BIODIVERSITAS
Volume 24, Number 12, December 2023
Pages: 6692-6703

ISSN: 1412-033X
E-ISSN: 2085-4722
DOI: 10.13057/biodiv/d241231

Arbuscular Mycorrhizal Fungi (AMF) diversity and population in UPV Nature Trail, Miagao, Iloilo, Philippines

EDGAR PHILIP T. DE ASIS♥, FRITZIE MARIE M. DEMETILLO, DIANA P. PAGUNTALAN
Division of Biological Sciences, College of Arts and Sciences, University of the Philippines Visayas. Miagao, Iloilo 5023, Philippines.
Tel.: +63-939-8807774, ♥email: etdeasis@up.edu.ph

Manuscript received: 18 September 2023. Revision accepted: 24 December 2023.

Abstract. *De Asis EPT, Demetillo FMM, Paguntalan DP. 2023. Arbuscular Mycorrhizal Fungi (AMF) diversity and population in UPV Nature Trail, Miagao, Iloilo, Philippines. Biodiversitas 24: 6692-6703.* Arbuscular Mycorrhizal Fungi (AMF) are soil microorganisms that form the most prevalent mutualistic associations with plant species. Studies revealed its global distribution in various terrestrial habitats, but available local literature remains few. This study investigated AMF diversity in the University of the Philippines Visayas (UPV) Nature Trail, Miagao, Iloilo, Philippines. AMF spores were isolated using wet sieving, decanting, and centrifugation. A total of 2815 individual spores were documented, with 114 distinct morphospecies representing 16 genera, nine families, and four orders classified. *Glomus clarum*, *Acaulospora* sp.7, and *Scutellospora pellucida* tallied the highest abundance across all points. *Scutellospora pellucida* (FOC=83.3%) recorded the highest species richness, followed by *Ambispora* sp. (FOC=77.78%), then *Acaulospora mellea* and *Glomus australe* (FOC=72.22%). Overall, Shannon-Weiner diversity index (H=3.6019) and Simpson diversity index (D=0.0420) revealed a very high AMF diversity in the trail, while the Pielou evenness index (J=0.7605) suggested a semi-balanced number of individuals among each morphospecies. A more abundant, even, and diverse, albeit not statistically significant, AMF community was recorded in forested areas compared to non-forested areas of the trail. Results generally suggest that the AMF community is diverse and abundant regardless of the location, ecosystem type, and faunal association.

Keywords: AMF abundance, Arbuscular Mycorrhizal Fungi (AMF), diversity, morphospecies, UPV Nature Trail

INTRODUCTION

Endomycorrhiza or Arbuscular Mycorrhizal Fungi (AMF) are ubiquitous soil microorganisms that are associated with almost 90% of plant species (Aggangan et al. 2015; Fasusi et al. 2021). This group of fungi belongs to phylum *Glomeromycota* which is characterized by finely branched hyphal structures, called arbuscules or hyphal coils, that colonize the cortical cells of plant roots (Pagano et al. 2016). The arbuscules are dedicated structures where the mineral and carbohydrate exchange occur. They penetrate cortical root cells and form balloon-like vesicles and branch out arbuscules allowing its host plant to capture minerals thereby expanding its absorptive capacity (Soriano et al. 2021).

AMF are known for their notably high affinity for phosphorus, which they assist in absorbing, along with nitrogen, carbon, water, and other nutrients, in exchange for photosynthetically fixed carbon sources from their plant symbionts. Furthermore, AMF promotes resistance against fungal pathogens via interaction with soil microbes by initiating root surface resistance to invading pests and pathogens (Soriano et al. 2021). The presence of AMF has also been demonstrated to improve the tolerance of their host plant to abiotic stresses, such as adverse soil and extreme climate conditions. At a larger scale, the symbiosis significantly influences plant-plant interactions and the ecology of plant communities, and thus it can also have a profound effect on agricultural productivity, bioremediation (Aggangan and Cortes 2018) and as well as the conservation and rehabilitation of habitats (Davison et al. 2015; Liu et al. 2021).

With an approximately 2.5 billion occupancies of tropical vegetation in the world, 900,000 hectares of these important formations are damaged annually (Marinho et al. 2018; International Sustainability Unit 2015; Roberts et al. 2017). In this regard, it becomes importantly significant to identify the biological communities present in tropical forests. In the Philippines, various ecosystems within its ideal geographic location and tropical climate occur, ranging from terrestrial forests, grasslands to agroecosystems. Within these, the majority of vegetation depends on the beneficial associations with soil mycorrhizal fungi for efficient growth and survival (Marinho et al. 2018). Despite this fact, field surveys on the occurrence of AMF in the country remain elusive, particularly in the Western Visayas region.

The Nature Trail inside the University of the Philippines-Visayas (UPV) campus, located in the town of Miagao, Iloilo Province, south of Panay Island is a known biodiversity hotspot. It is a terrain situated behind the new administration building and was launched as an official trail in 2018. The trail spans approximately two kilometers in a terrain that is composed of sloping hills, forested areas, glades, and a small, dried creek. Aside from being a place of leisure and recreation, the trail has been an interesting area for fieldwork in various research studies and laboratory activities. However, there has been no published literature on the indigenous species of AMF in this area.

As of 2022, there have been 327 morphologically described species of AMF, distributed in four orders, 11-17 families, and 39-49 genera, depending on the classification system followed (Wijayawardene et al. 2020; CICG 2022).

Published information on field surveys of endomycorrhizal diversity inside the UPV Miag-ao campus can provide wanting implications in relation to its diverse ecosystem. With this, the present study aims to provide baseline information of AMF species diversity and population present along the UPV Nature Trail, Miagao, Iloilo, Philippines. To do this: a) AMF spores are isolated from soil samples from different points across the trail with varying vegetation types. These soil samples are present within one meter point vicinity near associated plant species; b) the isolated AMF spores are then subjected to characterization following morphological features as basis for identification: color, shape, spore wall, and hyphal structures.

MATERIALS AND METHODS

Study site

The study was conducted in the Nature Trail (10°38 '38''N, 122°13'51"E) located inside the University of the Philippines-Visayas (UPV) campus in the town of Miagao, Iloilo, Western Visayas, Philippines (Figure 1). This sampling site consists of litters of leaves from a variety of terrestrial plant species situated in a hilly topographic location following the town's terraneous land formation. The entire trail spans approximately two kilometers, which starts from Phase 1 of the Nature Trail behind the UPV New Admin Building and across the UPV Reforestation Program Office and ends beside the UPV New Teacher's Dorm.

Rhizosphere sampling and plant diversity assessment

The sampling method used to determine the collection sites for the soil samples was the systematic random sampling technique. A total of six localized areas or points with fixed 250 m intervals each have been established within the UPV Nature Trail. Within the one-meter vicinity of the point, a 500 g soil sample was taken at a depth of 10-30 cm from the rhizosphere using a garden shovel (Soriano et al. 2021). Any weeds, leaf debris, and litter at the soil surface were removed before placing the soil samples in properly labeled Ziploc bags. After which, soil samples were transported and stored in a refrigerator until laboratory usage. For the assessment of associated plant diversity, all plant species found within the 3 m diameter of each point were documented and identified.

AMF spore isolation

The standard procedure for Glomalean spore isolation using wet sieving and decanting methods according to Soriano et al. (2021) was conducted. First, the soil samples were air-dried for 30 min and pulverized. Then, three 50g subsamples representing the replicates of each sampling point were obtained and reweighed. Each replicate was added to 750 mL of distilled water and mixed thoroughly to disintegrate soil aggregates, then allowed to settle for 10 min. Once settled, the supernatant was discarded through mesh screens following the nos. 18, 40, 170, and 400 with sizes 1, 0.420, 0.088, and 0.037 mm, respectively. This process was repeated four times until the color of the mixture became virtually clear. The acquired residues or filtered spores at the mesh screen 400 (0.037 mm) were washed with water, transferred into 50 mL tubes, and centrifuged for two rounds at 3000 RPM for three minutes. Next, the supernatant was discarded and replaced by a 60% sucrose solution. After that, centrifuge tubes were shaken vigorously for three seconds before undergoing another round of centrifugation at 2000 RPM for two minutes. Spores were finally re-sifted in sieve No. 400 and rinsed with distilled water before pouring onto Petri dishes for storage or immediate examination under a stereomicroscope.

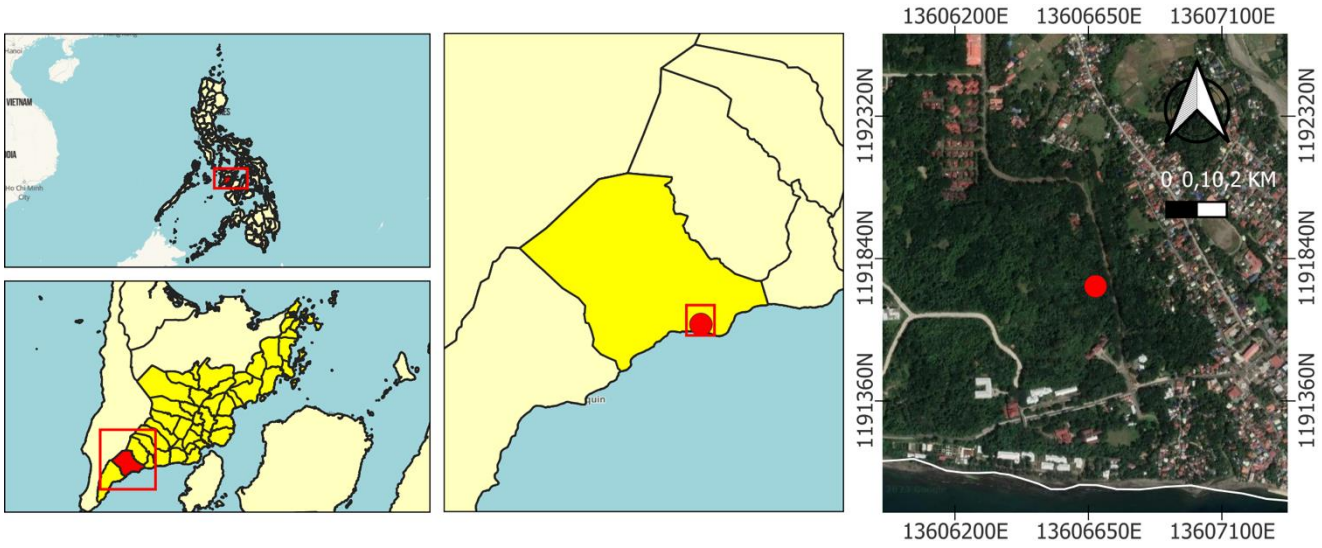

Figure 1. Map showing the location of the University of the Philippines Visayas in Miagao, Iloilo, Philippines

AMF spore identification and characterization

Isolated spores from the rhizosphere soil samples were first examined under a stereomicroscope with a 20X magnification. Then, intact and viable spores were mounted in glass slides using a micropipette and dissecting needles. They were subjected to documentation and further examination under a photomicroscope in 400X and 600X magnification. For identification and classification, the following morphological attributes were used: color, shape, spore wall, and endophytic elements, such as hypha, arbuscules, coils, or vesicles. The morphotype identities of AMF spores were ultimately verified based on existing literature (Aggangan et al. 2015; Kamble et al. 2018; Islam et al. 2022), monographs, the AMF handbook of Souza (2015), and the online database, International Collection of Vesicular Arbuscular Mycorrhizal Fungi (INVAM).

Calculation and analysis of AMF diversity

The biodiversity of AMF in the study site was calculated and quantified using the Shannon-Weiner diversity index (H'), Pielou Evenness index (J), and Simpson Diversity Index (D), as shown below (Soriano et al. 2021). Species richness was determined by the total count of AMF species among the samples, while relative abundance was measured by: (Total number of individuals in a species/Total number of spores) x 100. Mean diversity values were further subjected to a one-way analysis of variance (ANOVA) and Tukey's test for comparison.

Shannon-Wiener Index (H') = $-\sum_{i=1}^{S} pi \ln pi$

Where: s = number of species and p_i = proportion of individuals of each species belonging to the ith species of the total number of individuals

Pielou Evenness index (J) = $\frac{H}{H' max}$

Where: H'max = lnS and S = richness.

Simpson Index (D) = $1 - \frac{\sum n(n-1)}{N(N-1)}$.

Where: n = number of individuals in a single species and N = total number of individuals in a population

RESULTS AND DISCUSSION

Overall species diversity

A total of 2815 individual spores of 114 morphospecies of AMF belonging to four orders (Archaeosporales, Diversisporales, Glomerales, and Paraglomerales), nine families (Ambisporaceae, Archaeosporaceae, Acaulosporaceae, Diversisporaceae, Gigasporaceae, Pascisporaceae, Glomeraceae, Claroideoglomeraceae, and Paraglomeraceae), and 16 genera were documented from the three rhizosphere soil subsamples of each of the six points established within the UPV Nature Trail in Miagao, Iloilo (Figure 2). Of these, 48 species were only described but unidentified under the Phylum Glomeromycota (Figure 3).

The order with the highest number of species known is order Diversisporales with 34 identified species. Following it is Order Glomerales with 26 species, then Order Archeaosporales with 4 identified species, and lastly Order Paraglomerales with the least species identified (n=1).

On the family level, Glomeraceae had the highest recorded number of species (n=24), followed by Acaulosporaceae with 20 species. This is followed by Gigasporaceae (n=9), Diversisporaceae (n=4), then Claroideoglomeraceae, Ambisporaceae, and Archaeosporaceae where all have two species reported. The family with the least identified morphospecies are Pascisporaceae and Paraglomeraceae, both having only one species identified.

Among all the morphospecies identified throughout the established points in the trail, *Glomus clarum* is found to be the most abundant (N=248) comprising 8.81% of the total morphospecies, followed by *Acaulospora* sp.7 (N=212) comprising 7.53%, *Scutellospora pellucida* (N=191) which is 6.79% of the total number of spores, *Glomus* sp.1 (N=186) comprising 6.61% and *Ambispora* sp. (N=165) being 5.86% of the overall frequency. On the other hand, the lowest frequency was recorded in the following species: *Acaulospora brasiliensis*, *Acaulospora* sp.1. *Glomus albidum*, *Glomus hoi*, and *Rhizophagus clarus*, where N=1 (Table 2). Biodiversity calculations revealed that the Shannon-Weiner diversity index (H) across all points in the trail is 3.6019, the Simpson diversity index (D) is 0.0420, while the Pielou evenness index (J) is 0.7605.

AMF distribution across points

The occurrence of AMF species on each subsample of each point was recorded and its frequency of occurrence was calculated by dividing the presence of the species by the total number of points established. The summary of the occurrence of AMF species is tabulated in Table 2.

All points were dominated by *Scutellospora pellucida* (FOC=83.3%), followed by *Ambispora* sp. (FOC=77.78%,) and *Acaulospora mellea* and *Glomus australe* both having an FOC of 72.22%. Among the unidentified morphospecies, only Unidentified sp.36 and Unidentified sp.43 have the highest occurrence across all points (FOC=22.22%) only present in three points (points 4, 5, and 6) in four subsamples and two points (points 5 and 6) in four subsamples, respectively.

Meanwhile, identified morphospecies with the least occurrence across all points having an FOC of 5.56% appearing only in one subsample include *Acaulospora brasiliensis*, *Ac. gerdemanii*, *Ac.* sp.1, *Ac.* sp.2, *Ac.* sp.6, *Ac.* sp.10, *Archaeospora* sp., *Glomus albidum, Glomus hoi, Paraglomus albidum, Rhizophagus clarus, Sclerocystis pubescens, S. sinuosa,* and *Scutellospora arenicola.* Additionally, this also includes unidentified species #1, #2, #4, #6, #7, #9, #11, #12, #15, #16, #19, #21, #22, #23, #24, #26, #28, #32, #34, #37, #38, #39, #41, #45, #46, #47, and #48.

AMF species that occur in all sampling points are considered generalist species. Those identified and reported in the trail include *Acaulospora denticulate, Acaulospora mellea, Acaulospora* sp.4, *Ambispora* sp., *Claroideoglomus etunicatum, Diversispora epigea, Glomus occultum, Glomus pallidum, Glomus* sp.1, *Glomus* sp.2, and *Scutellospora pellucida.*

Table 1. Overall individual frequency of AMF morphospecies recorded across six points within the UPV Nature Trail, Philippines

Species	Overall freq. (N)	Relative abund. (%)
Acaulospora brasiliensis	1	0.04
Acaulospora cavernata	13	0.46
Acaulospora denticulate	24	0.85
Acaulospora foveata	10	0.36
Acaulospora gerdemanii	8	0.28
Acaulospora lacunosa	8	0.28
Acaulospora laevis	9	0.32
Acaulospora mellea	120	4.26
Acaulospora sp.*1*	1	0.04
Acaulospora sp.*2*	2	0.07
Acaulospora sp.*3*	35	1.24
Acaulospora sp.*4*	145	5.15
Acaulospora sp.*5*	3	0.11
Acaulospora sp.*6*	2	0.07
Acaulospora sp.*7*	212	7.53
Acaulospora sp.*8*	2	0.07
Acaulospora sp.*9*	13	0.46
Acaulospora sp.*10*	5	0.18
Acaulospora spinosa	15	0.53
Acaulospora tuberculata	3	0.11
Ambispora fennica	19	0.67
Ambispora sp.	165	5.86
Archaeospora sp.	3	0.11
Archaeospora trappei	70	2.49
Claroideoglomus claroideum	37	1.31
Claroideoglomus etunicatum	93	3.30
Diversispora aurantium	67	2.38
Diversispora celata	3	0.11
Diversispora epigea	59	2.10
Entrophospora sp.	36	1.28
Funneliformis coronatum	10	0.36
Gigaspora albida	17	0.60
Gigaspora rosea	28	0.99
Gigaspora sp.	11	0.39
Glomus albidum	1	0.04
Glomus australe	127	4.51
Glomus clarum	248	8.81
Glomus fasciculatum	9	0.32
Glomus flavisporum	11	0.39
Glomus geosporum	17	0.60
Glomus halonatum	39	1.39
Glomus hoi	1	0.04
Glomus intraradices	15	0.53
Glomus macrocarpum	145	5.15
Glomus maculosum	8	0.28
Glomus multisubstensum	11	0.39
Glomus occultum	106	3.77
Glomus pallidum	57	2.02
Glomus sp.*1*	186	6.61
Glomus sp.*2*	59	2.10
Glomus versiforme	4	0.14
Glomus warcuppi	58	2.06
Intraspora sp.	7	0.25
Paraglomus albidum	3	0.11
Pascispora sp.	15	0.53
Rhizophagus clarus	1	0.04
Sclerocystis pubescens	2	0.07
Sclerocystis taiwanensis	2	0.07
Scutellospora arenicola	2	0.07
Scutellospora calospora	29	1.03
Scutellospora dipurpurescrns	18	0.64
Scutellospora pellucida	191	6.79
Scutellospora sp.	16	0.57
Scutellospora verrucosa	12	0.43
Septoglomus constrictum	21	0.75
Unidentified species #1	1	0.04
Unidentified species #2	1	0.04
Unidentified species #3	3	0.11
Unidentified species #4	1	0.04
Unidentified species #5	6	0.21
Unidentified species #6	1	0.04
Unidentified species #7	1	0.04
Unidentified species #8	1	0.04
Unidentified species #9	3	0.11
Unidentified species #10	2	0.07
Unidentified species #11	1	0.04
Unidentified species #12	1	0.04
Unidentified species #13	2	0.07
Unidentified species #14	3	0.11
Unidentified species #15	1	0.04
Unidentified species #16	2	0.07
Unidentified species #17	20	0.71
Unidentified species #18	6	0.21
Unidentified species #19	1	0.04
Unidentified species #20	3	0.11
Unidentified species #21	2	0.07
Unidentified species #22	1	0.04
Unidentified species #23	1	0.04
Unidentified species #24	16	0.57
Unidentified species #25	2	0.07
Unidentified species #26	2	0.07
Unidentified species #27	4	0.14
Unidentified species #28	1	0.04
Unidentified species #29	2	0.07
Unidentified species #30	5	0.18
Unidentified species #31	4	0.14
Unidentified species #32	2	0.07
Unidentified species #33	2	0.07
Unidentified species #34	1	0.04
Unidentified species #35	2	0.07
Unidentified species #36	9	0.32
Unidentified species #37	1	0.04
Unidentified species #38	1	0.04
Unidentified species #39	1	0.04
Unidentified species #40	5	0.18
Unidentified species #41	1	0.04
Unidentified species #42	2	0.07
Unidentified species #43	11	0.39
Unidentified species #44	2	0.07
Unidentified species #45	1	0.04
Unidentified species #46	1	0.04
Unidentified species #47	1	0.04
Unidentified species #48	1	0.04
Total	2815	100

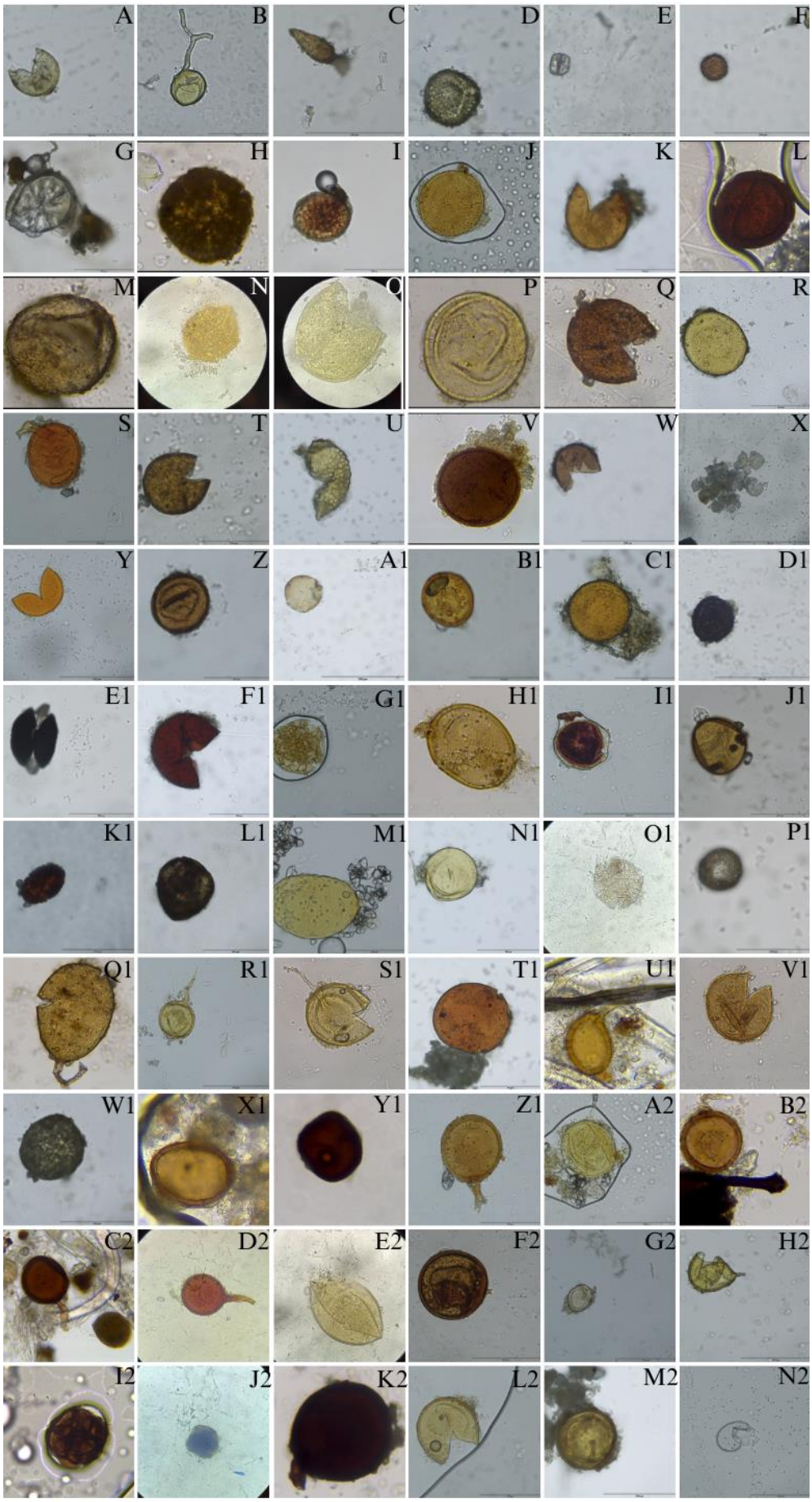
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U
V
W
X
Y
Z
A1
B1
C1
D1
E1
F1
G1
H1
I1
J1
K1
L1
M1
N1
O1
P1
Q1
R1
S1
T1
U1
V1
W1
X1
Y1
Z1
A2
B2
C2
D2
E2
F2
G2
H2
I2
J2
K2
L2
M2
N2

Figure 2. Photomicrograph of the 66 identified morphospecies of AMF spores from UPV Nature Trail. From Order *Archaeosporales*, Family Ambisporaceae: (A) *Ambispora* sp. Walker, Vestberg and Schüßler (B) *Ambispora fennica* Walker et al.; Family Archaeosporacea (C) *Archaeospora* sp. Morton and Redecker (D) *A. trappei* Ames and Linderman (E) *Instraspora* sp.. Order Diversisporales, Family Family Acaulosporaceae (Morton and Benny): (F) *Acaulospora brasiliensis* comb. nov (G) *Acaulospora cavernata* Błaszk. (1989) (H) *Acaulospora denticulata* Sieverd. & S. Toro (1987) (I) *Acaulospora foveata* Trappe & Janos, in Janos & Trappe (1982) (J) *Acaulospora gerdemanii* N. C. Schenck & T. H. Nicolson (K) *Acaulospora lacunosa* J.B. Morton (1986) (L) *Acaulospora laevis* (M) *Acaulospora mellea* Spain & N.C. Schenck (N) *Acaulospora* sp.1 (O) *Acaulospora* sp.2 (P) *Acaulospora* sp.3 (400x) (Q) *Ac*. sp 4. (R) *Ac*. sp.5 (S) *Ac*. sp.6 (T) *Ac*. sp.7 (U) *Ac*. sp.8 (V) *Ac*. sp.9 (W) *Ac*. sp.10 (X) *Ac*. Spinosa C. Walker & Trappe (1981) and (Y) *Ac*. tuberculata Janos & Trappe (1982); Family Diversisporaceae (Walker and Schüßler): (Z) *Diversispora aurantium* Błaszk., Blanke, Renker & Buscot (A1) *Diversispora celata* C. Walker, Gamper & A. Schüßler (B1) *Diversispora epigea* B.A. Daniels & Trappe and (C1) *Entrophospora* sp. R.N. Ames & R.W. Schneid; Family Gigasporaceae (Morton and Benny): (D1) *Gigaspora albida* N.C. Schenck & G.S. Sm. (1982) (E1) *Gigaspora rosea* T.H. Nicolson & N.C. Schenck (1979) (F1) *Gigaspora* sp. (Gerdemann and Trappe) (G1) *Scutellopora arenicola* Koske Koske & Halvorson (1990/1989) (H1) *Scutellopora calospora* Nicolson and Gerd. (I1) *Scutellospora dipurpurescens* J.B. Morton & Koske (1988) (J1) *Scutellospora pellucida* T.H. Nicolson & N.C. Schenck, Mycologia 71: 189 = *Cetraspora pellucida* (K1) *Scutellospora* sp. Walker and Sanders and (L1) *Scutellospora verrucosa* Walker and Sanders; Family Pascisporaceae (Walker, Błaszk., Schüßler and Schwarzott): (M1) *Pascispora* sp. Sieverd. and Oehl. From Order Glomerales, Family Glomeraceae Piroz. and Dalpé emend Oehl, Silva and Sieverd: (N1) *Funneliformis coronatum* C. Walker & A. Schüssler (2010) (O1) G*lomus albidum S*ilva & Sieverd., comb. nov.=*Paraglomus albidum (*P1) G*lomus australe S*.M. Berch (1983) (Q1) G*lomus clarum R*ose and Trappe (1980) (R1) G*lomus fasciculatum G*erdemann and Nicolson (S1) G*lomus flavisporum T*rappe & Gerd. (1974) (T1) G*lomus geosporum G*erdemann and Nicolson (U1) *Glomus halonatum R*ose and Trappe (1980) (V1) *Glomus hoi S*.M. Berch & Trappe (1985) (W1) *Glomus intraradices S*chenck and Smith (1982) (X1) *Glomus macrocarpum T*ulasne and Tulasne (Y1) *Glomus maculosum M*iller and Walker (1986) (Z1) *Glomus multisubstensum M*ukerji et al. (1983) (A2) *Glomus occultum W*alker (1982) (B2) *Glomus pallidum I*.R. Hall (1977) (C2-D2) *Glomus* sp.*1, 2 T*ulasne and Tulasne, emend. Walker and Schüßler (E2) G*lomus versiforme* (F2) G*lomus warcuppi Mc*Gee (1986) (G2) R*hizophagus clarus T*.H. Nicolson & N.C. Schenck (H2) S*clerocystis pubescens* Sacc. & Ellis Höhn. (1910) (I2) S*clerocystis sinuosa Gerd*. & B.K. Bakshi (1976) (J2) S*clerosytics taiwanensis* C.G. Wu & Z.C. Chen (1987) and (K2) Se*ptoglomus constrictum (T*rappe) Sieverd. et al.; Family Claroideoglomeraceae (Walker and Schüßler): (L2) *Claroideoglomus claroideum* Schenck and Sm., Walker and Schüßler and (M2) *Claroideoglomus etunicatum* W.N. Becker & Gerd., C. Walker & A. Schüßler comb. nov. =G*lomus etunicatum W*.N. Becker & Gerd. (1977). From Order Paraglomerales, Family Paraglomeraceae Morton and Redecker: (N2) *Paraglomus albidum S*ilva & Sieverd. Images with no scale are viewed under 400x magnifciation. Images with 100µm and 200µm are viewed under 400x and 600x magnification, respectively (Souza 2015)

Diversity indices

The Shannon-Weiner diversity indices of different subsamples across all points range from 2.3997 to 5.1043. Whereas, the Pielou Evenness index values range from 0.7763 to 1.4728. The Simpson diversity indices range from 0.0535 to 0.1598. Interestingly, after subjecting the mean diversity indices of Shannon-Weiner (p_H=0.422), Pielou Evenness (p_J=0.087), and Simpson (p_D=0.516) to Welch's One-Way Analysis of Variance (ANOVA), results show that there is no significant difference for all points at a 5% level of significance. All p-values obtained by the diversity indices are all greater than 0.05. In other words, the diversity and evenness among all points from different locations in the trail are fairly similar. Furthermore, this means that all data are normally distributed, thus post hoc analysis using the Tukey HSD test was not conducted.

Across different ecosystem types, a higher Shannon-Weiner diversity index was recorded in the forested areas of the trail (points 1-3) compared to the non-forested areas (points 4-6). The same result is also observed in terms of the Pielou Evenness index. On the other hand, a higher Simpson diversity index was calculated in the non-forested areas of the trail. Generally, all of these results indicate that the AMF community in the rhizosphere of the forest areas is more diverse and even, in comparison to that of the non-forested areas (i.e., grassland, dried creek, glade) of the trail.

Associated local fauna among points in the UPV Nature Trail

Generally, the vegetation in points 1-3 can be described as forest-type, whereas points 4 and 5 are grassland. Point 6 has been observed to have grassland areas, but it primarily exhibits vegetation characteristic of glades. In point 1, a total of nine plant species were identified within the point vicinity, which includes *Swietenia macrophylla* King, *Morinda citrifolia* Linn., *Corypha utan* Lam., *Artocarpus blancoi* Merr., *Leea indica* (Burm. f.) Merr., *Flemingia strobilifera* Linn., *Saribus* sp., *Leea* sp., and *Antidesma* sp.point 2 had eight plant species, including *Corypha utan* Lam., *Swietenia macrophylla* King, *Milletea* sp., *Artocarpus blancoi* Merr., *Leea indica* (Burm. f.) Merr., *Cassia* sp., *Terminalia* sp., and one unidentified plant species. There were 12 plant species in point 3, which include *Swietenia macrophylla* King, *Caesalpinia sappan* L., *Melanolepis multigradulosa* (Reinw. ex Blume) Rchb.f. & Zoll., *Morinda citrifolia* Linn., *Macaranga tanarius* (L.) Müll. Arg., *Peltophrorum* sp., *Urena lobata* L., *Flemingia strobilifera* Linn, *Cyperus* sp., and three unidentified plant species. In point 4, only two plant species were found in the vicinity, predominated by *Uraria* sp. and one unidentified plant species. Point 5 had a total of five plant species, mainly dominated by *Bambusa* sp. Other plant species found within point vicinity include *Corypha utan* Lam., *Leea* sp., *Ixora* sp., and one unidentified plant species. Lastly, only three plant species were documented around point 6. *Chromolaena odorata* (L.) R.M.King & H.Rob was the most prevalent species, followed by *Urena lobata* L. and one unidentified grass species.

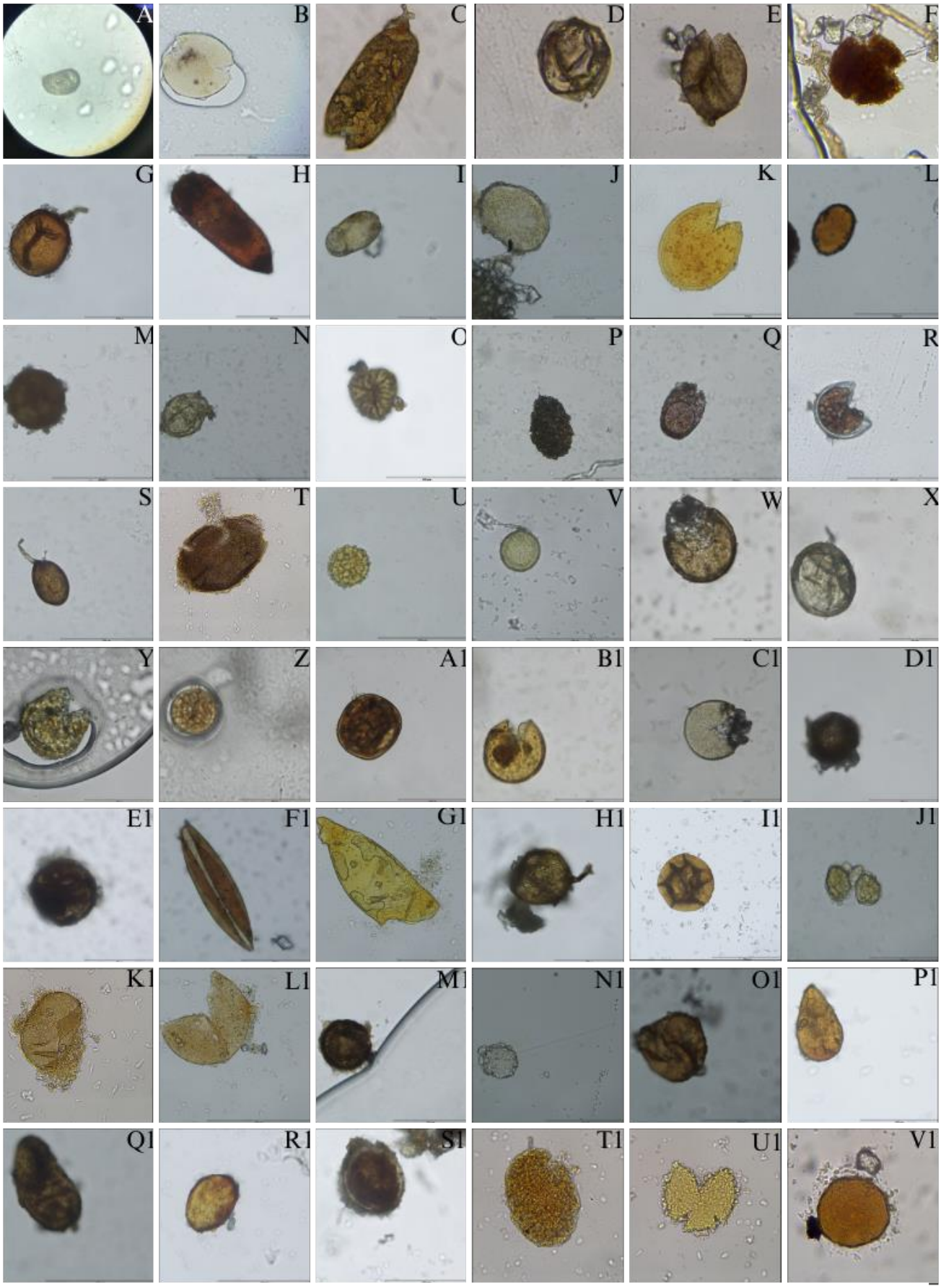

Figure 3. Photomicrographs of 48 unidentified AMF species isolated across all six points from the UPV Nature Trail, Philippines

Table 2. Species composition of AMF collected from the six different points established in the UPV Nature Trail, Philippines

Species	P1			P2			P3			P4			P5			P6			TC*	FOC**
	S1	S2	S3	S1	S2	S3	S1	S2	S3	S1	S2	S3	S1	S2	S3	S1	S2	S3		
Scutellospora pellucida	-	+	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	15	83.33
Ambispora sp.	+	+	-	+	+	+	-	+	+	+	+	+	-	+	+	-	+	+	14	77.78
Acaulospora mellea	-	+	+	+	+	-	+	+	+	+	+	+	-	+	-	+	+	-	13	72.22
Glomus australe	+	-	-	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	13	72.22
Acaulospora sp.*4*	-	+	+	+	-	-	+	+	+	+	+	+	-	+	-	+	+	-	12	66.67
Claroideoglomus etunicatum	+	+	-	+	+	+	+	-	-	-	+	+	+	-	-	+	+	+	12	66.67
Glomus sp.*2*	-	+	+	-	+	+	+	+	-	-	+	-	+	+	+	-	+	+	12	66.67
DIversispora epigea	-	-	+	+	+	-	-	+	+	-	-	+	+	+	+	-	+	+	11	61.11
Glomus occultum	+	-	+	+	-	+	+	+	-	-	-	+	+	+	+	+	-	-	11	61.11
Glomus sp.*1*	+	+	-	-	-	+	+	+	+	-	+	-	-	-	+	+	+	+	11	61.11
Glomus clarum	+	+	-	+	+	+	+	+	+	-	+	-	-	-	-	+	-	-	10	55.56
Acaulospora denticulate	-	+	-	+	+	-	+	-	+	-	+	+	-	+	-	-	+	-	9	50.00
Acaulospora sp.*7*	-	-	-	-	-	-	+	+	+	+	+	+	-	-	-	+	+	+	9	50.00
Claroideoglomus claroideum	+	-	+	-	+	-	-	+	-	+	-	+	-	+	+	+	-	-	9	50.00
Diversispora aurantium	-	-	-	+	+	+	-	-	+	-	+	+	-	-	-	+	+	+	9	50.00
Glomus pallidum	+	+	-	-	+	-	-	+	-	-	+	+	+	-	-	+	-	+	9	50.00
Scutellospora sp.	+	+	+	+	+	+	-	-	-	-	+	-	-	+	-	-	+	-	9	50.00
Gigaspora rosea	-	-	-	+	+	-	+	-	-	+	+	-	+	+	+	-	-	-	8	44.44
Glomus macrocarpum	+	+	-	+	-	+	+	+	-	-	-	-	-	-	-	+	+	-	8	44.44
Entrophospora sp.	+	+	-	-	-	+	-	-	-	+	+	+	-	-	+	-	-	-	7	38.89
Glomus warcuppi	-	-	+	-	-	-	+	+	+	-	-	+	+	-	-	-	+	-	7	38.89
Acaulospora foveata	+	-	-	-	-	-	+	+	-	-	+	-	-	+	-	-	-	+	6	33.33
Ambispora fennica	-	-	-	-	-	+	+	+	+	-	-	-	-	-	+	-	+	-	6	33.33
Gigaspora sp.	+	+	-	-	-	-	+	-	-	+	+	-	-	-	-	-	+	-	6	33.33
Glomus halonatum	+	-	-	-	-	+	-	+	-	-	-	-	+	+	-	+	-	-	6	33.33
Scutellospora calospora	+	+	-	-	+	-	+	+	-	-	-	-	-	-	-	+	-	-	6	33.33
Scutellospora dipurpurescrns	+	-	+	-	-	-	-	-	-	-	-	+	+	+	-	-	+	-	6	33.33
Glomus fasciculatum	-	+	+	-	+	-	-	-	-	+	-	-	-	-	+	-	-	-	5	27.78
Glomus multisubstensum	-	-	-	-	+	-	-	+	-	-	-	+	+	-	+	-	-	-	5	27.78
Acaulospora lacunosa	-	-	-	-	+	-	-	-	-	+	+	-	-	-	+	-	-	-	4	22.22
Acaulospora laevis	-	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	4	22.22
Archaeospora trappei	-	-	-	-	+	+	-	+	-	-	+	-	-	-	-	-	-	-	4	22.22
Glomus geosporum	+	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	+	-	4	22.22
Glomus intraradices	-	+	-	-	-	+	-	-	-	-	+	-	-	-	-	-	+	-	4	22.22
Pascispora sp.	+	-	+	-	+	-	-	-	-	+	-	-	-	-	-	-	-	-	4	22.22
Septoglomus constrictum	-	+	-	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	4	22.22
Unidentified species #36	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-	-	+	4	22.22
Unidentified species #43	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	+	4	22.22
Acaulospora sp.*3*	-	-	-	+	-	+	+	-	-	-	-	-	-	-	-	-	-	-	3	16.67
Acaulospora sp.*5*	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	+	-	3	16.67
Acaulospora tuberculata	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+	-	-	3	16.67
Funneliformis coronatum	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	-	-	-	3	16.67
Gigaspora albida	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	+	+	3	16.67
Glomus flavisporum	+	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	3	16.67
Glomus maculosum	+	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-	-	3	16.67
Scutellospora verrucosa	+	+	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	3	16.67
Unidentified species #5	-	+	-	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	3	16.67
Unidentified species #31	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	-	-	-	3	16.67
Acaulospora cavernata	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	+	-	2	11.11
Acaulospora sp.*8*	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	2	11.11
Acaulospora sp.*9*	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	2	11.11
Acaulospora spinosa	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	2	11.11
Diversispora celata	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	11.11
Glomus versiforme	+	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	2	11.11
Intraspora sp.	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	11.11
Sclerocystis taiwanensis	+	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #3	-	+	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #10	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #13	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-	-	-	-	2	11.11
Unidentified species #14	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #17	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #18	-	-	-	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #20	-	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-	-	-	2	11.11

Unidentified species #25	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #27	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #29	-	-	-	-	-	-	-	-	+	-	-	-	-	-	+	-	-	-	2	11.11
Unidentified species #30	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	2	11.11
Unidentified species #33	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	2	11.11
Unidentified species #35	-	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	2	11.11
Unidentified species #40	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	2	11.11
Unidentified species #42	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	2	11.11
Unidentified species #44	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	2	11.11
Acaulospora brasiliensis	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	1	5.56
Acaulospora gerdemanii	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	1	5.56
Acaulospora sp.*1*	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Acaulospora sp.*2*	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Acaulospora sp.*6*	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Acaulospora sp.*10*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	1	5.56
Archaeospora sp.	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	1	5.56
Glomus albidum	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Glomus hoi	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	1	5.56
Paraglomus albidum	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	1	5.56
Rhizophagus clarus	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	1	5.56
Sclerocystis pubescens	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	1	5.56
Sclerocystis sinuosa	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	1	5.56
Scutellospora arenicola	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #1	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #2	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #4	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #6	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #7	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #8	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #9	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #11	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #12	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #15	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #16	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #19	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #21	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #22	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #23	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #24	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #26	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #28	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #32	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	1	5.56
Unidentified species #34	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	1	5.56
Unidentified species #37	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	1	5.56
Unidentified species #38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	1	5.56
Unidentified species #39	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	1	5.56
Unidentified species #41	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	1	5.56
Unidentified species #45	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	1	5.56
Unidentified species #46	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	1	5.56
Unidentified species #47	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	1	5.56
Unidentified species #48	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	1	5.56

Note: P: Points established in the trail where soil samples were collected (i.e., P1, P2, P3, P4, P5, P6); S: Soil subsamples taken from each point (i.e., S1, S2, S3); *TC: Total Collection; **FOC: Total frequency of occurrence (%): Number of presence in 18 subsamples/Total number of subsamples (n=18); "+": indicates presence; "-": indicates absence

Overall, in terms of the frequency of occurrence of plant species documented, point 3 was recorded to have the highest (n = 12), while Point 4 had the lowest (n = 2). *S. macrophylla* was seen to be the most prevalent plant species for the first three points in the sampling site. On the other hand, the last three points were dominated by grass. There were five different plant species across all points in the trail that could only be documented but not identified.

Soil parameters, such as color and texture, within each point were also described. For points 1-3, the soil color observed was mainly light shades of gray and brown. Meanwhile, the soil in the latter points appeared to have darker brown tones to almost black. The soil texture among all points was observed to be dry. Only point 5 had a clayish texture, most likely as an attribute of the dried creek.

Discussion

Overall species diversity in the trail

The present study recorded a total of 114 AMF morphospecies in the rhizosphere soils of the UPV Nature Tail. They represent four orders, nine families, and 16 genera. Of these, 48 had never been described previously and had no resemblance with any other AMF species to our knowledge. As this was the first survey of AMF species conducted in the region and only about 327 AMF species have thus far been described worldwide in the Phylum Glomeromycota (CICG 2022), the reported number of unidentified species is not surprising. Whereas, the number of documented morphospecies in this study is relatively higher than those previously reported in other areas of the country. For instance, Soriano et al. (2021) had described only 13 AMF morphospecies in a rust-afflicted Moluccan albizia (*Falcataria moluccana*) stand in Laguna.

Out of the 2815 individual AMF spores recorded, the highest species richness (i.e., no. of species) was observed in *Acaulospora* and *Glomus* species, which represent the families Acaulosporaceae and Glomeraceae and the orders Diversisporales and Glomerales, respectively. A parallel result was reported by the earlier studies conducted in the Philippines (Aggangan et al. 2015; Soriano et al. 2021). The generally high abundance of these genera is associated with their tolerance to soil acidity (Tran et al. 2019), and ability for easy colonization (Shi et al. 2019), propagation, and habitat variability (Öpik et al. 2013). On the other hand, *Paraglomus* species were found rarest in the trail, similar to the findings of Rodríguez-Echeverría et al. (2017). This can be attributed to the fact that only two species in this genus, the only in the Paraglomeraceae family, have been discovered.

Biodiversity calculations through the Shannon-Weiner diversity index (H), Pielou evenness index (J), and Simpson diversity index (D) all reveal that the rhizosphere soils on the UPV Nature Trail host a highly diverse AMF community, as expected in a tropical region (Marinho et al. 2019). The Shannon-Weiner diversity index (H), which measures both species richness and evenness, ranges from 0 to Hmax and is interpreted as the higher the value the more diverse the species are in the habitat. Hence, the index obtained in the study (H=3.6019) signifies a high diversity of AMF species in the area. Notedly, it is higher than the usual range of indices, which is 1.5-3.5 (Ortiz-Burgos 2016) but is comparable to that of Shi et al. (2019), which reported a >2 diversity in two tropical forests of China. The Simpson diversity index calculated in the study (D=0.0420) also supports this result, as the values usually range from 0 to 1, with lower numbers indicating high diversity. In terms of the Pielou evenness index (J), with values ranging from 0 to 1 and 1 representing a community with perfect evenness, the overall value obtained in this study (J=0.7605) falls within the semi-balanced scale (Hussain et al. 2022). This suggests that each AMF species in the trail occurs in almost similar numbers.

Comparison of AMF spatial distribution

The recorded distribution of AMF morphospecies across the 18 rhizosphere subsamples of the six sampling points along the trail revealed that *Scutellospora pellucida* dominated the area with an 83.33% total frequency of occurrence (FOC). Meanwhile, several species recorded the lowest FOC of 5.56%, as they appeared in only one subsample. According to Pereira et al. (2014), the FOC may serve as a basis for delineating the adaptability of AMF species to different environmental and soil conditions. Similarly, Bonfim et al. (2016) proposed that dominance of AMF species in various environments indicates high plasticity and adaptability to various biotic and abiotic impacts. Therefore, *S. pellucida*, which was found in almost all subsamples (TC=15/18), along with other species present in all sampling points (*Acaulospora denticulate*, *Acaulospora mellea*, *Acaulospora* sp.4, *Ambispora* sp., *Claroideoglomus etunicatum, Diversispora epigea, Glomus occultum, Glomus pallidum, Glomus* sp.1, and *Glomus* sp.2), may be considered generalists or highly adaptable organisms.

Among the six sampling points established within the UPV Nature Trail, higher AMF species richness and abundance were recorded in points 1-3, which represent the forested areas of the trail, in comparison to points 4-6 from the non-forested locations (i.e., grassland, dried creek, and glade). Furthermore, the same trend was observed in terms of the diversity indices, indicating that the AMF community in the rhizosphere soils within the forest areas is more diverse and even than that of the non-forested. As the fungal community assemblage is typically correlated positively to greater plant diversity, one can presume that the diversity of AMF species is significantly greater in the forested portions of the trail compared to its open areas or grasslands. However, despite the difference in numbers observed among the location types, there was surprisingly no significant difference among the mean diversity indices of all points. In other words, since the results for all three diversity indices (H, J, D) were fairly similar, thus the occurrence of AMF communities is generally diverse and abundant regardless of their inhabited ecosystem type or location. This finding, however, may only be applicable to the study area as extensive sampling and further research are required to generalize the results.

Association of AMF and the local vegetation in the trail

As observed, there was higher species richness, abundance, evenness, and diversity of AMF spore morphospecies documented from the rhizosphere soils collected from the forested areas of the trail compared to that of the non-forested areas. Interestingly, the species richness of plants within the study site was also observed to be higher in the forested areas than in the open locations (i.e., grassland, dried creek, and glade). This finding corroborates the presumed positive correlation between AMF and plant diversity (Hiiesalu et al. 2014; Xu et al. 2016). The plant diversity hypothesis suggests that as the diversity of plants in an ecosystem increases, more soil microbial niches emerge, which increases the likelihood for soil microorganisms, such as AMF, to find a viable plant host (Ma et al. 2023). Similarly, the greater the diversity of AMF abundance and diversity, the more improved the ability of plants to absorb nutrients. As AMF facilitates

nutrient uptake, interspecific competition between plants is lowered, thereby enabling more species to coexist. Zhang et al. (2021) mentioned a previous comparative study wherein a higher AMF diversity and a significant reduction in phosphorus deficiency were recorded in macrocosms with a more diverse plant composition. These support the notion that plants and AMF foster mutual promotion. Surprisingly, however, a one-way ANOVA of the mean diversity indices reveals no significant difference in the diversity of AMF among the different points with different vegetation. Previous reports by Davison et al. (2015), Xu et al. (2017), and Ma et al. (2023) even showed that grasslands tend to have a higher AMF abundance and diversity, in contrast with the results of this study. According to Solís-Rodríguez et al. (2020), aside from vegetation, abiotic factors, such as the chemical properties of the soil at the time the samples were collected, also have a significant role in structuring AMF communities. Plant host-specificity may not always be the main contributor to AMF diversity (Melo et al. 2019; Xu et al. 2022).

Tropical ecosystems, including the UPV Nature Trail, are recognized as conservation hotspots of AMF, as they harbor 75% of the currently identified Glomeromycotan species (Błaszkowski and Chwat 2013; Sieverding et al. 2014; Marinho et al. 2018). Whether or not the relatively higher fungal diversity, abundance, and richness observed in forested areas were related to the relatively greater plant diversity remains unknown and must be further investigated. But in essence, several factors are considered to influence AMF distributions and diversity. This includes abiotic (e.g., soil physicochemical properties) and biotic (e.g., host plant) factors, and intrinsic properties of species (e.g., dispersal ability), as proposed by Chaudhary et al. (2018), and also species life histories (Solís-Rodríguez et al. 2020).

In conclusion, a total of 2815 Glomeromycotan spores were documented in the rhizosphere of the Nature Trail inside the University of the Philippines Visayas Campus in Miagao, Iloilo, Philippines, of which 114 morphospecies from 16 genera, nine families, and four orders were identified. Biological indices revealed that the diversity of AMF morphospecies across all the points was relatively high but had no significant differences. This suggests that AMF can be abundant in both forested and non-forested areas. Generally, this indicates that endomycorrhizal fungi possess widespread distribution, plasticity, and high adaptability regardless of their habitat. This study provides baseline information for the indigenous AMF morphospecies in the UPV Nature Trail, Miagao, Iloilo, Philippines. Additionally, this can lay the initial groundwork for further studies and extended research on AMF communities in the region and the country. Such development can lead to a more established directory of identified AMF morphospecies and their possible implications for overall ecosystem health.

ACKNOWLEDGEMENTS

Gratitude is expressed to the University of the Philippines Visayas-Office of the Vice Chancellor for Planning and Development (UPV-OVCPD), most especially to the Site Development and Reforestation Project (SDRP) and Physical Design Team for permission to conduct our study in the UPV Nature Trail, provision of site maps, and for ensuring our safety during the conduct of the study. We are also grateful for the assistance of the National Institute of Molecular Biology and Biotechnology-UPV (NIMBB-UPV) for offering us laboratory services. Quality images would not have been taken if not for the high-end photomicroscope lent by our esteemed professors from the Division of Biological Sciences—Dr. Resurrecion Sadaba and Dr. Eric Rizo.

REFERENCES

Aggangan N, Pampolina N, Cadiz N, Raymundo A. 2015. Assessment of plant diversity and associated mycorrhizal fungi in the mined-out sites of Atlas mines in Toledo City, Cebu for Bioremediation. J Environ Sci Manag 18: 71-86. DOI: 10.47125/jesam/2015_1/08.

Aggangan NS, Cortes AD. 2018. Screening mined-out indigenous mycorrhizal fungi for the rehabilitation of mine tailing areas in the Philippines: Rehabilitation of mine tailings. Reforesta 6: 71-85. DOI: 10.21750/REFOR.6.06.59.

Błaszkowski J, Chwat G. 2013. *Septoglomus deserticola* emended and new combinations in the emended definition of the family *Diversisporaceae*. Acta Mycol 48:89-103. DOI: 10.5586/am.2013.011.

Bonfim JA, Vasconcellos RL, Gumiere T, de Lourdes Colombo Mescolotti D, Oehl F, Nogueira Cardoso EJ. 2016. Diversity of arbuscular mycorrhizal fungi in a Brazilian Atlantic forest toposequence. Microb Ecol 71: 164-177. DOI: 10.1007/s00248-015-0661-0.

Chaudhary VB, Cuenca G, Johnson NC. 2018. Tropical-temperate comparison of landscape-scale arbuscular mycorrhizal fungal species distributions. Divers Distrib 24:116-128. DOI: 10.1111/ddi.12664.

Davison J, Moora M, Öpik M, Adholeya A, Ainsaar L, Bâ A, Burla S, Diedhiou AG, Hiiesalu I, Jairus T, Johnson NC. 2015. Global assessment of arbuscular mycorrhizal fungus diversity reveals very low endemism. Science 349: 970-973. DOI: 10.1126/science.aab11.

Fasusi OA, Amoo AE, Babalola OO. 2021. Propagation and characterization of viable arbuscular mycorrhizal fungal spores within maize plant (*Zea mays* L.). J Sci Food Agric 101: 5834-5841. DOI: 10.1002/jsfa.11235.

Hiiesalu I, Pärtel M, Davison J, Gerhold P, Metsis M, Moora M, Öpik M, Vasar M, Zobel M, Wilson SD. 2014. Species richness of arbuscular mycorrhizal fungi: Associations with grassland plant richness and biomass. New Phytol 203: 233-244. DOI: 10.1111/nph.12765.

Hussain NA, Ali AH, Lazem LF. 2022. Ecological indices of key biological groups in Southern Iraqi marshland during 2005-2007. Mesopotamian J Mar Sci 27: 112-125. DOI: 10.58629/mjms.v27i2.162.

CICG. 2022. International Culture Collection of Glomeromycota. https://sites.google.com/site/cicgfma/home.

International Sustainability Unit. 2015. Tropical Forests: A Review. Clarence Hall, London.

Islam M, Al-Hashimi A, Ayshasiddeka M, Ali H, El Enshasy HA, Dailin DJ, Sayyed RZ, Yeasmin T. 2022. Prevalence of mycorrhizae in host plants and rhizosphere soil: A biodiversity aspect. PLoS One 17 (3): e0266403. DOI: 10.1371/journal.pone.0266403.

Kamble VR, Lanjekar SS, Yadav YR, Kolekar MM, Chandore AN. 2018. A new record: Incidence of arbuscular mycorrhizal fungi (AMF) in *Eleocharis konkanensis* an endemic sedge of Maharashtra (India). Intl J Curr Microbiol Appl Sci 7 (05): 2243-2258. DOI: 10.20546/ijcmas.2018.705.261.

Liu HQ, Lu XB, Li ZH, Tian CY, Song J. 2021. The role of root-associated microbes in growth stimulation of plants under saline conditions. Land Degrad Dev 32: 3471-3486. DOI: 10.1002/ldr.3955.

Ma X, Xu X, Geng Q, Luo Y, Ju C, Li Q, Zhou Y. 2023. Global arbuscular mycorrhizal fungal diversity and abundance decreases with soil available phosphorus. Global Ecol Biogeogr 32: 1423- 1434. DOI: 10.1111/geb.13704.

Marinho F, da Silva IR, Oehl F, Maia LC. 2018. Checklist of arbuscular mycorrhizal fungi in tropical forests. Sydowia 70: 107-127. DOI: 10.12905/0380.sydowia70-2018-0107.

Marinho F, Oehl F, da Silva IR, Coyne D, da Nobrega Veras JS, Maia LC. 2019. High diversity of arbuscular mycorrhizal fungi in natural and anthropized sites of a Brazilian tropical dry forest (Caatinga). Fungal Ecol 40: 82-91. DOI: 10.1016/j.funeco.2018.11.014.

Melo CD, Walker C, Krüger C, Borges PA, Luna S, Mendonça D, Fonseca HM, Machado AC. 2019. Environmental factors driving arbuscular mycorrhizal fungal communities associated with endemic woody plant *Picconia azorica* on native forest of Azores. Ann Microbiol 69: 1309-1327. DOI: 10.1007/s13213-019-01535-x.

Öpik M, Zobel M, Cantero JJ, Davison J, Facelli JM, Hiiesalu I, Jairus T, Kalwij JM, Koorem K, Leal ME, Liira J. 2013. Global sampling of plant roots expands the described molecular diversity of arbuscular mycorrhizal fungi. Mycorrhiza 23: 411-430. DOI: 10.1007/s00572-013-0482-2.

Ortiz-Burgos S. 2016. Shannon-weaver diversity index. In: Kennish MJ (eds.). Encyclopedia of Estuaries. Dordrecht, The Netherlands. DOI: 10.1007/978-94-017-8801-4_233.

Pagano MC, Oehl F, Silva GA, Maia LC, Silva DK, Cabello MN. 2016. Advances in arbuscular mycorrhizal taxonomy. In: Pagano M (eds.). Recent Advances on Mycorrhizal Fungi. Fungal Biology. Springer, Cham. DOI: 10.1007/978-3-319-24355-9.

Pereira CM, da Silva DK, de Almeida Ferreira AC, Goto BT, Maia LC. 2014. Diversity of arbuscular mycorrhizal fungi in Atlantic forest areas under different land uses. Agric Ecosyst Environ 185: 245-252. DOI: 10.1016/j.agee.2014.01.005.

Roberts P, Hunt C, Arroyo-Kalin M, Evans D, Boivin N. 2017. The deep human prehistory of global tropical forests and its relevance for modern conservation. Diversity (Basel) 11 (10): 181. DOI: 10.3390/d11100181.

Rodríguez-Echeverría S, Teixeira H, Correia M, Timóteo S, Heleno R, Öpik M, Moora M. 2017. Arbuscular mycorrhizal fungi communities from tropical Africa reveal strong ecological structure. New Phytol 213: 380-390. DOI: 10.1111/nph.14122.

Shi Z, Yin K, Wang F, Mickan BS, Wang X, Zhou W, Li Y. 2019. Alterations of arbuscular mycorrhizal fungal diversity in soil with elevation in tropical forests of China. Diversity 11 (10): 181. DOI: 10.3390/d11100181.

Sieverding E, da Silva GA, Berndt R, Oehl F. 2014. *Rhizoglomus*, a new genus of the *Glomeraceae*. Mycotaxon 129: 373-386. DOI: 10.5248/129.373.

Solís-Rodríguez UR, Ramos-Zapata JA, Hernández-Cuevas L, Salinas-Peba L, Guadarrama P. 2020. Arbuscular mycorrhizal fungi diversity and distribution in tropical low flooding forest in Mexico. Mycol Prog 19: 195-204. DOI: 10.1007/s11557-019-01550-x.

Soriano JK, Manalo MM, Pampolina NM, Carandang WM. 2021. Diversity of Endomycorrhizas in *Falcataria moluccana* (Miq.) Barneby & J.W. Grimes affected by Gall Rust Disease in Laguna, Philippines. Philippine J Sci 150: 1779-1788. DOI: 10.56899/150.6b.14.

Souza T. 2015. Handbook of Arbuscular Mycorrhizal Fungi. Esperança, PB, Paraíba, Brazil. DOI: 10.1007/978-3-319-24850-9.

Tran BTT, Watts-Williams SJ, Cavagnaro TR. 2019. Impact of an arbuscular mycorrhizal fungus on the growth and nutrition of fifteen crop and pasture plant species. Funct Plant Biol 46: 732-742. DOI: 10.1071/FP18327.

Wijayawardene NN, Hyde KD, Al-Ani LK, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev DV, Saxena RK, Tokarev YS. 2020. Outline of Fungi and fungi-like taxa. Mycosphere 11: 1060-1456. DOI: 10.5943/mycosphere/11/1/8.

Xu T, Veresoglou SD, Chen Y, Rillig MC, Xiang D, Ondřej D, Hao Z, Liu L, Deng Y, Hu Y, Chen W. 2016. Plant community, geographic distance and abiotic factors play different roles in predicting AMF biogeography at the regional scale in northern China. Environ Microbiol Rep 8: 1048-1057. DOI: 10.1111/1758-2229.12485.

Xu M, Li X, Cai X, Li X, Christie P, Zhang J. 2017. Land use alters arbuscular mycorrhizal fungal communities and their potential role in carbon sequestration on the Tibetan Plateau. Sci Rep 7: 3067. DOI: 10.1038/s41598-017-03248-0.

Xu X, Chen C, Zhang Z, Sun Z, Chen Y, Jiang J, Shen Z. 2022. The influence of environmental factors on communities of arbuscular mycorrhizal fungi associated with *Chenopodium ambrosioides* revealed by MiSeq sequencing investigation. Sci Rep 7: 45134. DOI: 10.1038/srep45134.

Zhang J, Quan C, Ma L, Chu G, Liu Z, Tang X. 2021. Plant community and soil properties drive arbuscular mycorrhizal fungal diversity: A case study in tropical forests. Soil Ecol Lett 3 (1): 52-62. DOI: 10.1007/s42832-020-0049-z.