. bombycis* may weaken the host and increase susceptibility to secondary colonization by opportunistic microorganisms. The co-occurrence of *Aspergillus* sp. with microsporidian infection observed in the present study may therefore reflect secondary colonization or opportunistic growth associated with deteriorating host tissues. However, the present study did not experimentally determine whether these infections were causally related.

The presence of *Trichoderma* sp. in soil samples is of particular interest because this genus is widely recognized for its antagonistic activity against plant pathogens. Sharma & Sharma (2020) reported that *Trichoderma* can suppress pathogens such as *Fusarium* sp. through competition and other antagonistic interactions. However, the classification of the *Trichoderma* isolates in the present study as entomopathogenic endophytic fungi (EEFs) requires evidence demonstrating both endophytic colonization and entomopathogenic activity. Isolation from soil alone is insufficient to establish EEF status. Therefore, EEF classification should be interpreted according to the criteria and biological assays used in the present study. Endophytic fungi may nevertheless have potential as biological control agents because some plant-associated fungi can contribute to plant defense and pathogen suppression.

The three isolates selected for the antagonism assay were *S. subtropicum* KuBi1, *B. bassiana* BGRSP, and *C. oxysporum* KeTi1. The selection was based on their occurrence among the recovered entomopathogenic fungal taxa and their suitability as representative isolates for evaluating antagonistic activity against *Fusarium* sp. KuBi1 was obtained from *Rhizoecus* sp. associated with a forestry nursery, BGRSP was recovered from dead farmer-reared silkworms, and KeTi1 was obtained from secondary-forest soil beneath candlenut trees using *Dorcus* sp. larvae as insect bait. These isolates represent distinct ecological sources as well as two genera of entomopathogenic fungi that are not commonly encountered: *S. subtropicum* and *C. oxysporum*. In contrast, *Fusarium* sp. was isolated from *Pseudococcus* sp. associated with *Durio zibethinus*. Because isolation from an insect host alone does not demonstrate entomopathogenicity, *Fusarium* sp. is referred to here as an isolate recovered from *Pseudococcus* sp. rather than as an entomopathogenic fungus.

Morphological Characteristics of Selected Fungal Isolates. The selected *S. subtropicum, B. bassiana* and *C. oxysporum* isolates showed distinct macroscopic and microscopic characteristics, whereas *Fusarium* sp. displayed the characteristic morphology of the genus (Figure 4). *B. bassiana* and *S. subtropicum* both belong to the family Cordycipitaceae (Hypocreales) and are recognized as entomopathogenic fungi. Morphologically, the two genera appear similar, characterized by white colonies and hyaline hyphae. They can only be distinguished by their conidia: in *Beauveria*, the conidia tend to aggregate tightly into clusters associated with short phialides, whereas *Simplicillium* produces conidia from solitary (non-clustered) phialides. *C. oxysporum* has greenish-gray or olive-gray colonies with a smooth, wrinkled surface. Microscopic observation reveals septate, branched hyphae with long, unbranched conidiophores. The conidia were oval to cylindrical, while the conidiophores were erect and branched. *Fusarium* sp. was characterized by crescent-shaped macroconidia. These morphological characteristics supported identification at the genus level under the conditions used in this study.

Insect associated samples showed that entomopathogenic fungi can be recovered from different insect taxa and developmental stages, as observed in *B. mori* and *T. helena* pupae (Figure 3).

Entomopathogenic fungi have been reported to infect insects at multiple developmental stages, including eggs, larvae, pupae, nymphs, and adults (Leyte-Lugo et al., 2025). The occurrence of fungal infection in *T. helena* pupae is also consistent with evidence that pupae can remain susceptible to fungal infection under suitable conditions (Naeem-Ullah et al., 2025). Thus, both naturally occurring and reared insects may serve as sources of entomopathogenic fungal isolates. However, the ecological role and pathogenicity of individual isolates should be confirmed experimentally rather than inferred solely from their occurrence in insect cadavers.

The diversity of fungal isolates recovered in this study was also reflected in their colony and microscopic characteristics (Figure 5). The recovered taxa included *Aspergillus, Beauveria, Simplicillium, Penicillium, Cordyceps, Fusarium, Cladosporium* and *Metarhizium.* Differences in colony morphology, pigmentation, and hyphal structures provide useful preliminary

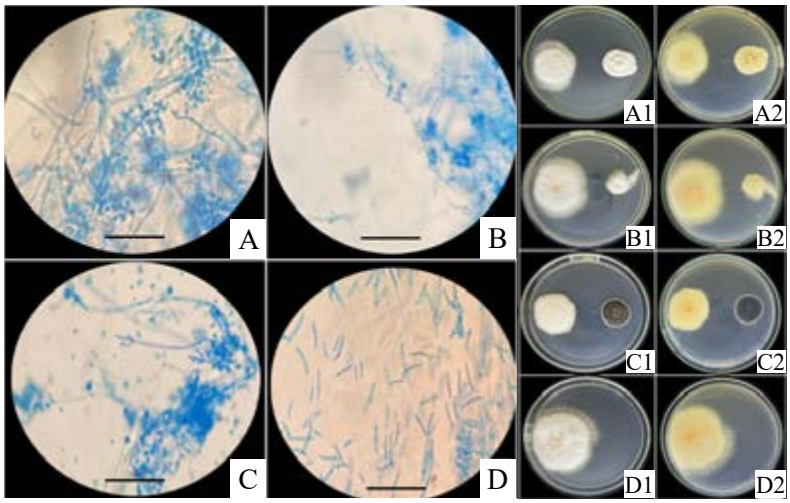


Figure 4. Morphological characteristics of selected fungal isolates and their antagonistic interactions with *Fusarium* sp. A–A2. *S. subtropicum* isolate KuBi1; B–B2. *B. bassiana* isolate BGRSP; C–C2. *C. oxysporum* isolate KeTi1; D–D2. *Fusarium* sp. isolate KtDu1 (control). For each isolate, the corresponding panels show the colony morphology and microscopic characteristics. Antagonistic interactions between the selected isolates and *Fusarium* sp. are shown from the front and reverse views. Microscopic observations were conducted at 400× magnification, with a scale bar of 5 µm. Photographs of fungal cultures were taken after 7 days of incubation.

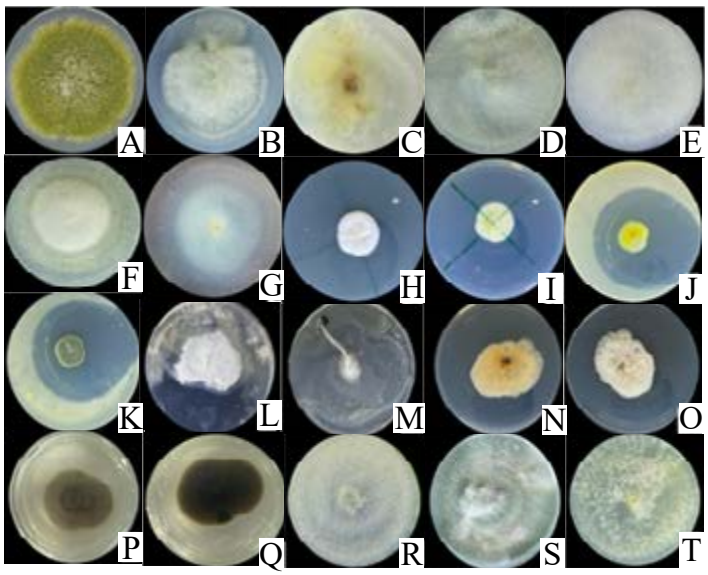


Figure 5. Fungal isolates obtained from insect associated samples. A-D. *Aspergillus* sp.; E-G. *Beauveria* sp.; H-I, *S. subtropicum*; J-K. *Penicillium* sp.; L-M. *Cordyceps* sp., N-O. *Fusarium* sp.; P-Q. *C. oxysporum*; R-T, *Metarhizium* sp. Photographs were taken after 10 days of incubation.

characteristics for genus-level identification. The frequent occurrence of *Beauveria* and *Metarhizium* is consistent with previous observations that these genera are important fungal pathogens of invertebrates in agricultural and natural ecosystems (McGuire & Northfield, 2020). Meanwhile, the occurrence of *Gibellula* sp. and *Cordyceps* sp. indicates additional fungal diversity associated with forest insects and other arthropods. Variation in colony morphology under culture conditions may also reflect differences in fungal physiology and metabolite production. Narsing et al. (2017) reported that changes in fungal colony characteristics can be associated with physiological responses and secondary metabolite production. Consequently, fungal isolates intended for biological control should be evaluated not only on the basis of taxonomic identity but also according to their physiological and ecological characteristics.

Endophytic fungal isolates obtained from leaves and roots of candlenut, mahogany, and other tree species showed differences in their occurrence among plant tissues (Figure 6). The recovery of fungi from apparently healthy, surface-sterilized plant tissues supports their classification as endophytic isolates under the isolation procedure used in this study. However, the presence of endophytic fungi does not necessarily demonstrate a mutualistic or symbiotic relationship, because endophytic associations may be neutral, beneficial, or context dependent. Xiong et al. (2023) emphasized that endophytic fungi associated with woody and foliar tissues may contribute to plant stress tolerance and defense through the production of bioactive compounds. Differences between leaf- and root-associated isolates may also reflect differences in tissue characteristics and environmental exposure, with roots being directly influenced by soil-associated microbial communities (Birt et al., 2022). These findings indicate that plant tissues may represent an important source of fungal isolates for subsequent screening of biological control traits.

Antagonistic Activity Against *Fusarium* sp. The selected *S. subtropicum, B. bassiana* and *C. oxysporum* isolates inhibited the radial growth of *Fusarium* sp. in dual-culture assays (Figure 4). The inhibition patterns differed among isolates, indicating variation in their antagonistic capacity. Such differences may be related to isolate-specific growth characteristics and interactions with the pathogen. Camele et al. (2023) reported that the antagonistic performance of *Beauveria* isolates can be influenced by fungal strain, nutrient availability, and the production of volatile compounds. In the present study, however, the mechanisms responsible for inhibition were not directly examined. Therefore, mechanisms such as mycoparasitism, antibiosis, competition for space and nutrients, or production of

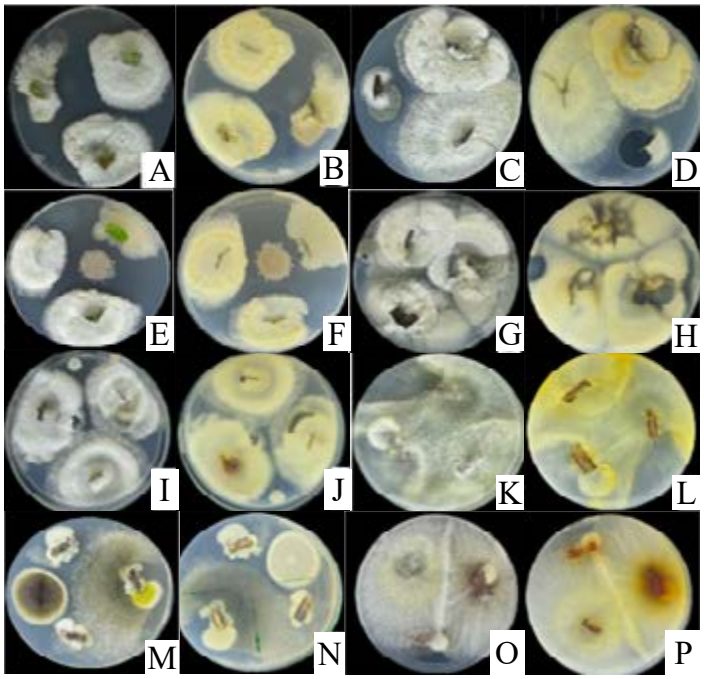


Figure 6. Endophytic fungal isolates obtained from plant tissues. A–F. Isolates obtained from candlenut (*Aleurites moluccana*) leaves; G–J. Isolates obtained from mahogany (*Swietenia mahagoni*) leaves; K–N. Isolates obtained from candlenut roots; O–P. Isolates obtained from mahogany roots. Photographs were taken after 10 days of incubation.

inhibitory metabolites should be regarded as possible explanations rather than confirmed mechanisms. These mechanisms have been proposed in previous studies of fungal antagonism (Bustamante et al., 2022; Prihatiningsih et al., 2022).

Radial growth of *Fusarium* sp. in the untreated control was significantly greater than that observed in dual cultures with the selected antagonistic isolates. The average colony diameter in the control was approximately 35 mm, whereas the colonies in cultures containing KeTi1, KuBi1, and BGRSP were approximately 15–18 mm after seven days (Figure 7). One-way ANOVA indicated a significant effect of treatment on *Fusarium* sp. radial growth ($p < 0.05$). Post-hoc analysis placed the untreated control in a separate statistical group, whereas the three antagonistic isolates were grouped together. Thus, the three isolates significantly reduced *Fusarium* sp. radial growth relative to the control, but no significant difference was detected among KeTi1, KuBi1, and BGRSP.

The observed inhibition may involve several biological interactions commonly associated with antagonistic fungi, including competition for nutrients and space, production of antimicrobial compounds, and direct interaction with pathogen hyphae (Ren et al., 2020; Nehra et al., 2022). Previous studies have also reported that some *Beauveria* and *Metarhizium* strains produce secondary metabolites and volatile compounds that can influence the growth of other fungi, including beauvericin, bassianolide, and other bioactive compounds (Zhang et al., 2020; González-Mas et al., 2021). Nevertheless, the production of these compounds was not measured in the present study. In addition, the nutrient composition and physical conditions of the culture medium can strongly influence fungal growth and antagonistic interactions (Köhl et al., 2019). Therefore, the inhibition observed in vitro demonstrates antagonistic potential but does not by itself establish the specific mechanism responsible for pathogen suppression.

The percentage inhibition of radial growth (PIRG) further demonstrated the antagonistic potential of the three isolates (Figure 8). The mean PIRG values ranged from approximately 47% to 56%. KeTi1 and

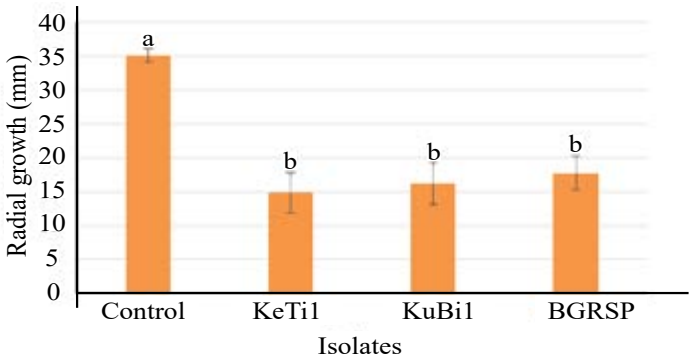


Figure 7. Radial growth of *Fusarium* sp. in control and in dual cultures with antagonistic fungal isolates after 7 days of incubation. Different letters indicate significant differences among treatments according to analysis of variance (ANOVA) followed by the HSD test at $P < 0.05$.

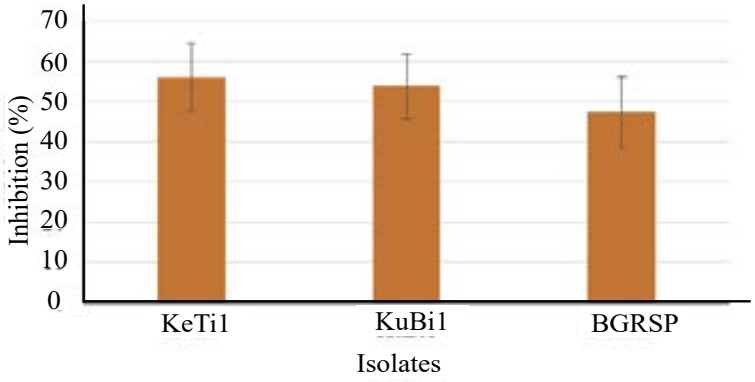


Figure 8. Percentage inhibition of radial growth (PIRG) of *Fusarium* sp. by antagonistic fungal isolates after seven days of incubation. Different letters indicate significant differences among treatments according to analysis of variance (ANOVA) followed by the HSD test at $P < 0.05$.

KuBi1 showed numerically higher inhibition than BGRSP, although the differences among the isolates were relatively small. These results indicate that all three isolates were able to suppress the radial growth of *Fusarium* sp. under the in vitro conditions tested. The quantitative PIRG values provide a more direct measure of antagonistic performance than qualitative descriptions such as "moderate" or "strong" inhibition.

The inhibition levels observed in the present study may be associated with the combined effects of competition and the production of fungal metabolites or hydrolytic enzymes, as suggested by previous studies (Karim et al., 2022). *Beauveria* sp. species have been reported to produce biologically active compounds, including beauvericin, bassianolide, and destruxins, that can affect other microorganisms and fungal growth (Paschapur et al., 2021; Shahbaz et al., 2024). *Simplicillium* and *Cladosporium* have been extensively studied as endophytic fungi; for instance, entomopathogenic *Simplicillium* can control soybean rust (*Phakopsora pachyrhizi*) (Nada et al., 2025), while *C. oxysporum* in addition to being an endophyte can function as a plant growth promoting endophyte (PGPE) that stimulates plant growth (Yang et al., 2023). However, the presence and contribution of these compounds in the present isolates remain to be experimentally verified. Differences in antagonistic performance among fungal strains may also be associated with their genetic and ecological backgrounds, as antagonistic activity is frequently strain dependent and influenced by ecological origin (Chiellini et al., 2019).

Overall, the in vitro assays demonstrate that *S. subtropicum* KuBi1, *B. bassiana* BGRSP, and *C. oxysporum* KeTi1 have potential to suppress the growth of *Fusarium* sp. under dual-culture conditions. The lack of a significant difference among the three isolates suggests that their antagonistic performance was comparable under the conditions tested, although KeTi1 and KuBi1 showed numerically higher PIRG values. These isolates may therefore be considered candidates for further development as biological control agents for forestry and nursery systems. However, their effectiveness as endophytic inoculants or direct biological control agents should be evaluated under greenhouse and field conditions, together with studies of colonization ability, host compatibility, environmental stability, and the mechanisms underlying pathogen suppression.

CONCLUSION

This study demonstrated that diverse fungal isolates were obtained from insect associated samples, soil, and plant tissues, including insects at larval, pupal, and adult stages, as well as leaf and root tissues. A total of 72 fungal isolates were recovered and classified into entomopathogenic (EP), entomopathogenic endophytic (EEF), and endophytic (END) groups based on their respective sources and observed characteristics. Isolate KuBi1 (*S. subtropicum*), BGRSP (*B. bassiana*), and KeTi1 (*C. oxysporum*), showed potential as candidate entomopathogenic fungi for further development as microbial pest-control agents. In vitro antagonistic assays demonstrated that all three selected isolates suppressed the radial growth of *Fusarium* sp., with the highest percentage inhibition of radial growth (PIRG) reaching 56% by isolate KeTi1. These findings indicate that the selected isolates have potential as biological control agents; however, further greenhouse and field studies are required to validate their efficacy, establish their stability and colonization capacity, and assess their suitability for development as environmentally friendly biopesticides.

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AUTHORS' CONTRIBUTIONS

SN and SHL conceptualized and designed the study. SN, SHL, and MBM conducted the fungal isolation procedures. SN collected the data. SN and MBM analyzed and interpreted the data. SN and AP prepared the initial draft of the manuscript. All authors

contributed to the review of the research workflow, data analysis, interpretation of the results, and overall manuscript structure. All authors read and approved the final version of the manuscript.

COMPETING INTEREST

The authors declare no conflicts of interest related to this article.

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