HAYATI
Journal of Biosciences

Vol. 33 No. 4, July 2026 851-863
DOI:10.4308/hjb.33.4.851-863
ISSN: 1978-3019
EISSN: 2086-4094

Research Article

Unravelling Arbuscular Mycorrhizal Community in Kaolin Post-Mining and Tropical Heath Forest Ecosystems in Belitung Regency, Indonesia

Muhammad Hilman Aulia[1], Nampiah Sukarno[1,2*], Rika Indri Astuti[1,2], Adi Yulandi[3], Kartini Kramadibrata[4], Sri Listiyowati[2]

[1]*Study Program of Microbiology, Graduate School, IPB University, Bogor 16680, Indonesia*
[2]*Department of Biology, Faculty of Mathematics and Natural Sciences, IPB University, Bogor 16680, Indonesia*
[3]*School of Bioscience, Technology, and Innovation. Atma Jaya Catholic University of Indonesia, Jakarta 12930, Indonesia*
[4]*Indonesian Mycological Society, Bogor Branch, Bogor, Indonesia*

ARTICLE INFO

Article history:
Received June 17, 2025
Received in revised form January 6, 2026
Accepted January 9, 2026
Available Online March 5, 2026

KEYWORDS:
AMF spore,
heath forest,
high-throughput sequencing,
morphology,
post-mining land,
SSU

ABSTRACT

Arbuscular Mycorrhizal (AM) symbiosis plays a vital role in supporting plant growth in restored degraded land and natural forests. This study examined AM communities present within the root and the rhizosphere of kaolin post-mining land areas and tropical heath forests using both spore morphology and metagenomic approaches. Soil and plant root samples were collected from three distinct zones: the kaolin post-mining land, ecotone, and heath forest, and used to establish trap cultures with *Pueraria javanica*. Spore-based identification revealed nine AMF species belonging to five genera, with *Acaulospora* and *Glomus* being the most dominant. Metagenomic analysis of 18S rRNA sequences from colonized *P. javanica* roots revealed 33 AMF-associated Amplicon Sequence Variants (ASVs), dominated by *Glomus* and *Rhizophagus*. Diversity indices indicated medium diversity levels across all sites, with the ecotone showing the highest evenness and species richness. Differences in AM communities between morphological and molecular approaches highlight the importance of integrating both methods to understand their diversity comprehensively. This baseline information contributes to the potential use of AMF as bio-restoration agents in the kaolin post-mining ecosystems. To our knowledge, this is the first report of AM communities in the kaolin post-mining land and tropical heath forest.

1. Introduction

Arbuscular Mycorrhiza (AM) is a mutualistic symbiosis between fungi of the phylum Glomeromycota and plant roots, characterized by the formation of internal and external hyphae that contribute to enhanced plant growth and improved soil characteristics (Smith and Read 2008; Chen *et al.* 2018). Arbuscular Mycorrhizal Fungi (AMF) comprises 240 species based on their morphological characteristics (Krüger *et al.* 2012; Redecker *et al.* 2013). AMF is associated with more than 90% of flowering plant species, bryophytes, and ferns (Ahanger *et al.* 2014). Plants benefit from this interaction through improved mineral nutrient and water uptake and enhanced stress tolerance (Salam *et al.* 2017). Additionally, AMF protects plant roots from root pathogen attacks (Yang *et al.* 2014) and promotes plant growth by assisting in phosphate absorption from the soil (Das *et al.* 2022).

Studies on AMF diversity in Indonesia are relatively limited. AMF diversity influences the diversity of plants or vegetation in a given area (Guzman *et al.* 2021). AMF contribute to enhancing plant diversity because they are among the most abundant organisms in the rhizosphere, with associations involving more than 200,000 plant host species (Lee *et al.* 2013; van der Heijden *et al.* 2015). However, AMF diversity can decline due to

*Corresponding Author
E-mail Address: nampiah@apps.ipb.ac.id

mining activities, which cause physical disturbances to the soil, including loosening and compaction, affecting soil structure and permeability. These soil changes can also lead to reduced plant diversity, as AMF are obligate symbionts of plants (Berruti *et al.* 2016).

One of the mining activities in Indonesia is kaolin mining in Belitung Regency. Kaolin is a mining product in Belitung commonly used to make cement and ceramics (Subari *et al.* 2021). This activity harms the ecological conditions of the environment, especially on sandy soil structure, acidic pH (4-5), and low organic matter content (Wang 2017; Sukarman *et al.* 2020). In addition, studies related to kaolin mining also impact the diversity, composition, and function of bacterial and fungal communities in the rhizosphere, and the magnitude of this impact also depends on the plant species (Xiao *et al.* 2024; Armanisa *et al.* 2025). Post-mining land management can be done through land restoration mechanisms to restore soil conditions to be productive again. However, there are barriers in the ecological restoration process, namely the topsoil, vegetation, and soil biodiversity that are lost, resulting in environmental conditions that are different from before. There is a need for assistance from soil microorganisms, including AMF, which forms a community structure in the plant rhizosphere. The relationship between plants, soil, and mycorrhizal fungi is important for restoring ecological functions and processes in disturbed soil ecosystems such as post-mining land ecosystems (Krüger *et al.* 2017).

To restore post-mining land, it is necessary to analyze the status and diversity of AMF in the post-mining area as well as in the surrounding natural forest, which serves as a control for comparison since AMF diversity influences the composition of the overlying vegetation community (Tedersoo *et al.* 2020). The natural forest surrounding the kaolin post-mining area is a heath forest. Heath forest is a tropical ecosystem that grows on podzolic soil with sandy texture, low nutrient content, and low pH (Luizão *et al.* 2007). The presence of AMF colonization structures in plant roots, such as entry points, internal hyphae, coils, arbuscules, and vesicles, can determine the host status of arbuscular mycorrhizae. AMF diversity in an area can be categorized into two types: the morphological diversity of spores in the soil rhizosphere and the molecular diversity of the functional symbiotic structures present in the roots colonized by AMF (Bowles *et al.* 2016; Zhang *et al.* 2021).

The advantage of identifying AMF diversity based on spore morphology lies in its ability to distinguish species using shape, color, wall ornamentation, and size. However, some limitations exist, such as low spore abundance, since particular AMF species can reproduce vegetatively without producing spores. Therefore, complementary data from molecular identification of AMF based on their functional symbiotic structures in plant roots are necessary (Nuryana *et al.* 2020). Currently, there is no available information on the status and morphological and molecular diversity of AMF in the kaolin post-mining lands and heath forests as controls in Belitung Regency for an initial study on the application of AMF as land restoration agents.

2. Materials and Methods

2.1. Soil and Seed Sampling, Environmental Data, and Preparation of Trap Culture Pots

Soil and seed sampling was carried out in September 2023, starting with a plant inventory in three ecosystems, namely around the kaolin post-mining area (Pt, 2°44'17.2"S 107°40'49.9"E), ecotone (Ek, 2°43'52.3"S 107°41'08.0"E), and heath forest (Hk, 2°43'20.1"S 107°41'17.1"E), Tanjungpandan, Belitung Regency, Indonesia (Figure 1). Plant inventory was carried out using the exploration method (plotless sampling) (Kusmana 2017). Soil samples were taken from four sides of the rhizosphere area of each plant in the three ecosystems as much as ±250 g with a depth of 30 cm below the ground surface and composited into 1 kg and then made into a trap culture pot following the reference of Brundrett *et al.* (1996). A composite soil sample of 500 g from each plant rhizosphere was mixed with 500 g of sterile zeolite. The mixture was put into a pot and then planted with *Pueraria javanica* plants. The plants were watered with distilled water and cared for until they were at least 3 months old so that their spores and roots could be harvested.

Environmental data regarding the physical properties and nutrient content of the soil were tested by analyzing soil texture (pipette method), pH (H_2O), C-organic (Walkley & Black (Titration)), total N (Kjeldahl), available phosphate (Bray 1 (Spectrophotometer)), total phosphate (HCl 25% (Spectrophotometer)), macronutrients (Ca, Mg, and K) (NH_4OAc pH 7.0 (AAS)) using analysis services at the Laboratory of the Department of Soil Science and Land Resources, Faculty of Agriculture, IPB University. Temperature and humidity were measured using the Extech Environmental Meter 4 in 1.

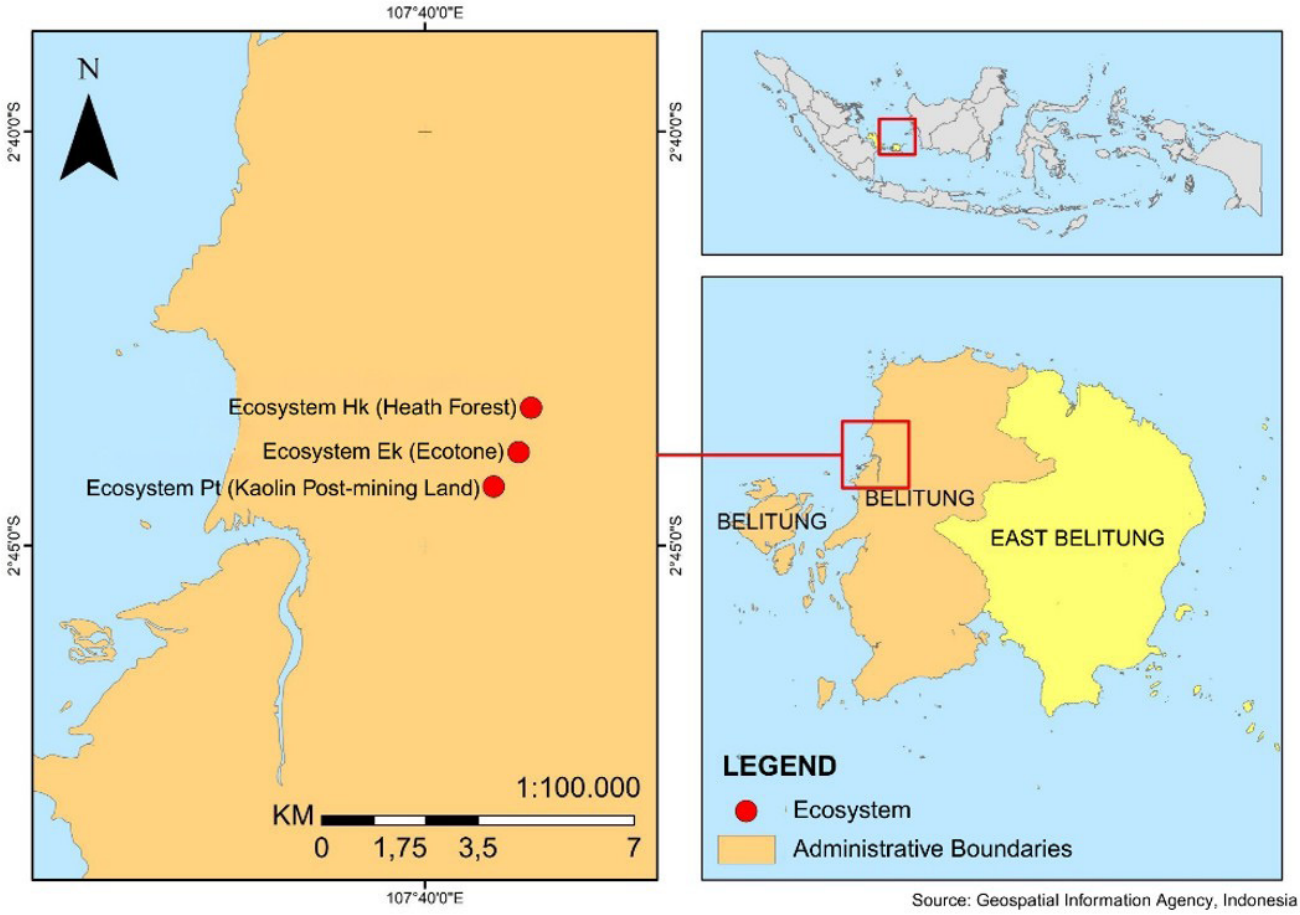

Figure 1. Map of the sampling site in Tanjungpandan, Belitung Regency, Indonesia (Source: Geospatial Information Agency, Indonesia)

2.2. Metagenomic Analysis using Next Generation Sequencing (NGS) from Root Samples

The roots of *P. javanica* plants from 16 trap culture pots from three ecosystems were composited into three samples so that there was only one sample in each ecosystem. Using a mortar and pestle, 250 mg of roots were crushed with liquid nitrogen. Root DNA extraction using the Geneaid Genomic DNA Mini Kit (Plant) followed the manufacturer's instructions. DNA quality and quantity were analyzed using nanodrop (MaestroGen Inc., Taiwan). DNA samples were sent to PT Genetika Science and forwarded to 1st BASE (Malaysia) for sequencing. DNA samples were amplified with the universal fungal 18s V4 rRNA primers 528F (5'-GCG GTA ATT CCA GCT CCA A-3') and 706R (5'-AAT CCR AGA ATT TCA CCT CT-3'). Library preparation was carried out using the final PCR products. The final libraries were sequenced on the Illumina platform to produce sequence pairs with a length of ~350 bp. Cutadapt and DADA2 were used to correct sequencing errors and remove low-quality sequences and chimera errors. The obtained ASV (Amplicon Sequence Variants) data were used for taxonomic classification based on the PR2 version 4.7.2 (18S) and MaarjAM databases (Öpik *et al.* 2010). Diversity analysis (Shannon, Simpson, and Inverse Simpson), downstream, and visualization were performed using RStudio (R vision 4.2.3) (https://www.R-project.org/), krona tools (https://github.com/marbl/Krona), PICRUSt2 (https://github.com/picrust/picrust2), and phyloseq (https://joey711.github.io/phyloseq/).

2.3. Spore Isolation

Spore isolation was performed using a wet sieving and decanting technique (Brundrett *et al.* 1996). A 50 g sample from the cultivation pots was mixed with 300 ml of distilled water. The mixture was filtered through stacked sieves (125, 106, and 50 µm). Spores remaining on the sieves were transferred to a tube and centrifuged at 3,000 rpm, 27°C, for 5 minutes. The supernatant was discarded, leaving a pellet, to which 25 mL of a 50% sugar solution was added and mixed thoroughly. Subsequently, it was centrifuged for 2 minutes at the

same speed and temperature. The supernatant containing the spores was filtered and transferred to a petri dish.

2.4. Spore Morphological Identification

Spore morphology was identified by observing the preparation under a microscope (Brundrett *et al.* 1996). Spores were placed on a glass slide that had been given PVLG solution and Melzer dye, then covered using a cover glass to be observed under an Olympus CX33 Compound Microscope with an additional Sony Exmor CMOS Sensor Camera at a magnification of 1000×. The characteristics observed for spore morphological identification followed the guidelines on the INVAM website (https://invam.ku.edu/) and the Glomeromycota Species List (http:/www.amf-phylogeny.com/), including size, shape, colour, wall layers, ornaments, and hyphae found on the spore wall. A total of 30 spores were observed for the morphological characteristics of each species.

2.5. Spore Diversity Analysis

The diversity of AMF spores, species dominance, evenness, and total frequency of occurrence (FOC) were analyzed and calculated based on Magurran (1988). Diversity was determined using the Shannon diversity index (H'). Species dominance and evenness were assessed using the dominance index (D) and Simpson's evenness index (E_1/D), respectively.

$$\text{FOC species } i = \frac{\text{number of occurrences of species } i}{\text{total number of occurrences}} \times 100\%$$

$$\text{Total FOC}_{\text{species } i} = \frac{\text{total number of occurrences of species } i}{\text{total number of fungal isolates}} \times 100\%$$

$$H' = -\Sigma\,(pi \times \ln pi) \qquad D = \Sigma\,(pi)^2 \qquad E_{1/D} = \frac{1/D}{S}$$

$$pi = ni / N \qquad D = 1 - D \text{ or } 1 / D$$

Where:
ni : number of individuals of species *i*
N : total number of individuals
pi : proportion of species *i*
S : total number of taxa recorded (species richness)

3. Results

3.1. Plant Inventory and Environmental Data

The plant inventory conducted around the Kaolin Lake area, Tanjungpandan, Belitung Regency, identified 16 plant species distributed across three sampling ecosystems, as detailed in Table 1. The Post-mining land ecosystem (Pt), located near Kaolin Lake (post-mining land), had the lowest number of plant species, with only four species recorded. Five plant species were found in the ecotone ecosystem (Ek), while the highest number of species was observed in the heath forest ecosystem (Hk), with seven plant species identified. The rhizosphere of each host plant from these three sampling ecosystems was collected and used to establish a trap culture.

The results of physical properties and soil nutrient content testing from the three ecosystems, the kaolin post-mining land (Pt), ecotone (Ek), and heath forest (Hk), are presented in Table 2. Each ecosystem exhibited distinct physical and chemical soil characteristics. Soil pH showed slight variation across the sites, with the highest value at Pt (4.77), followed by Ek (4.49), and the lowest at Hk (4.41). Organic carbon (C-organic) content was highest in Ek (6.72%), followed by Hk (3.59%), and lowest in Pt (0.69%). A similar trend was observed for total nitrogen (N), although the differences were not statistically significant, *i.e.* Ek (0.20%), Hk (0.13%), and Pt (0.04%). Total phosphorus (P) content was highest in Ek (154.1 ppm) and lowest

Table 1. Diversity of plant species at three sampling ecosystems

Kaolin post-mining (Pt) (2°44'17.2"S 107°40'49.9"E)	Ecotone (Ek) (2°43'52.3"S 107°41'08.0"E)	Heath forest (Hk) (2°43'20.1"S 107°41'17.1"E)
Dillenia suffruticosa (Pt1)	*Dillenia suffruticosa* (Ek1)	*Syzygium bankense* (Hk1)
Dicranopteris linearis (Pt2)	*Daemonorops rubra* (Ek2)	*Arthrophyllum diversifolium* (Hk2)
Acacia mangium (Pt3)	*Ploiarium alternifolium* (Ek3)	*Eurya nitida* (Hk3)
Melastoma malabathricum (Pt4)	*Malaleuca leucadendron* (Ek4)	*Syzygium lepidocarpa* (Hk4)
	Elaeocarpus valentonii (Ek5)	*Calophyllum lanigerum* (Hk5)
		Melastoma malabathricum (Hk6)
		Tristaniopsis merguensis (Hk7)

Table 2. Soil properties content from three sampling ecosystems

Ecosystem	pH	C org (%)	N total (%)	P total (ppm)	P available (ppm)	Ca	Mg	K	Texture (%)		
						(Cmol(+)/kg)			Sand	Ash	Clay
	H_2O	Walkey & Black	Kjeldahl	(HNO_3:$HClO_4$)	Bray I	*N* NH_4OAc pH 7.0			Pippete method		
Pt	4.77	0.69	0.04	76.7	2.38	0.18	0.09	0.06	76.68	13.91	9.41
Ek	4.49	6.72	0.20	154.1	1.09	0.17	0.19	0.17	48.34	20.77	30.88
Hk	4.41	3.59	0.13	135.1	1.39	0.07	0.12	0.12	70.68	9.18	20.14

in Pt (76.7 ppm), whereas the trend was reversed for available phosphorus. Macronutrients (Ca, Mg, and K) also varied across ecosystems. Calcium (Ca) was highest in Pt (0.18 Cmol(+)/kg), while magnesium (Mg) and potassium (K) were highest in Ek (0.19 and 0.17 Cmol(+)/kg, respectively). Soil texture also differed among the sites, *i.e.* Pt and Hk were predominantly sandy, while Ek had a sandy-clay texture. The results of temperature and humidity measurements carried out in the three ecosystems are presented in Table 3.

Table 3. Environmental parameters

Ecosystem	Temperature (°C)	Humidity (%)
Pt	35.77–36.84	46.34–50.91
Ek	31.94–32.31	60.62–63.86
Hk	33.22–34.68	50.44–56.57

3.2. Metagenomic Analysis (NGS) from Root Samples

Identification of the 18S rRNA V4 region using NGS from three root samples resulted in 132 ASVs representing six fungal phyla namely Ascomycota, Basidiomycota, Glomeromycota, Mucoromycota, Rozellomycota, and Zoopagomycota namely along with one unclassified phylum. ASVs not belonging to the phylum Glomeromycota were removed (99 ASVs, 75%), leaving 33 ASVs (25%) classified within Glomeromycota, which represent the AMF community across the three ecosystems Pt, Ek, and Hk, with their distribution and abundance shown in Table 4. The relative abundance of Glomeromycota ASVs was highest in Pt (16%), followed by Ek (7%) and Hk (4%) (Figure 2A). The ASVs within Glomeromycota were classified into three classes: Archaeosporomycetes, Glomeromycetes, Paraglomeromycetes, and one unclassified class. There were differences in class composition among the samples. The dominant class across all three sites was consistently Glomeromycetes. In contrast, Archaeosporomycetes, Paraglomeromycetes, and unclassified classes were found in relatively small proportions at Ek (2%) and Hk (3% and 2%, respectively) (Figure 2B).

At the family level, the identified AMF were classified into four families—Acaulosporaceae, Ambisporaceae, Glomeraceae, and Paraglomeraceae—and one unclassified family. The most dominant family across all three ecosystems was Glomeraceae, comprising 100% in Pt, 86% in Ek, and 95% in Hk. Acaulosporaceae (12%) and the unclassified family (2%) were found exclusively in Ek. Ambisporaceae (3%) and Paraglomeraceae (2%) were found only at Hk (Figure 3A). At the genus level, the AMF composition varied across the three ecosystems. Two genera were identified in Pt, three genera plus one unclassified genus in Ek, and four genera in Hk. *Glomus* and *Rhizophagus* were found in all ecosystems. In Pt, *Glomus* was more dominant (56%) than *Rhizophagus* (44%). Ek was dominated by *Rhizophagus* (62%), followed by *Glomus* (13%), an unclassified genus (13%), and *Acaulospora* (12%). In Hk, the highest abundance was also *Rhizophagus* (70%), followed by Glomus (25%), with minor proportions of *Ambispora* (3%) and *Paraglomus* (2%) (Figure 3B). A phylogenetic tree constructed from the 33 ASVs is presented in Figure 4.

AMF Diversity analysis in root samples was conducted based on differences in ASV abundance that had been translated into genus-level taxa for each sample and measured using three indices: Shannon, Simpson, and Inverse Simpson. The results showed that Ek had the highest Shannon index at 1.09, followed by Hk at 0.77 and Pt at 0.69. For the Simpson index, the highest value was found in Hk at 0.80, followed by Pt at 0.76, and the lowest in Ek at 0.70. The highest Inverse Simpson index was found in Hk at 5.08, followed by Pt at 4.24, and the lowest in Ek at 3.37 (Figure 5).

3.3. Spore Morphological Identification

Nine AMF species were obtained from 16 pot trap cultures. Taxonomically, these species belong to the class Glomeromycetes, comprising three orders (Diversisporales, Gigasporales, and Glomerales), five families (Acaulosporaceae, Entrophosporaceae,

Table 4. Glomeromycota ASV

ASV	Ecosystem			Total	BLAST MaarjAM
	Kaolin post-mining (Pt)	Ecotone (Ek)	Heath forest (Hk)		
ASV114	0	26	0	26	Uncultured *Acaulospora*
ASV98	0	45	0	45	Uncultured *Acaulospora*
ASV136	0	0	17	17	Uncultured *Ambispora*
ASV40	145	7	12	164	Uncultured *Glomus*
ASV45	143	0	0	143	Uncultured *Glomus*
ASV69	84	0	0	84	Uncultured *Glomus*
ASV85	0	0	64	64	Uncultured Glomeromycotina
ASV91	0	54	0	54	Uncultured *Glomus*
ASV93	52	0	0	0	Uncultured *Glomus*
ASV99	41	0	0	41	Uncultured *Glomus*
ASV111	0	0	28	28	Uncultured *Glomus*
ASV113	0	0	27	27	Uncultured *Glomus*
ASV121	22	0	0	22	Uncultured *Glomus*
ASV125	20	0	0	20	Uncultured *Glomus*
ASV138	0	16	0	16	Uncultured *Glomus*
ASV139	15	0	0	15	Uncultured *Glomus*
ASV142	13	0	0	13	Uncultured *Glomus*
ASV167	0	0	7	7	Uncultured *Glomus*
ASV144	0	13	0	13	Uncultured mycorrhizal fungus
ASV158	0	0	9	9	Uncultured *Paraglomus*
ASV87	59	0	0	59	Uncultured *Rhizophagus*
ASV141	0	0	15	15	Uncultured *Rhizophagus*
ASV17	0	255	149	404	Uncultured *Rhizophagus*
ASV34	195	0	0	195	Uncultured *Rhizophagus*
ASV38	0	0	176	176	Uncultured *Rhizophagus*
ASV51	118	0	0	118	Uncultured *Rhizophagus*
ASV58	0	102	0	102	Uncultured *Rhizophagus*
ASV78	72	0	0	72	Uncultured *Rhizophagus*
ASV86	0	62	0	62	Uncultured Glomeromycotina
ASV122	0	0	22	22	Uncultured *Rhizophagus*
ASV133	0	0	18	18	Uncultured *Rhizophagus*
ASV155	0	0	10	10	Uncultured *Rhizophagus*
ASV104	33	0	0	33	Uncultured *Glomus*
Total	1012	580	554	2146	
Count ASV	14	9	13	33	

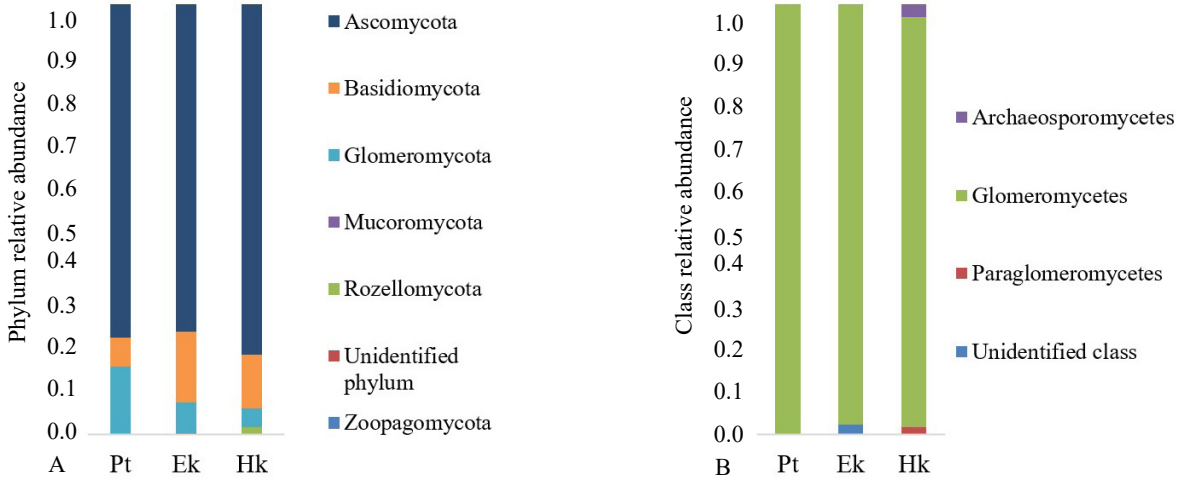

Figure 2. Distribution of abundance of phylum (A) and class (B) in *P. javanica* roots

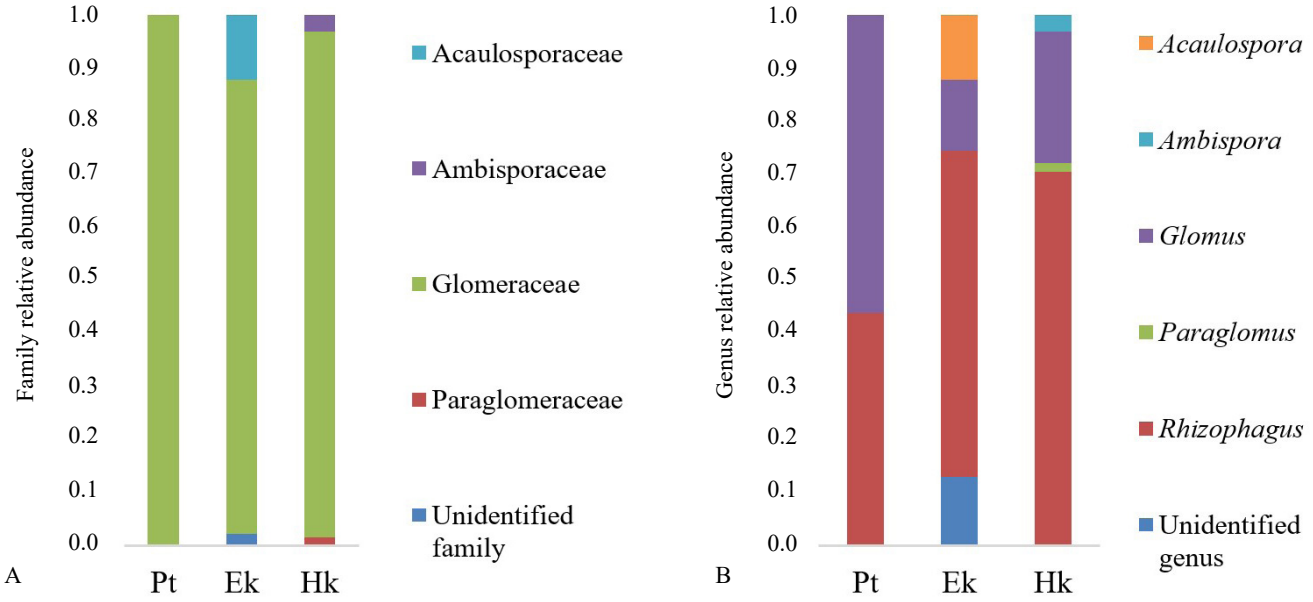

Figure 3. Distribution of abundance of family (A) and genus (B) in *P. javanica* roots

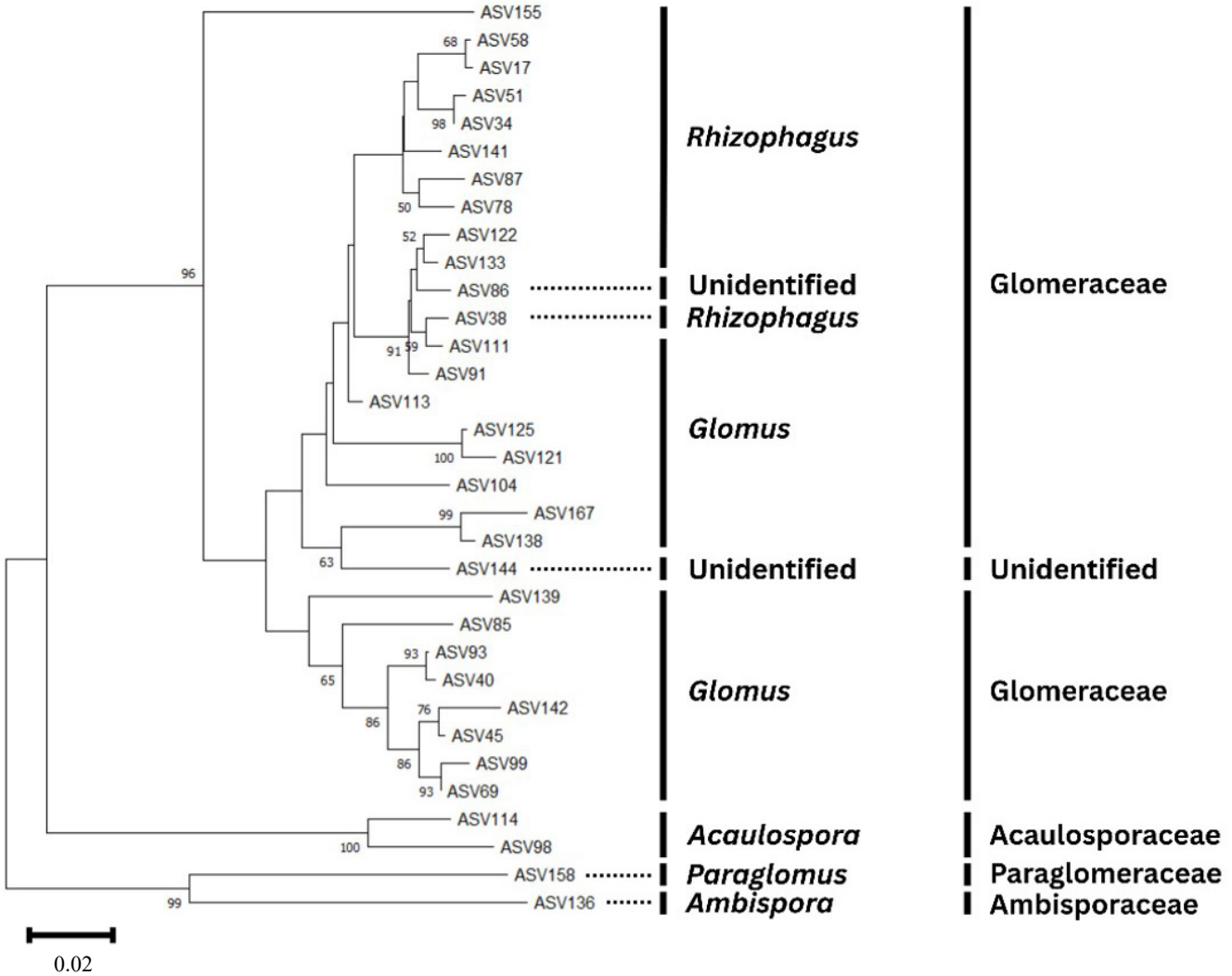

Figure 4. Phylogenetic tree of 33 ASVs in three samples using NGS

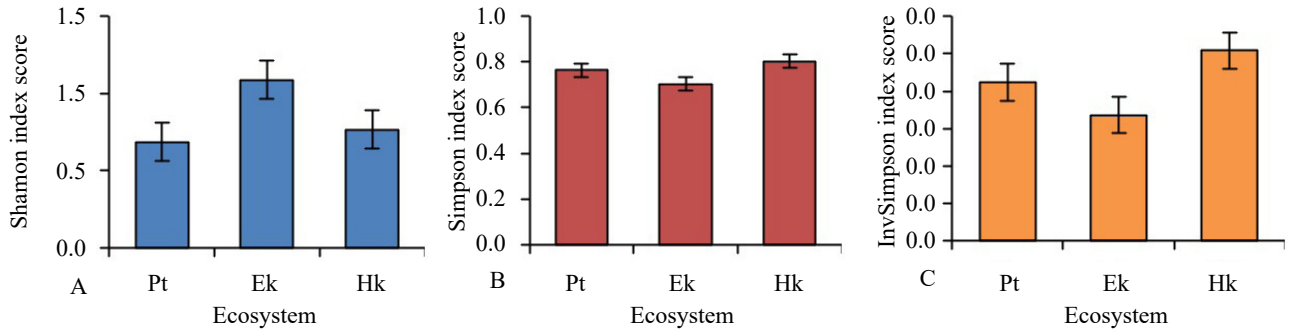

Figure 5. Diversity analysis of metagenomic samples in three sampling ecosystems. (A) Shannon index score, (B) simpson index score, and (C) InvSimpson index score

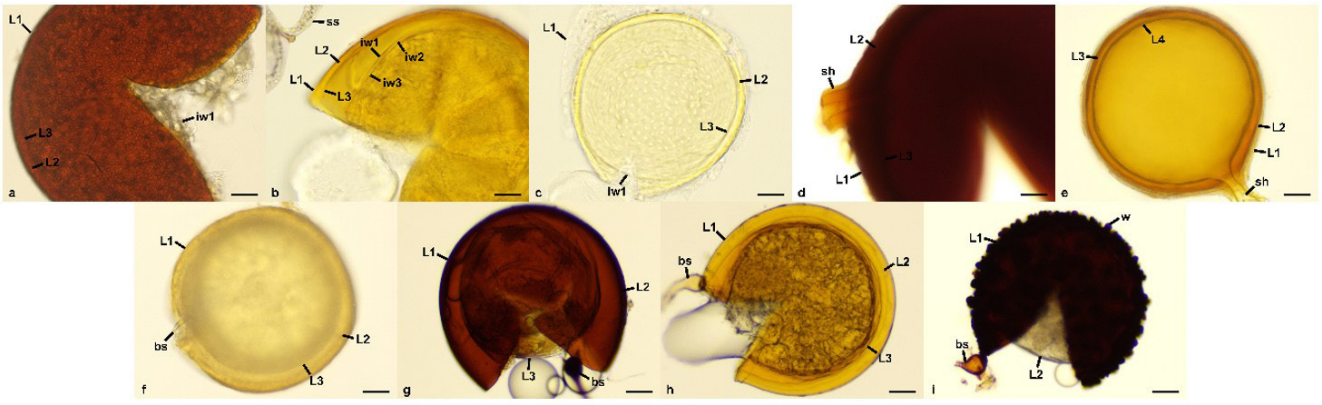

Figure 6. Spore morphology, (A) *Acaulospora foveata*, (B) *A. mellea*, (C) *A. scrobiculata*, (D) *Glomus ambisporum*, (E) *Claroideoglomus claroideum*, (F) *Gigaspora albida*, (G) *G. decipiens*, (H) *G. margarita*, (I) *Racocetra gregaria*, L1, L2, L3 = Layer 1-3; iw1, iw3 = inner wall 1-3; ss = sporiferous saccule; sh = subtending hyphae; bs = bulbous suspensor; scale 50 µm

Gigasporaceae, Glomeraceae, and Racocetraceae), and five genera (*Acaulospora, Glomus, Claroideoglomus, Gigaspora*, and *Racocetra*). The identified species were *Acaulospora foveata, Acaulospora mellea, Acaulospora scrobiculata, Claroideoglomus claroideum, Glomus ambisporum, Gigaspora albida, Gigaspora decipiens, Gigaspora margarita,* and *Racocetra gregaria*, which were distributed across the three ecosystems. The morphological characteristics of each AMF species are presented in Figure 6.

3.4. Spore Diversity Analysis

The diversity and total frequency of occurrence (FOC) analysis of each AMF species across the three ecosystems is presented in Table 5. The genera isolated from all sites were *Acaulospora* (n = 1709, 60.07%) followed by *Glomus* (n = 552, 19.40%), *Gigaspora* (n = 324, 11.39%), *Claroideoglomus* (n = 249, 8.75%) and *Racocetra* (n = 11, 0.39%) (Figure 7). Based on the total frequency of occurrence, the most frequent species were *A. foveata* (29.31%), *A. mellea* (23.20%), and *G. ambisporum* (19.40%) – categorized as very frequent. Moderately frequent species included *G. margarita* (9.31%), *C. claroideum* (8.75%), and *A. scrobiculata* (7.56%). Less frequent species was *G. albida* (1.34%) – categorized as rare. Scarce species were *G. decipiens* (0.74%) and *R. gregaria* (0.39%) (Table 5).

Based on ecosystem differences, Ek (ecotone) yielded the highest number of isolated AMF spores with 1,010 spores, followed by Hk (954 spores) and Pt (881 spores). Species richness also increased from Pt to Hk. Pt contained seven species, namely *A. foveata, A. mellea, G. ambisporum, C. claroideum, G. albida, G. decipiens,* and *G. margarita*. Ek hosted eight species. Hk exhibited the highest richness with nine species. The diversity index (Shannon's H') indicated that Ek had the highest diversity (H' = 1.49) compared to Pt (1.43) and Hk (1.47). However, the dominance index (D) was highest in Pt (0.31), followed by Hk (0.30) and Ek (0.27), suggesting greater dominance of particular species in Pt. Evenness index (E1/D) was also highest in Ek (0.46), followed by Pt (0.45) and Hk (0.36) (Table 5).

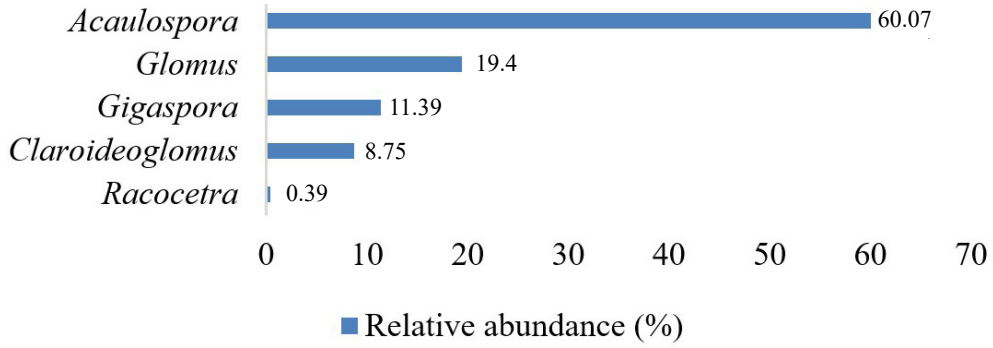

Figure 7. Abundance of the AMF genus originating from three sampling ecosystems

Table 5. Overall summary of AMF spore occurrence at three sampling locations

AMF species	Frequency of occurrence at each ecosystem (FOC, %)			Total FOC (%)
	Kaolin post-mining (Pt)	Ecotone (Ek)	Heath forest (Hk)	
	ΣPt	ΣEk	ΣHk	
Acaulospora foveata	7.83	30.99	47.38	29.31
Acaulospora mellea	8.97	37.33	21.38	23.20
Acaulospora scrobiculata	0	17.52	3.98	7.56
Glomus ambisporum	49.83	7.62	3.77	19.40
Claroideoglomus claroideum	19.52	3.27	4.61	8.75
Gigaspora albida	1.48	1.88	0.63	1.34
Gigaspora decipiens	0.79	0.59	0.84	0.74
Gigaspora margarita	11.58	0	17.09	9.31
Racocetra gregaria	0	0.79	0.31	0.39
Summary				
Total spore number	881	1010	954	2845
Total isolate/species	7	8	9	24
Shannon Diversity (H')	1.43	1.49	1.47	
Simpson Dominance (D)	0.31	0.27	0.30	
Simpson Evenness (E1/D)	0.45	0.46	0.36	

4. Discussion

Land use activities such as mining can significantly affect the composition and diversity of arbuscular mycorrhizal fungal (AMF) species in the kaolin post-mining ecosystems in Belitung Regency. Therefore, studying AMF diversity in a given area is essential to maximize their ecological functions. AMF diversity can be assessed through two main approaches: spore morphological diversity in the rhizosphere and molecular diversity in the functional symbiotic structures of colonized plant roots. However, direct field surveys of AMF diversity often yield less accurate results due to the high proportion of damaged or low-quality spores, which may introduce bias during identification. In addition, differences in sporulation rates and spore production among AMF species can also influence the observed diversity in natural settings (Sukarno *et al.* 2023). As a solution, the trap culture method can be used to obtain and propagate mixed AMF spore inocula from natural habitats (Dobo *et al.* 2017; Suting and Devi 2021). Nonetheless, several studies have noted that this method still has limitations, as the AMF community that develops in culture may only represent species tolerant to disturbances, such as hyphal or mycelial damage during sampling (Chagnon *et al.* 2013).

Before using *P. javanica* as the host plant in the trap culture pot system, a germination trial was conducted using seeds from 16 plant species collected from field samples. The aim was to make the trap culture conditions more closely resemble the original field environment. However, none of the seeds successfully germinated. This failure is likely due to environmental differences between Belitung and Bogor, particularly in elevation, humidity, and temperature. Belitung is located at an average elevation of 200 meters above sea level with a relative humidity of around 55% and temperature around 33°C (BPS Kabupaten Belitung 2020), while Bogor is situated at approximately 265

meters above sea level with a humidity of around 70% and temperature around 26°C (BPS Kota Bogor 2023). The selection of *P. javanica* as the host plant was based on several considerations, *i. e.* its extensive root growth that facilitates rapid colonization by AMF, its ability to withstand heat and drought stress, and its perennial nature, which allows for a longer growth cycle without the need for repeated planting (Lapanjang *et al.* 2023).

The survey of AM communities in roots was conducted using a metagenomic approach. A total of 132 ASVs were obtained from six different fungal phyla. This broad taxonomic range resulted from using primers targeting all taxonomic levels within the fungal kingdom, necessitating data extraction specific to the phylum Glomeromycota to represent the AMF community. Some taxa remained unidentified at the class to genus levels, likely due to the limited availability of publicly accessible AMF DNA sequence databases from environmental samples. Additionally, the short sequencing reads (~350 bp) generated by the Illumina platform may contribute to unclassified taxa, as most available AMF sequences in the SSU rRNA region are typically between ~800–1800 bp in length. The application of full-length SSU sequencing, long-read approaches (e.g., SSU-ITS-LSU), or alternative molecular markers such as ITS or LSU may provide new insights into the taxonomy of currently unidentified AMF taxa (Delavaux *et al.* 2022).

The relative abundance composition of AMF DNA sequences from root samples varied across taxonomic levels from class to genus among the three ecosystems. Overall, the taxonomic composition at both class and genus levels was lower in Pt compared to Ek and Hk. *Glomus* and *Rhizophagus* generally dominated all three ecosystems. However, *Acaulospora* and an unidentified genus were additionally found in Ek, and *Ambispora* and *Paraglomus* were detected in Hk. Total nitrogen content in Ek (0.20%) and C (0.13%) was considerably higher than in Pt (0.04%). Similarly, potassium content in Ek (0.17 $cmol^{(+)}$/kg) and C (0.12 $cmol^{(+)}$/kg) was also higher than in Pt (0.06 $cmol^{(+)}$/kg). These differences may explain why only two AMF genera were detected in Pt, whereas more genera were present in the other sites. Higher total nitrogen in soil reduces interspecific competition among AMF for nitrogen uptake, potentially supporting greater AMF diversity (Zhang *et al.* 2025). In addition, elevated potassium levels can enhance mutualistic interactions between AMF and plant roots, promoting a more diverse AMF community (Han *et al.* 2023).

Diversity analysis results based on the metagenomic approach in root samples varied among the three sampling ecosystems. Based on the three diversity indices calculated (Shannon, Simpson, and Inverse Simpson), Ek exhibited the highest Shannon index value but the lowest for both the Simpson and Inverse Simpson indices. Although Ek had the highest Shannon index, the values ranging from 0.69 to 1.09 indicate low diversity, as no more than four genera were detected. Simpson index values, ranging from 0.70 to 0.80, suggest that all three ecosystems were still highly dominated by two genera, *Glomus* and *Rhizophagus*. The Inverse Simpson index values ranged from 3.37 to 5.08, indicating moderate diversity and evenness. The physicochemical properties of the soils in each ecosystem may influence the observed variation in diversity. The highest clay content was found in Ek, reaching 30.88%. Ek also had the highest organic carbon content (6.72%) and the lowest available phosphorus (1.09 ppm). Clay soils with high organic matter and good water-holding capacity can enhance the diversity and stability of AMF communities (Fors *et al.* 2023).

Each identified AMF spore species based on spore morphology originated from a different host plant, as AMF tends to colonize specific plant species preferentially. The diversity of AMF spores can be influenced by habitat conditions, host plant type, and root exudates (Hugoni *et al.* 2018). Morphologically, *Acaulospora* can be identified by its acaulosporoid spore development, in which the spore forms on the neck of a sporiferous saccule (da Silva *et al.* 2022). *Claroideoglomus* and *Glomus* can be identified by their glomoid spore formation, where spores develop at the tip of a subtending hypha. *Gigaspora* and *Racocetra* are AMF spores belonging to the family Gigasporaceae. These two genera exhibit gigasporoid spore formation, with spores developing at the tip of a bulbous suspensor structure (Walker *et al.* 2018).

The physicochemical properties of the soil may influence the differences in the total occurrence frequency of each AMF spore. The diversity index (H′) showed that Ek had the highest value (1.49) compared to the other two ecosystems, while the dominance index (D) was highest in Pt (0.31). The highest diversity in Ek is likely due to the relatively even proportion of individuals among species. In contrast, although Hk had the most significant number of species, it was dominated by *A. foveata*, resulting in the lowest evenness index (E1/D) at this site (0.36).

Spore abundance, species richness, and AMF diversity indices can be influenced by soil characteristics such as pH, organic carbon, nitrogen, P_2O_5, magnesium, calcium, and soil texture (Tuheteru *et al.* 2022). A diversity index value ranging from 1–3 indicates moderate diversity; an evenness index between 0.3–0.6 reflects moderate evenness; and a dominance index of 0–0.5 indicates low dominance (Herman *et al.* 2024). Using a host plant consortium, as opposed to a single host plant as applied in this study, may also enhance the spore diversity produced in trap culture pots (Tenzin *et al.* 2022). The frequent occurrence of *Acaulospora* and *Glomus* in this study is likely due to their adaptive capacity to degraded environments such as post-mining lands (Tuheteru *et al.* 2020). The dominance of these two AMF groups may be attributed to their generalist and ruderal traits which characterized by rapid sporulation, strong responsiveness to host plants, and high tolerance to disturbance (Ohsowski *et al.* 2014; Maulani *et al.* 2025).

Differences in the composition and diversity of AMF were observed between the metagenomic approach on root samples and the morphological identification of spores in the rhizosphere of trap culture pots. The metagenomic analysis detected *Ambispora* and *Paraglomus*, but their spores were not found morphologically in the rhizosphere. Conversely, morphological analysis revealed *Claroideoglomus, Gigaspora,* and *Racocetra*, which were not detected in the metagenomic sequencing of roots. Such discrepancies between morphological and molecular results are common due to each method's distinct detection targets and inherent limitations. Molecular approaches can detect living or dormant AMF colonizing roots without spores (Redecker *et al.* 2013). However, they also suffer from limitations such as primer specificity, PCR amplification biases, chimera formation, and the limited availability of reference databases (Hart *et al.* 2015).

On the other hand, morphological identification is widely used and supported by numerous taxonomic references, such as morphospecies descriptions of Glomeromycota. Nonetheless, this approach may be biased toward only detecting actively sporulating AMF, and morphologically similar (cryptic) species may be difficult to distinguish or overlook, potentially underestimating AMF diversity. Combining both approaches offers the most comprehensive insight into AMF community composition (Cofré *et al.* 2025).

Acknowledgements

The authors thank the Indonesia Endowment Fund for Education Agency (LPDP RI), Ministry of Finance, Republic of Indonesia, for scholarship and research funds during their Master's Program education. The author also would like to thank the Secretariat of Scientific Authority for Biodiversity, National Research and Innovation Agency (BRIN), Republic of Indonesia and Agency for Natural Resources Conservation of South Sumatera (BKSDA Sumatera Selatan), Ministry of Environment and Forestry, Republic of Indonesia for the research permission.

References

Ahanger, M.A., Tyagi, S.R., Wani, M.R., Ahmad, P., 2014. Drought tolerance: role of organic osmolytes, growth regulators, and mineral nutrients, in: Ahmad, P., Wani, M. (Eds.), *Physiological Mechanisms and Adaptation Strategies in Plants Under Changing Environment.* Springer, New York, pp. 25–55. https://doi.org/10.1007/978-1-4614-8591-9_2

Armanisa, K., Rusmana, I. Astuti, R.I., 2024. Diversity of rhizospheric bacterial community from kaolin mining site and their potential as plant growth promoting bacteria. *HAYATI Journal of Biosciences*. 32, 212-222.

Berruti, A., Lumini, E., Balestrini, R., Bianciotto, V., 2016. Arbuscular mycorrhizal fungi as natural biofertilizers: let's benefit from past successes. *Front. Microbiol.* 7, 1559. https://doi.org/10.3389/fmicb.2015.01559

Bowles, T.M., Barrios-Masias, F.H., Carlisle, E.A., Cavagnaro, T.R., Jackson, L.E., 2016. Effects of arbuscular mycorrhizae on tomato yield, nutrient uptake, water relations, and soil carbon dynamics under deficit irrigation in field conditions. *Sci. Total Environ.* 566, 1223–1234. https://doi.org/10.1016/j.scitotenv.2016.05.178

[BPS Kabupaten Belitung] Badan Pusat Statistik Kabupaten Belitung, 2020. Available at: https://belitungkab.bps.go.id/id/statistics-table/1/MTEyIzE=/luas-daerah--jumlah-pulau--tinggi-wilayah--dan-jarak-ke-ibukota-menurut-kecamatan--2019.html. [Date accessed: 2 June 2025]

[BPS Kota Bogor] Badan Pusat Statistik Kota Bogor, 2023. Available at: https://bogorkota.bps.go.id/id/statistics-table/2/NTgxIzI=/kelembaban-menurut-bulan-di-stasiun-pengamatan-badan-meteorologi-klimatologi-dan-geofisika--bmkg--kota-bogor--persen-.html. [Date accessed: 2 June 2025]

Brundrett, M.C., Bougher, N., Dell, B., Grove, T., Malajczuk, N., 1996. *Working with Mycorrhizas in Forestry and Agriculture*. Australian Centre for International Agricultural Research, Canberra.

Chagnon, P.L., Bradley, R.L., Maherali, H., Klironomos, J.N. 2013. A trait-based framework to understand life history of mycorrhizal fungi. *Trends Plant Sci.* 18, 484–491. https://doi.org/10.1016/j.tplants.2013.05.001

Chen, M., Arato, M., Borghi, L., Nouri, E., Reinhardt, D., 2018. Beneficial services of arbuscular mycorrhizal fungi–from ecology to application. *Front. Plant. Sci.* 9, 1270. https://doi.org/10.3389/fpls.2018.01270

Cofré, N., Grilli, G., Marro, N., Videla, M., Urcelay, C., 2025. Morphological spore-based characterisation and molecular approaches reveal comparable patterns in glomeromycotan communities. *Mycorrhiza.* 35, 19. https://doi.org/10.1007/s00572-025-01198-4

Das, D., Paries, M., Hobecker, K., Gigl, M., Dawid, C., Lam, H.M., Zhang, J., Chen, M., Gutjahr, C., 2022. PHOSPATE STARVATION RESPONSE transcription factors enable arbuscular mycorrhiza symbiosis. *Nat Commun.* 13, 477. https://doi.org/10.1038/s41467-022-27976-8

da Silva, K.J.G., Fernandes, J.A.L., Magurno, F., Leandro, L.B.A., Goto, B.T., Theodoro, R.C., 2022. Phylogenetic review of *Acaulospora* (*Diversisporales, Glomeromycota*) and the homoplasic nature of its ornamentations. *J. Fungi.* 8, 892. https://doi.org/10.3390/jof8090892

Delavaux, C.S., Ramos, R.J., Sturmer, S.L., Bever, J.D. 2022. Environmental identification of arbuscular mycorrhizal fungi using the LSU rDNA gene region: an expanded database and improved pipeline. *Mycorrhiza.* 32, 145–153. https://doi.org/10.1007/s00572-022-01068-3

Dobo, B., Asefa, F., Asfaw, Z., 2017. Effect of tree-enset-coffee based agro-forestry practices on arbuscular mycorrhizal fungi (AMF) species diversity and spore density. *Agroforest Syst.* 92, 525–540. https://doi.org/10.1007/s10457-016-0042-9

Fors, R.O., Sorci-Uhmann, E., Santos, E.S., Silva-Flores, P., Abreu, M.M., Viegas, W., Nogales, A., 2023. Influence of soil type, land use, and rootstock genotype on root-associated arbuscular mycorrhizal fungi communities and their impact on grapevine growth and nutrition. *Agriculture.* 13, 2163. https://doi.org/10.3390/agriculture13112163

Guzman, A., Montes, M., Hutchins, L., DeLaCerda, G., Yang, P., Kakouridis, A., Dahlquist-Willard, R.M., Fireston, M.K., Bowles, T., Kremen, C., 2021. Crop diversity enriches arbuscular mycorrhizal fungal communities in an intensive agricultural landscape. *New Phytol.* 231, 447–459. https://doi.org/10.1111/nph.17306

Hart, M.M., Aleklett, K., Chagnon, P.-L., Egan, C., Ghignone, S., Helgason, T., Lekberg, Y., Öpik, M., Pickles, B.J., Waller, L., 2015, Navigating the labyrinth: a guide to sequence-based, community ecology of arbuscular mycorrhizal fungi. *New Phytol.* 207, 235-247. https://doi.org/10.1111/nph.13340

Han, S., Wang, X., Cheng, Y., Wu, G., Dong, X., He, X., Zhao, G., 2023. Multidimensional analysis reveals environmental factors that affect community dynamics of arbuscular mycorrhizal fungi in poplar roots. *Front. Plant Sci.* 13, 1068527. https://doi.org/10.3389/fpls.2022.1068527

Herman, W., Iskandar, Budi, S.W., Pulunggono, H.B., Kurniati, Milantara, N., 2024. Dynamics of vegetation diversity and arbuscular mycorrhizal fungi in post-coal mining revegetation land in Sawahlunto, West Sumatra, Indonesia. *Biodiversitas.* 25, 4627-4641. https://doi.org/10.13057/biodiv/d251201

Hugoni, M., Luis, P., Guyonnet, J., Haichar, F.E., 2018. Plant host habitat and root exudates shape fungal diversity. *Mycorrhiza.* 28, 451–463. https://doi.org/10.1007/s00572-018-0857-5

Krüger, C., Kohout, P., Janoušková, M., Püschel, D., Frouz, J., Rydlová, J., 2017. Plant communities rather than soil properties structure arbuscular mycorrhizal fungal communities along primary succession on a mine spoil. *Front. Microbiol.* 8, 719. https://doi.org/10.3389/fmicb.2017.00719

Krüger, M., Krüger, C., Walker, C., Stockinger, H., Schüβler, A. 2012. Phylogenetic reference data for systematics and phylotaxonomy of arbuscular mycorrhizal fungi from phylum to species level. *New Phytol.* 193, 970-84. https://doi.org/10.1111/j.1469-8137.2011.03962.x

Kusmana, C., 2017. *Metode Survey dan Interpretasi Data Vegetasi.* IPB Press, Bogor.

Lapanjang, I., Zakaria, E., Edy, N., Barus, H.N. 2023. Effectiveness of multiple culture of arbuscular mycorrhizal fungi (AMF) from the rhizosphere of cocoa on host plant *Pueraria javanica. IOP Conf. Ser.: Earth Environ. Sci.* 1253, 1-6. https://doi.org/10.1088/1755-1315/1253/1/012032

Lee, E.H., Eo, J.K., Ka, K.H., Eom, A.H., 2013. Diversity of arbuscular mycorrhizal fungi and their roles in ecosystems. *Mycobiology.* 41, 121-125. https://doi.org/10.5941/MYCO.2013.41.3.121

Luizão F.J., Luizão R.C., Proctor J., 2007. Soil acidity and nutrient deficiency in central Amazonian heath forest soils. *Plant Ecol.* 192, 209-224. https://doi.org/10.1007/s11258-007-9317-6.

Magurran, A.E., 1988. *Ecological Diversity and Its Measurement.* Princeton University Press, New Jersey, USA.

Maulani, N.I., Sukarno, N., Yulandi, A., Listiyowati, S., Kramadibrata, K., Subagya, M., Anwar, S., 2025. Morphological and molecular identification of culturable arbuscular mycorrhizal fungi (AMF) associated with *Pternandra azurea* from Martabe Batang Toru Forest, North Sumatra, Indonesia. *HAYATI Journal of Biosciences*. 32, 1240-1250. https://doi.org/10.4308/hjb.32.5.1240-1250

Nuryana, I., Widada, J., Subandiyah, S., 2020. Molecular study of root colonization and diversity of arbuscular mycorrhizal fungi (AMF) associated with lesser yam (*Dioscorea esculenta*). *Journal of Physics: Conference Series.* 1665, 1–9. https://doi.org/10.1088/1742-6596/1665/1/012017

Ohsowski, B.M., Zaitsoff, P.D., Öpik, M., Hart, M.M. 2014. Where the wild things are: looking for uncultured Glomeromycota. *New Phytol.* 204(1): 171–179. https://doi.org/10.1111/nph.12894

Öpik, M., Vanatoa, A., Vanatoa, E., Moora, M., Davison, J., Kalwij, J.M., Reier, Ü., Zobel, M., 2010. The online database MaarjAM reveals global and ecosystemic distribution patterns in arbuscular mycorrhizal fungi (Glomeromycota). *New Phytol.* 188, 223–241. https://doi.org/10.1111/j.1469-8137.2010.03334.x

Redecker, D., Schüßler, A., Stockinger, H., Stürmer, S.L., Morton, J.B., Walker, C., 2013. An evidence-based consensus for the classification of arbuscular mycorrhizal fungi (Glomeromycota). *Mycorrhiza*. 23, 515–531. https://doi.org/10.1007/s00572-013-0486-y

Salam, E.A., Alatar, A., El-Sheikh, M.A. 2017. Inoculation with arbuscular mycorrhizal fungi alleviates harmful effects of drought stress on damask rose. *Saudi J. Biol. Sci.* 25, 1772–1780. https://doi.org/10.1016/j.sjbs.2017.10.015

Smith, S., Read, D., 2008. *Mycorrhizal Symbiosis*, third ed. Academic Press, San Diego, USA.

Subari, Erlangga, B.D., Maryani, E., Arifin, D.N., 2021. Potential utilization of quartz sand and kaolin from tin mine tailings for whiteware. *Min of Mineral Depos.* 15, 1-6. https://doi.org/10.33271/mining15.03.001

Sukarman, Gani, R.A., Asmarhansyah, 2020. Tin mining process and its effects on soils in Bangka Belitung Islands Province, Indonesia. *Sains Tanah: J. Soil Sci. Agroclimatol.* 17, 180-189. https://doi.org/10.20961/stjssa.v17i2.37606

Sukarno, N., Rahmawati, C., Listiyowati, S., Fadillah, W.N., Novera, Y., 2023. Isolation of arbuscular mycorrhizal fungi from rhizosphere of Bangka Island woody plants and their mycorrhizal structure culture characteristics. *Jurnal Sumberdaya HAYATI.* 9, 39-48. https://doi.org/10.29244/jsdh.9.2.39-48

Suting, E.G., Devi, N.O., 2021. Occurrence and diversity of arbuscular mycorrhizal fungi in trap cultures from limestone mining sites and un-mined forest soil of Mawsmai, Meghalaya. *Trop Ecol.* 62, 525–537. https://doi.org/10.1007/s42965-021-00144-7

Tedersoo, L., Bahram, M., Zobel, M. 2020. How mycorrhizal associations drive plant population and community biology. *Science.* 367, eaba1223. https://doi.org/10.1126/science.aba1223

Tenzin, U.W., Noirungsee, N., Runsaeng, P., Noppradit, P., Klinnawee, L., 2022. Dry-season soil and co-cultivated host plants enhanced propagation of arbuscular mycorrhizal fungal spores from sand dune vegetation in trap culture. *Journal of Fungi.* 8, 1061. https://doi.org/10.3390/jof8101061

Tuheteru, F.D., Husna, Albasri, Arif, A., Kramadibrata, K., Soka, G., 2020. Composition and diversity of arbuscular mycorrhizal fungi spore associated with different land-use types in tropical gold mine. *J Deg Mine Lands Manag.* 8, 2503–2512. https://doi.org/10.15243/jdmlm.2020.081.2503

Tuheteru, F.D., Husna, Albasri, Effendy, H.M., Arif, A., Basrudin, Tuheteru, E.J., Mulyono, S., Irianto, R.S.B., 2022. Diversity of arbuscular mycorrhizal fungi in asphalt post-mining land in Buton Island, Indonesia. *Biodiversitas.* 23, 6327-6334. https://doi.org/10.13057/biodiv/d231229

van der Heijden, M.G.A., Martin, F.M., Selosse, M.A., Sanders, I.R. 2015. Mycorrhizal ecology and evolution: the past, the present, and the future. *New Phytol.* 205, 1406-1423. https://doi.org/10.1111/nph.13288

Walker, C., Harper, C.J., Brundrett, M.C., Krings, M. 2018. Looking for arbuscular mycorrhizal fungi in the fossil record: an illustrated guide, in: Krings, M., Harper, C.J., Cúneo, N.R., Rothwell, G.W. (Eds.), *Transformative Paleobotany.* Academic Press, Edinburgh, pp. 481-517. https://doi.org/10.1016/B978-0-12-813012-4.00020-6

Wang, F., 2017. Occurrence of arbuscular mycorrhizal fungi in mining-impacted sites and their contribution to ecological restoration: mechanisms and applications. *Crit. Rev. in Env. Sci. Tech.* 7, 1901-1957. https://doi.org/10.1080/10643389.2017.1400853

Xiao, W., Zhang, Y., Chen, X., Sha, A., Xiong, Z., Luo, Y., Peng, L., Zou, L., Zhao, C., Li, Q. 2024. The diversity and community composition of three plants' rhizosphere fungi in Kaolin Mining areas. *Journal of Fungi.* 10, 306. https://doi.org/10.3390/jof10050306

Yang, H., Dai, Y., Wang, X., Zhang, Q., Zhu, L., Bian, X., 2014. Meta-analysis of interactions between arbuscular mycorrhizal fungi and biotic stressors of plants. *Sci. World J.* 2014, 1-7. https://doi.org/10.1155/2014/746506

Zhang, M.G., Shi, Z.Y., Yang, M., Lu, S.C., Wang, X.G. 2021. Molecular diversity and distribution of arbuscular mycorrhizal fungi at different elevations in Mt. Taibai of Qinling Mountain. *Front. Microbiol.* 12, 1-12. https://doi.org/10.3389/fmicb.2021.609386

Zhang, S., Yang, Z., Yang, X., Ma, X., Ma, Q., Ma, M., Zhang, J., 2025. Plant–soil interactions shape arbuscular mycorrhizal fungal diversity and functionality in Eastern Tibetan Meadows. *J. Fungi.* 11, 337. https://doi.org/10.3390/jof11050337