

Acta Botanica Hungarica 60(1–2), pp. 185–222, 2018
DOI: 10.1556/034.60.2018.1-2.9

ARBUSCULAR MYCORRHIZAL AND DARK SEPTATE ENDOPHYTE FUNGAL ASSOCIATIONS IN PLANTS OF DIFFERENT VEGETATION TYPES IN VELLIANGIRI HILLS OF WESTERN GHATS, SOUTHERN INDIA

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(Received 21 June, 2017; Accepted 16 August, 2017)

In recent years more attention is being paid to the presence of various non-pathogenic root fungal associations in plants of natural ecosystems for their role in various ecosystem processes. Despite their widespread reports in various ecosystems worldwide, our knowledge on root endophyte fungal association in plants from natural vegetation is far from complete. We assessed the arbuscular mycorrhizal (AM) and dark septate endophyte (DSE) fungal association in plants of Velliangiri Hills of the southern Western Ghats region, due to limited information on the root fungal association in this region. Of the 147 plant taxa (belonging to 46 families) investigated from five different vegetation types ranging from montane grasslands to tropical rainforest, 141 were colonised by AM fungi and co-occurrence of DSE fungi along with AM fungi was observed in 74 plant taxa. We report AM and DSE fungal associations for the first time in 61 and 42 plant species, respectively. Determination of AM morphological types indicated the frequent occurrence of intermediate type and AM morphology is reported for the first time in 64 plant taxa. Spore morphotypes belonging to eleven species (in six genera) were isolated from the different vegetation types. Arbuscular mycorrhizal fungal spore numbers neither differed significantly among vegetation types nor were related to AM fungal colonisation. Spores of *Funneliformis geosporum* was the most frequent spore morphotypes. Dark septate endophyte fungal association occurred in plants of all the vegetation types and was most frequent in herbs. Though no significant relationship was found between AM and DSE fungal colonisation within roots, a positive association was found in the occurrence of these two fungal groups.

Key words: AM fungi, *Arum*-type, DSE fungi, *Glomus*, intermediate type, *Paris*-type

INTRODUCTION

Arbuscular mycorrhizal (AM) fungi are the most common and widespread soil fungi associating with plant roots. Belonging to the phylum Glomeromycota, these fungi are presumed to associate with around 86% of the vascular plant taxa (Brundrett 2009). The AM fungal hyphal network in the soil plays an important role not only in initiating root colonisation, but also mediate nutrient uptake and their distribution among plants (Smith and Read 2008).

Thus, AM fungi create functional linkages between biotic and abiotic components of the soil system (Berruti *et al.* 2015), affecting ecosystem processes like plant growth and productivity, as well as the structure and diversity of natural plant communities (Yang *et al.* 2016). In spite of over a century of assessment of the mycorrhizal status of plant species from different ecosystems worldwide, only less than 10% of the vascular plants have been actually examined for their mycorrhizal status (Brundrett 2009). Even for the plant taxa whose mycorrhizal status is known, the data at times are inconsistent or conflicting due to various levels of misdiagnosis (Brundrett 2009). In addition, it is also essential to examine plant taxa over a range of environmental conditions and habitat types to ascertain factors that may possibly influence their mycorrhizal status.

Root colonisation patterns of AM fungi within plant roots are categorised as *Arum*-, *Paris*- or intermediate types based on the spread and location of the intraradical structures of the AM fungi (Dickson 2004). The colonisation pattern is termed *Arum*-type when the fungus spreads intercellularly with intracellular hyphae differentiating into arbuscules in root cortical cells. In the *Paris*-type AM morphology, the spread of the fungus is chiefly intracellular forming hyphal or arbusculate coils. The colonisation patterns sharing features of both *Arum*- and *Paris*-types are termed as intermediate types. Although root colonisation patterns have been reported for plants from different vegetation formations, these represent only a small percentage of plant taxa where mycorrhizal status have been investigated (Dickson *et al.* 2007). It has been suggested that *Arum*-type colonisation patterns predominate roots of plants with high root growth rates, while *Paris*-type colonisation patterns are formed by plants with slow growing and long lived roots (Brundrett *et al.* 1990, Dickson *et al.* 2007). Experimental evidence has shown substantial transport of phosphate to the plant host through the fungal interphase in the different types of AM morphologies (Dickson *et al.* 2007).

Arbuscular mycorrhizal fungal colonisation in plant roots are influenced by both the presence and density of AM fungal propagules. Even though, AM fungi can perennate through different types of propagules like soil hyphae and mycorrhizal roots, the major propagules of AM fungi are the spores (Berruti *et al.* 2015, Grilli *et al.* 2015). Spores are also used to determine AM fungal community composition in different ecosystems (Grilli *et al.* 2015). Only limited studies have examined the AM fungal community composition in tropical ecosystems (Öpik and Davison 2016). Such assessments included tropical vegetation in China (Yang *et al.* 2013, Yu *et al.* 2017, Zhang *et al.* 2004, Zhao *et al.* 2003), Panama (Mangan *et al.* 2004, Schappe *et al.* 2017), Brazil (da Silva *et al.* 2017, Sturmer and Siqueira 2006, Zangaro *et al.* 2007), Costa Rica (Lovelock *et al.* 2003, Picone 2000) and India (Devi *et al.* 2017, D'Souza and Rodrigues 2013, Kumar and Adholeya 2016, Muthukumar and Udaiyan 2000a, 2002, Muthukumar *et al.* 2006, Radhika and Rodrigues 2010, Ragupathy and Mahadevan 1993).

Plant roots in natural habitats are also frequently colonised by fungi with dematiaceous, septate hyphae forming microsclerotia or moniliform hyphae. These fungi are denoted as dark septate endophyte (DSE) fungi and often coexist with different mycorrhizal fungi (Mandyam and Jumpponen 2005, Newsham 2011). Although previous studies indicate a negative, neutral or positive influence of DSE fungi on plant performance, recent studies do indicate a positive effect of these fungi on plant growth and yield (Zhang *et al.* 2012). Mandyam and Jumpponen (2005) concluded that DSE fungi are prevalent in various habitats, but information on their prevalence in tropical ecosystems is scanty. Only limited studies (e.g. Muthukumar and Prabha 2013, Muthukumar *et al.* 2006, Rains *et al.* 2003, Uma *et al.* 2010) have examined the occurrence of DSE fungal association in tropical plant species.

Velliangiri Hills (long. 6° 40' to 7° 10' E and lat. 10° 55' to 11° 10' N) is a mountain range in the Nilgiri Biosphere Reserve of Western Ghats, Southern India. The mountain peaks vary in their altitudes from 520 to 1,800 m a. s. l. The mean annual rainfall is quite variable ranging from 500 to 7,000 mm. The average temperature ranges between 0 °C during winter and 41 °C during summer. The variability in altitudes and climatic conditions has resulted in different vegetation types ranging from grassland to tropical rainforest covering these hill ranges supporting a wide variety of flora and fauna (Murugesan and Balasubramanian 2008). The 48 km² hill range consists of around 1,715 species of angiosperms including 439 endemics (Murugesan 2005, see Ragupathy *et al.* 2008 and references there in). The vegetation in Velliangiri Hills is presently under immense threat as the result of various anthropogenic activities (Balasubramanian and Murugesan 2004, Ragupathy *et al.* 2008). A previous study has shown that AM and DSE fungal association occur in grasses of this region (Sathiyadash *et al.* 2010). Apart from that study, there is no information on root fungal associations in plants of Velliangiri Hills. So the aim of the present investigation was therefore to record the AM and DSE fungal association in plants of different vegetation types in Velliangiri Hills. We also assessed the extent of variation in fungal colonisation and AM fungal spore numbers across species, life-forms, and vegetation types. Further, we also isolated and identified spores of AM fungi in soil samples of the plant taxa investigated. The relationship between various fungal variables was also assessed.

MATERIALS AND METHODS

Sampling

The samples of roots and soils of 147 taxa (94 herbs, 19 shrubs, 15 under shrubs and 19 trees) were collected from five different vegetation types southern tropical thorn forest (ST), tropical moist deciduous forest (TM), tropical wet

evergreen forest (TW), shola forest (SH) and southern montane humid grassland (SM) in June 2009 (Table 1). More details on the vegetation types have been provided by Murugesan (2005) and Murugesan and Balasubramaniam (2008). Three plants were sampled for each taxon. Herbs were usually dug out and roots for shrubs and trees were traced back to the stem. Roots were washed clear of soil and preserved in formalin, acetic acid and 70% alcohol (5:5:90; v/v/v) solution and transported to the laboratory for processing. Soil shaken from roots and adjacent to plant roots was collected; air dried and packed individually in polythene bags. One-half of these soil samples were used for the enumeration and isolation of AM fungal spores. The other half of the soil sample from all the plants of a vegetation type was bulked to form a composite soil sample. This composite soil sample was used for determining soil characters.

Determination of soil characters

The air dried composite soil samples were sieved (2 mm grid) and three subsamples of the composite sample were analysed for the following characters. Soil pH and EC was determined in 1:2.5, soil:water (v/v) solution after incubation for 20 min, with digital pH and conductivity meters, respectively, soon after the soil samples were brought to the laboratory (Jones 2001). Total nitrogen (N), was determined using the micro-Kjeldahl method, available phosphorus (P) was determined with the method by Bray and Kurtz (1945) and exchangeable potassium (K) was measured with a digital flame photometer after extraction in an ammonium acetate solution (Jackson 1971).

Table 1

Soil characteristics (mean±standard error) and the number of plant taxa examined from the different vegetation types of Velliangiri Hills.

Soil type	Vegetation types [#]				
	ST	TM	TW	SH	SM
	Sandy soil	Sandy soil	Sandy clay loam	Sandy clay soil	Clay soil
pH	7.40±0.09	7.90±0.09	7.10±0.10	7.97±0.11	7.42±0.07
Ec (dSm ⁻¹)	0.10±0.01	0.60±0.02	0.60±0.01	0.69±0.22	0.80±0.05
Nitrogen (mg/kg)	7.60±0.24	7.70±0.21	7.30±0.13	10.80±0.38	16.20±0.36
Phosphorus (mg/kg)	0.84±0.03	0.62±0.02	0.74±0.04	0.13±0.01	0.60±0.02
Potassium (mg/kg)	24.00±1.41	22.00±1.00	23.00±0.84	17.40±0.41	16.20±0.36
No. of taxa examined	34	39	42	06	26

[#]ST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest; SH = shola forest; SM = southern montane humid grassland

Preparation of roots for AM and DSE fungal assessment

The root samples were washed free of FAA, cut into 1-cm pieces, cleared in 2.5% KOH (Koske and Gemma 1989), acidified with 5 N HCl and stained with trypan blue (0.05% in lacto glycerol) overnight. Roots that remained dark after clearing were bleached using alkaline H₂O₂ prior to acidification. Ten to thirty stained root bits were examined for each plant with a compound microscope (×400) for the presence of AM and DSE fungal structures. The percentage root length colonised by AM and DSE fungi and the root length containing different fungal structures were estimated according to the magnified intersection method (McGonigle *et al.* 1990). Ten intersection points were scored for each root bit. Only root specimens containing arbuscules/arbusculate coils were considered to be mycorrhizal. Melanised hyphae with regular septation and microsclerotia were used to designate DSE fungal association. The AM and DSE fungal status of plant species in the present study were compared to previous literature (Harley and Harley 1987, Wang and Qiu 2006) to assess the information on their endorhizal status.

Determination of AM fungal morphology

The AM-morphology was classified as *Arum*-, *Paris*- or intermediate types based on whether the fungal hyphae were passing through the intercellular spaces or within cells as coils, respectively, following the descriptions of Dickson (2004). We did not distinguish the intermediate subtype morphologies described by Dickson (2004) as only the whole and squashed roots were examined. However, when the parallel running hyphae were intracellular, the morphology was designated as intermediate type. The AM morphological types of the plant species was compared to those presented by Dickson *et al.* (2007).

Isolation, enumeration, and identification of AM fungal spores

Spores of AM fungi were recovered from 100 g soil samples by wet-sieving and decanting technique (Muthukumar *et al.* 1996). The residues from the sieves (710 and 37 µm) were collected over filter papers, spread on a Petri dish and viewed under a dissection microscope at ×40 magnifications. Only intact spores were counted. For enumeration, spore clusters and sporocarps were considered as one unit. Permanent slides of AM fungal spores for identification were prepared by transferring all the intact AM fungal spores onto a glass slide containing polyvinyl-alcohol-lacto glycerol with or without Melzer's reagent (Schenck and Perez 1990). Spores were cracked open for observation of spore wall characters. Spore characters were compared with the original descriptions present in databases established by the Schüßler laboratory (<http://>

www.amf-phylogeny.com/) and cultural database of INVAM (<http://www.invam.caf.wvu.edu>). Arbuscular mycorrhizal fungal nomenclature is that of Schüßler and Walker (2010). The frequency of each AM fungal spore morphotype was calculated as the number of plant taxa in which spore of a particular morphotype occurred by the total number of plant taxa examined $\times 100$.

Life-history attributes and plant nomenclature

Each plant taxon sampled during the survey was categorised for its life-form and life-cycle attributes as determined directly from the field observations or literature (Henry *et al.* 1987, 1989, Nair and Henry 1983, Prain 1981*a, b*, Toby and Hodd 1982). Plant nomenclature and authorities are as The Plant List (2013).

Statistical analysis

The data on soil characteristics were subjected to Analysis of Variance (ANOVA) and the means were separated using Duncan's Multiple Range Test (DMRT). Percentage frequency of occurrence of different fungal association in different habit was calculated using the formula: Number of taxa in a habit with specific fungal association/total number of taxa in the habit examined $\times 100$. Data on fungal colonisation and AM fungal spore numbers were analysed using Kruskal–Wallis non-parametric analysis to assess the significance of the variation among plant species and vegetation types. The relationship between various AM and DSE fungal variables were analysed by Pearson's correlation. We also used the probabilistic co-occurrence model using R package co-occur available on Comprehensive R Archive Network (<https://CRAN.R-project.org/package=cooccur>) to assess the nature of association (positive, negative or random) between AM and DSE fungi as well as the AM fungal species associated with different plant species (Griffith *et al.* 2016).

RESULTS

Soil properties

Soils of different vegetation types in Velliangiri Hills were sandy to sandy clay loam. All soils were near neutral to slightly alkaline and the pH significantly varied among the vegetation types ($F_{4,24} = 15.425$; $P < 0.001$). The EC significantly differed among the vegetation types ($F_{4,24} = 6.866$; $P < 0.001$), and ranged between 0.10 dSm^{-1} and 0.80 dSm^{-1} . The N ($F_{4,24} = 182.069$), P ($F_{4,24} = 109.062$) and K ($F_{4,24} = 15.276$) contents of the soils significantly ($P < 0.001$) varied among the vegetation types and ranged from 7.6 to 16.2 mg/kg , 0.13 to 0.84 mg/kg , and 16.2 to 24 mg/kg , respectively.

Occurrence of AM and DSE fungi in various vegetation types

One hundred and forty-one of the 147 plant taxa (46 families) examined from the different vegetation types had AM fungal structures in their roots (Table 2). Plants roots belonging to non-mycorrhizal families like Com-

Table 2

Life history attributes, arbuscular mycorrhizal, dark septate endophytic fungal association and colonisation morphology in angiosperms of Velliangiri Hills. Abbreviation: Vegetation type = VT, Habit = Ht, Fungal association = Fa, AM type = At, Plant status = Ps

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
Acanthaceae					
<i>Andrographis lineata</i> Nees	SM	H	AM*	I*	
<i>Justicia beddomei</i> (C. B. Clarke) Bennet	ST	S	AM*, DSE*	I*	
<i>Justicia tranquebariensis</i> L.	ST	US	AM*, DSE*	A*	
<i>Nilgiranthus asper</i> Santapau	SH	S	AM*, DSE*	I*	
<i>Pleocaulus sessilis</i> (Nees) Bremek.	SH	H	AM*	A*	
<i>Rostellularia japonica</i> (Thunb.) J. L. Ellis	TW	H	AM*	A*	
<i>Rungia apiculata</i> Bedd.	TW	US	AM*, DSE*	P*	
<i>Rungia latior</i> Nees	TW	H	AM*	I*	
<i>Strobilanthes asperrimus</i> Nees	SM	S	AM*, DSE*	I*	
<i>Strobilanthes</i> sp.	SM	H	AM, DSE	A	
Agavaceae					
<i>Sansevieria roxburghiana</i> Schult. et Schult. f.	ST	S	AM, DSE	I	EI
Anacardiaceae					
<i>Mangifera indica</i> L.	ST	T	AM, DSE	P	EI
Annonaceae					
<i>Goniothalamus</i> sp.	TW	H	AM	I	
Araceae					
<i>Arisaema leschenaultii</i> Blume Rumph.	TW	H	AM	A	
<i>Arisaema tortuosum</i> (Wall.) Schott.	TW	H	AM	I	
Asclepiadaceae					
<i>Cynanchum callialatum</i> Buch.-Ham. ex Wight	TW	S	AM	I	
Asteraceae					
<i>Acmella paniculata</i> (Wall. ex DC.) R. K. Jansen	TW	H	AM, DSE*	A	EI
<i>Ageratum houstonianum</i> Mill.	TW	H	AM*, DSE*	A*	
<i>Anaphalis beddomei</i> Hook. f.	TW	US	AM*	I*	
<i>Anaphalis brevifolia</i> DC.	TW	H	AM*, DSE*	I*	
<i>Anaphalis busua</i> (Buch.-Ham.) DC.	TW	H	AM*, DSE	I*	

Table 2 (continued)

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
<i>Anaphalis elliptica</i> (DC.) DC.	TW	H	AM*	A*	
<i>Anaphalis lawii</i> (Hook. f.) Gamble.	TW	H	AM*	I*	
<i>Bidens biternata</i> (Lour.) Murr. et Sherff.	TM	H	AM*, DSE*	A*	
<i>Bidens pilosa</i> L.	TM	H	AM*, DSE*	I*	
<i>Bidens</i> sp.	TM	H	AM, DSE	I	
<i>Chromolaena odorata</i> (L.) R. M. King et H. Rob.	ST	S	AM*	A*	
<i>Conyza japonica</i> (Thunb.) Less. ex Less.	TW	H	AM*, DSE*	I*	
<i>Conyza leucantha</i> (D. Don) Ludlow et P. H. Raven	TM	H	AM *	A*	
<i>Emilia scabra</i> DC.	SH	H	AM*	A*	
<i>Emilia</i> sp.	SH	H	AM	A	
<i>Erigeron aegypticus</i> L.	TM	H	AM*	A*	
<i>Erigeron bonariensis</i> L.	TM	H	AM*, DSE*	I*	
<i>Erigeron trilobus</i> (Decne.) Boiss.	TM	H	AM*, DSE*	A*	
<i>Helichrysum</i> sp.	SM	H	AM, DSE	I	
Balsaminaceae					
<i>Impatiens jerdoniae</i> Wight	TW	T	NM	–	
<i>Impatiens minor</i> (DC.) Bennet	TW	H	AM*	I*	
Boraginaceae					
<i>Cynoglossum zeylanicum</i> (Vahl) Brand	TM	H	AM*, DSE*	A*	
Caesalpinaceae					
<i>Cassia</i> sp.	ST	US	AM	A	
Capparaceae					
<i>Crataeva magna</i> (Lour.) DC.	ST	T	AM, DSE*	A*	EI
Cannabaceae					
<i>Cannabis sativa</i> L.	SM	H	AM*	I*	EI
Commelinaceae					
<i>Commelina imberbis</i> Ehrenb. ex Hassk.	SM	H	AM*	I*	
<i>Commelina</i> sp.	SM	H	AM	A	
Cruciferae					
<i>Brassica juncea</i> (L.) Czern.	TW	H	NM	–	EI
Cucurbitaceae					
<i>Cucumis prophaterum</i> L.	ST	H	AM*, DSE*	I*	
<i>Gynostemma pentaphyllum</i> (Thunb.) Makino	TM	H	AM*	I*	
<i>Gynura</i> sp.	TM	H	AM, DSE	I	

Table 2 (continued)

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
<i>Mukia leiosperma</i> (Wight et Arn.) Wight	ST	H	AM*, DSE*	I*	
<i>Zehneria maysorensis</i> (Wight et Arn.) Arn.	TW	H	AM*, DSE*	A*	RA
<i>Zehneria scabra</i> Sond.	TW	H	NM	–	EI
Cyperaceae					
<i>Cyperus cyperinus</i> (Retz.) Suringar	SM	H	AM	I	
<i>Cyperus rotundus</i> L.	SM	H	NM	–	EI
<i>Cyperus</i> sp.	SM	H	AM	I	
<i>Fimbristylis falcata</i> (Vahl) Kunth	SM	H	AM, DSE*	A	
<i>Fimbristylis ovata</i> (Burm. f.) J. Kern	SM	H	AM, DSE*	I	
<i>Fimbristylis strigosa</i> Govind.	SM	H	AM, DSE*	I*	
Dioscoreaceae					
<i>Dioscorea oppositifolia</i> L.	ST	H	AM*	A*	
<i>Dioscorea tomentosa</i> J. Koenig ex Spreng.	ST	H	AM	I	
Eriocaulaceae					
<i>Eriocaulon</i> sp.	SM	H	AM, DSE	A	
Euphorbiaceae					
<i>Acalypha racemosa</i> Wall. ex Baill.	ST	US	AM*, DSE*	A*	EI
<i>Breynia retusa</i> (Dennst.) Alston.	TM	H	AM*	I*	EI
<i>Bridelia retusa</i> (L.) A. Juss.	TM	T	AM	I	EI
<i>Bridelia stipularis</i> (L.) Blume	TM	S	AM, DSE	I	
<i>Euphorbia indica</i> Lam.	TM	H	AM*	A*	EI
<i>Euphorbia tortilis</i> Rottler ex Ainslie	TM	H	AM*	I*	
<i>Flueggea leucopyrus</i> Willd.	TM	S	AM	I	
<i>Glochidion heyneanum</i> (Wight et Arn.) Wight.	TW	T	AM, DSE	I	
<i>Mallotus philippensis</i> (Lam.) Müll. Arg.	TM	T	AM, DSE	I	EI
<i>Mallotus tetracoccus</i> (Roxb.) Kurz	TM	T	AM, DSE	I	
<i>Phyllanthus emblica</i> L.	TM	T	AM	A*	
<i>Phyllanthus maderaspatensis</i> L.	ST	H	AM*	A*	
<i>Phyllanthus missionis</i> Hook. f.	ST	US	AM	A	
<i>Phyllanthus reticulatus</i> Poir.	ST	S	AM*, DSE*	A*	
<i>Phyllanthus urinaria</i> L.	TM	H	AM	I	
Gentianaceae					
<i>Exacum</i> sp.	SM	H	AM	P	
<i>Swertia</i> sp.	SM	H	AM	P	

Table 2 (continued)

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
Haloragaceae					
<i>Laurembergia coccinea</i> Kanitz	TW	H	AM*	I*	
Juncaceae					
<i>Juncus prismatocarpus</i> R. Br.	SM	H	AM*, DSE*	I*	
Labiatae					
<i>Leucas marrubioides</i> Desf.	TW	H	AM*	A*	
<i>Leucas rosmarinifolia</i> Benth.	TW	S	AM*, DSE*	I*	
<i>Leucas</i> sp.	TW	S	AM, DSE	A	
<i>Orthosiphon pallidus</i> Royle ex Benth.	ST	US	AM*	I*	
<i>Orthosiphon rubicundus</i> (D. Don) Benth.	ST	H	AM*, DSE*	I*	EI
<i>Orthosiphon</i> sp.	ST	H	AM, DSE	A	
<i>Pogostemon</i> sp.	SH	H	AM, DSE	I	
<i>Scutellaria</i> sp.	TW	H	AM, DSE	I	
Lauraceae					
<i>Neolitsea scrobiculata</i> Gamble	TW	T	AM	I	
Liliaceae					
<i>Asparagus racemosus</i> Willd.	TM	H	AM	A	
<i>Urginea indica</i> (Roxb.) Kunth.	TM	H	AM	A	
Malvaceae					
<i>Urena lobata</i> L.	ST	US	AM*	I*	EI
<i>Urena</i> sp.	ST	H	AM	A	
Mimosaceae					
<i>Albizia</i> sp.	TM	T	AM, DSE	I	
<i>Pithecellobium dulce</i> (Roxb.) Benth.	TM	T	AM, DSE	I	
Oleaceae					
<i>Jasminum ritchiei</i> C. B. Clarke	TM	S	AM	A	
Oxalidaceae					
<i>Biophytum longipedunculatum</i> Govind.	TW	H	AM*, DSE*	A	
<i>Biophytum sensitivum</i> (L.) DC.	TW	H	AM, DSE*	A	
<i>Oxalis corniculata</i> L.	TW	H	AM, DSE	I	
Papilionaceae					
<i>Crotalaria clavata</i> Wight et Arn.	ST	S	AM	I	
<i>Crotalaria</i> sp.	ST	US	AM	I	
<i>Crotalaria verrucosa</i> L.	ST	H	AM, DSE*	A*	

Table 2 (continued)

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
<i>Pterocarpus marsupium</i> Roxb.	ST	T	AM	I	
<i>Vigna unguiculata</i> (L.) Walp.	ST	H	AM, DSE*	A	EI
Plantaginaceae					
<i>Plantago erosa</i> Wall.	TM	H	AM, DSE*	A	
<i>Plantago</i> sp.	TM	H	AM, DSE	A	
Poaceae					
<i>Arundinella</i> sp.	SM	H	AM	I	
<i>Brachiaria</i> sp.	SM	H	AM, DSE	I	
<i>Cymbopogon citratus</i> (DC.) Stapf	TW	H	AM, DSE	I	EI
<i>Cyrtococcum</i> sp.	TW	H	AM	I	
<i>Eleusine indica</i> (L.) Gaertn.	TW	H	AM	P	
<i>Heteropogon contortus</i> (L.) P Beauv. ex Roem. et Schultes	TW	H	AM, DSE*	I	
<i>Ischaemum</i> sp.	TW	H	AM, DSE	A	
<i>Jansenella griffithiana</i> (C. Muell) Bor.	SM	H	AM*, DSE*	P*	
<i>Panicum notatum</i> Retz.	SM	H	AM*	A*	
<i>Panicum sparsicomum</i> Nees ex Steud.	SM	H	AM*, DSE*	I*	RA
<i>Polytrias indica</i> (Houtt.) Veldkamp.	TW	H	AM	I	
<i>Tripogon</i> sp.	SM	H	NM	–	
Polygalaceae					
<i>Polygala</i> sp.	SM	H	AM, DSE	I	
Polygonaceae					
<i>Persicaria barbata</i> (L.) H. Hara	SM	H	AM*	I*	EI
<i>Persicaria chinense</i> (L.) H. Gross.	TW	US	AM*, DSE*	I*	EI
<i>Persicaria lanigerum</i> (R. Br.) Sojak.	TW	H	AM*	A	
Rhamnaceae					
<i>Ziziphus rugosa</i> Lam.	TM	T	AM*, DSE*	I*	EI
Rosaceae					
<i>Rubus ellipticus</i> Sm.	TW	S	AM*	A*	EI, B
Rubiaceae					
<i>Canthium rheedii</i> DC.	SH	H	AM*	A*	
<i>Canthium travancoricum</i> Bedd.	TW	T	AM	I	
<i>Catunaregam spinosa</i> (Thunb.) Triveng.	TW	T	AM, DSE	I	
<i>Knoxia sumatrensis</i> (Retz.) DC.	SM	H	AM	I	

Table 2 (continued)

Family/Plant species	VT ^a	Ht ^b	Fa ^c	At ^d	Ps ^e
<i>Psyrdrax dicoccos</i> Gaertn.	TW	T	AM	P	RA
Rutaceae					
<i>Clausena heptaphylla</i> (Roxb.) Wight et Arn.	TM	S	NM	–	
<i>Glycosmis</i> sp.	TM	S	AM	I	
<i>Toddalia asiatica</i> (L.) Lam.	TM	S	AM, DSE	A	
Sapindaceae					
<i>Dimocarpus longan</i> Lour.	TM	T	AM	A	EI
<i>Filicium decipiens</i> (Wight et Arn.) Thwaites	TM	T	AM, DSE	I	EI
Scrophulariaceae					
<i>Scoparia dulcis</i> L.	TM	US	AM*	I*	
<i>Torenia hirsuta</i> Willd.	TM	H	AM*, DSE*	I*	
Solanaceae					
<i>Solanum americanum</i> Mill.	ST	H	AM	A	EI
<i>Solanum ferox</i> L.	ST	H	AM*, DSE*	I*	
<i>Solanum grandiflorum</i> Ruiz et Pav.	ST	US	AM*	I*	
<i>Solanum trilobatum</i> L.	ST	US	AM*, DSE*	I*	EI
<i>Solanum viarum</i> Dunal	ST	US	AM*	I*	EI
Thunbergiaceae					
<i>Thunbergia fragrans</i> Roxb.	ST	H	AM, DSE*	I	
<i>Thunbergia</i> sp.	ST	H	AM, DSE	I	
Umbelliferae					
<i>Polyzygus tuberosus</i> Walp.	TM	H	AM, DSE*	I	
Urticaceae					
<i>Pouzolzia</i> sp.	TM	US	AM, DSE	I	
Verbenaceae					
<i>Lantana camara</i> L.	ST	S	AM, DSE*	A	EI
<i>Tectona grandis</i> L.	ST	T	AM, DSE	I	
Vitaceae					
<i>Cayratia auriculata</i> (Roxb.) Gamble	TM	H	AM, DSE	I	
<i>Tetrastigma</i> sp.	TM	S	AM, DSE	I	

^aST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest; SH = shola forest; SM = southern montane humid grassland; ^bH = herb; S = shrub; US = under shrub; T = tree; ^cAM = arbuscular mycorrhizal; DSE = dark septate endophyte; NM = non-mycorrhizal; ^dA = *Arum*-type; P = *Paris*-type; I = intermediate type; ^eEI = economically important; B = species useful in plant breeding; RA = rare; * = first report

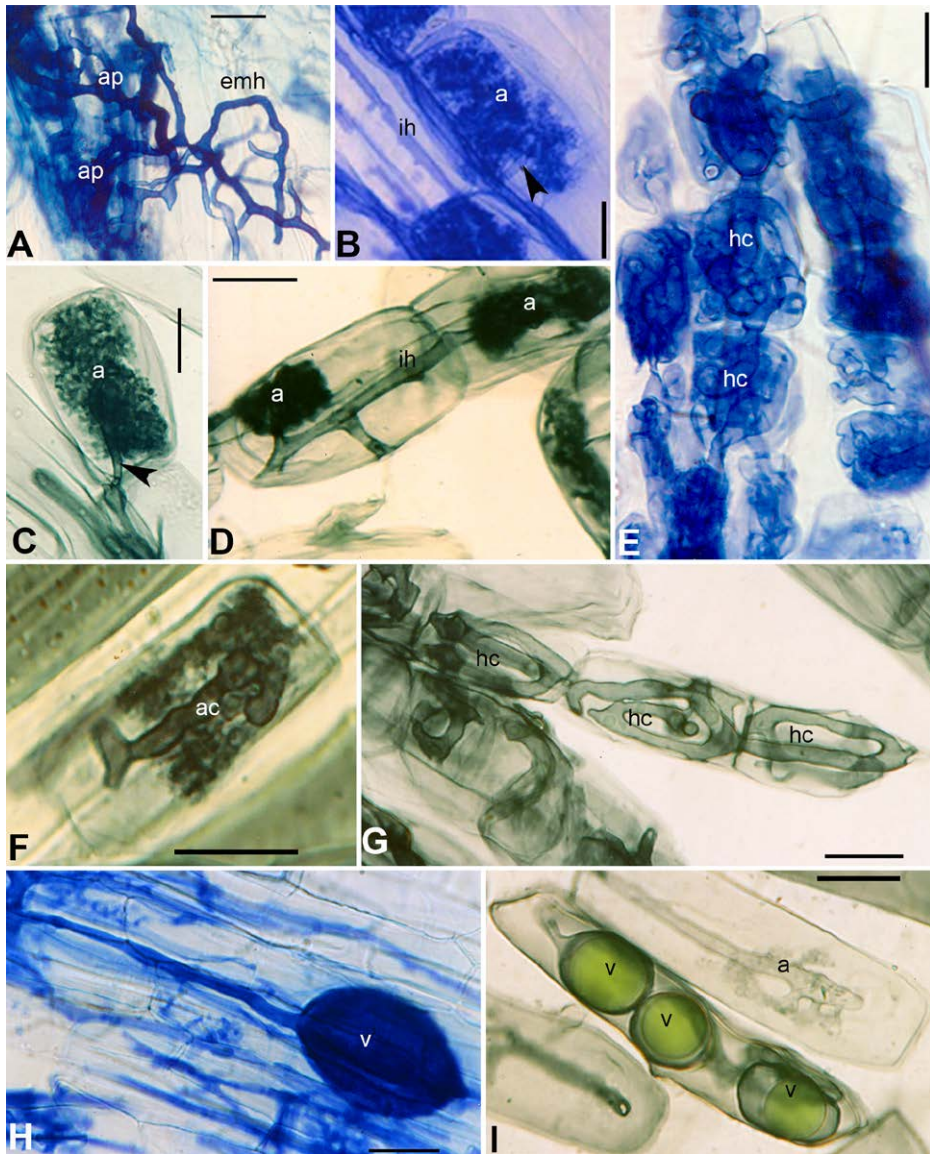


Fig. 1. Arbuscular mycorrhizal (AM) fungal association and morphology in plants of Velliangiri Hills. A = Extraradical hyphae (emh) and appressoria (ap) on the root surface of *Scutellaria* sp.; B = intracellular linear hyphae (ih), arbuscule (a) and arbuscular trunk (arrow head) in *Phyllanthus emblica*; C = arbuscular trunk (arrow head) and arbuscule (a) in *Brachiaria* sp.; D = intracellular linear hyphae (ih) and arbuscule (a) in *Panicum notatum*; E = intracellular hyphal coils (hc) in *Swertia* sp.; F = arbusculate coils (ac) in *Polygala* sp.; G = intracellular hyphal coils (hc) in *Orthosiphon* sp.; H = intercellular vesicle (v) in *Nilgirianthus asper*; I = intracellular vesicles (v) and arbuscule (a) in *Polygala* sp. Scale bars: 50 µm

melinaceae, Cyperaceae, Capparaceae and Juncaceae had AM fungal structures. The entry of AM fungi into roots was characterised by an appressorium on the root surface (Fig. 1A). The AM fungal structures within roots included arbuscules, intra- and intercellular hyphae, hyphal and arbusculate coils and inter or intracellular vesicles (Fig. 1B–C). Non-mycotrophy was low (4%, 6/147) and occurred in plant species of SM, TM, and TW. All the plant species examined from the ST were mycorrhizal. Ninety-two percent (24/26) of the plant species in SM, 97% (38/39) from the TM and 93% (39/42) from TW were mycorrhizal (Fig. 3).

Melanised, regularly septate hyphae, and microsclerotia characterised DSE fungal associations (Fig. 2A–D) and were found in 74 plant roots examined from different vegetation types. DSE fungal association was more frequent (62%) in southern tropical thorn forests compared to other forest types (Table 2 and Fig. 3). Plant species in six of nine monocot families and 26 of 37 dicot families had DSE fungal association. All the plants possessing DSE fungal association also harboured AM fungi. Further, 88% of the economically impor-

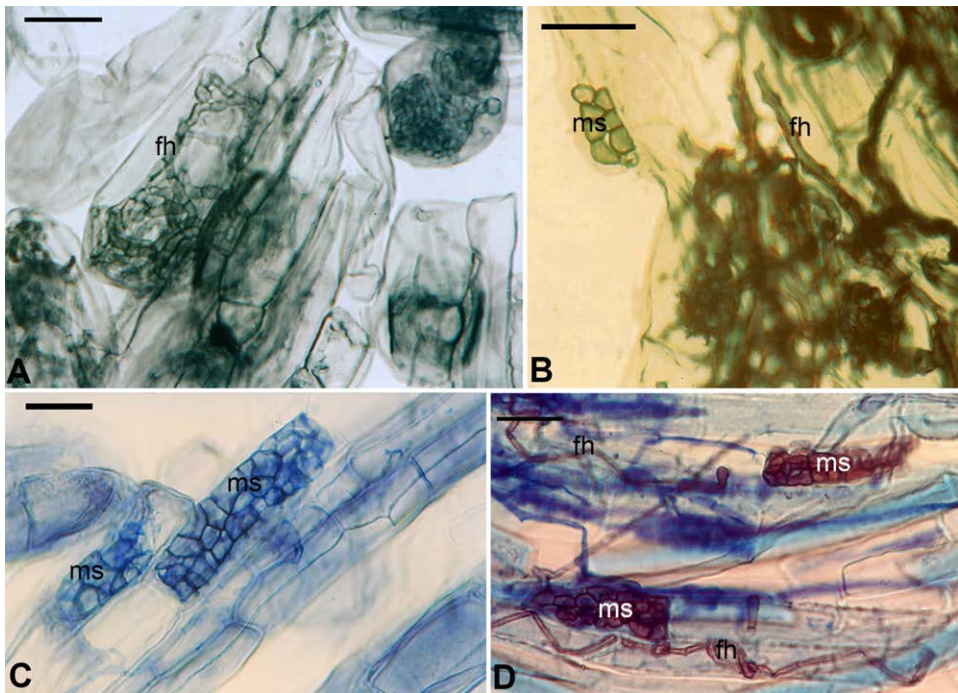


Fig. 2. Dark septate endophyte (DSE) fungal association in angiosperms of Velliangiri Hills. A = Dark septate intracellular fungal hyphae (fh) in *Scutellaria* sp.; B = septate fungal hyphae (fh) and microsclerotia (ms) in *Torenia* sp.; C = microsclerotia (ms) in *Nilgirianthus asper*; D = septate fungal hyphae (fh) and microsclerotia (ms) in *Brachiaria* sp. Scale bars: 50 μ m

tant plant species had AM and 30% had DSE fungal association. Of the three rare plant species examined in the present study, *Zehneria maysorensis* (Cucurbitaceae) and *Panicum sparsicomum* (Poaceae) had dual colonisation of AM and DSE and *Psydrax dicoccos* (Rubiaceae) was colonised only by AM fungi.

AM and DSE fungal association in plant life-forms in different vegetation types

All the herbs examined from ST and TM were mycorrhizal. Ninety-two percent of the herbs in the SM and 93% of herbs in the TW were mycorrhizal. All shrubs examined from the ST, TW, SM and 86% of those examined from the TM were colonised by AM fungi. All the under shrubs examined from three forests such as ST, TM, and TW had AM fungal associations. Similarly, all the trees in the ST, TM forests and 83% of tree species in the TW had AM fungal associations (Table 2 and Fig. 3).

Herbs were frequently colonised by DSE fungi in all the vegetation types. Thirty-eight percent of the herbs in the SM, 90% of herbs in the ST, 57% in the TM and 46% in TW had DSE fungal associations. Thirty percent of the under shrubs in the ST and 50% in the TM had DSE fungal association. Seventy-five percent of trees from the ST, 67% from the TM and 17% from the TW are colonised by AM fungi respectively (Table 2 and Fig. 3).

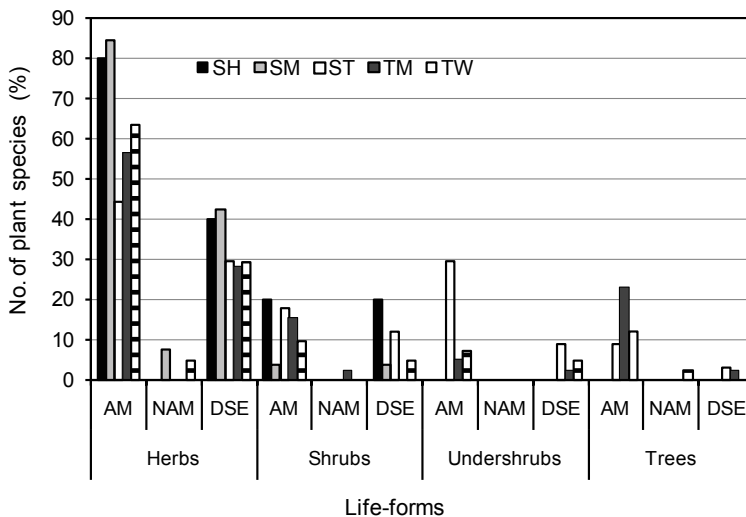


Fig. 3. The occurrence of arbuscular mycorrhizal (AM), non-mycorrhizal (NAM) and dark septate endophyte (DSE) fungal association in plants of various vegetation types and life-forms in Velliangiri Hills. SH = Shola forest; SM = southern montane humid grassland; ST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest

AM fungal morphology in different vegetation types

Intermediate type AM morphology was frequent in plant species examined from different vegetation types (Table 2 and Fig. 4). The *Paris*-type AM morphology was maximum (13%) in plants from the SM and minimum (2.94%) in plants from the ST (Fig. 4). In general, intermediate type AM was more frequent (57%) than the typical *Arum*- and *Paris*-types (34% to 5%) in different vegetation types (Table 2).

Extent of AM and DSE fungal association

Total root length colonisation (%RLTC) ranged between 14.78% (*Plantago erosa*, Plantaginaceae) and 82.95% (*Neolitsea scrobiculata*, Lauraceae) and was significantly different between plant taxa ($X^2_{146} = 203.617$; $P < 0.01$). The percentage root length with hyphae (%RLH) ranged between $< 1\%$ (*Emilia scabra*, Asteraceae) and 46.91% (*Panicum sparsicomum*, Poaceae), hyphal coils (%RLHC) ranged between 1.94% (*Solanum grandiflorum*, Solanaceae) and 70.49% (*Exacum* sp., Gentianaceae), arbuscules / arbusculate coils (%RLA/AC) ranged between $< 1\%$ (*Persicaria barbata*, Polygonaceae) and 54.29% (*Bridelia stipularis*, Euphorbiaceae), vesicles (%RLV) ranged between < 1 (*Emilia* sp., Asteraceae) and 21.52% (*Helichrysum* sp., Asteraceae) (Table 3 and Fig. 1). Significant differences ($P < 0.01$) existed between species for AM fungal variables such as %RLH ($X^2_{146} = 193.471$), %RLV ($X^2_{146} = 197.152$), %RLA ($X^2_{146} = 192.847$), and %RLHC ($X^2_{146} = 202.510$). In contrast, the differences for plant species among different forest types for %RLH ($X^2_4 = 1.785$), %RLV ($X^2_4 =$

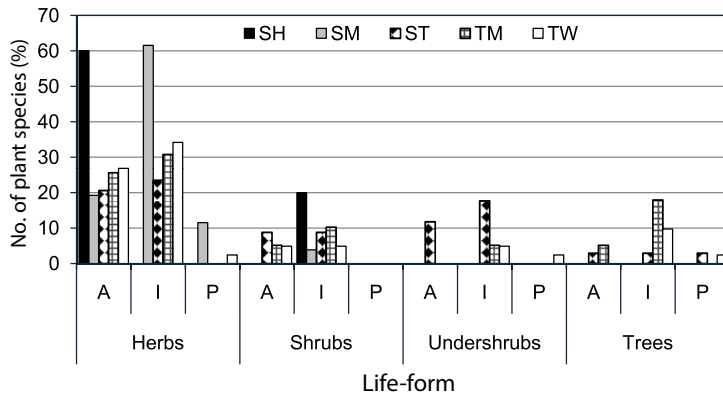


Fig. 4. Incidence of arbuscular mycorrhizal morphological types in plant species of various life-forms and vegetation types of Velliangiri Hills. SH = Shola forest; SM = southern montane humid grassland; ST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest. A = *Arum*-; P = *Paris*-; I = intermediate type

0.611), %RLHC ($X^2_4 = 3.107$), %RLTC ($X^2_4 = 1.953$) are not significant ($P > 0.05$). Nevertheless, significant differences existed for %RLA/AC ($X^2_4 = 10.917$; $P < 0.05$) among vegetation types. Average total colonisation was higher (50.34%) in plants from tropical moist deciduous forests compared to other vegetation types.

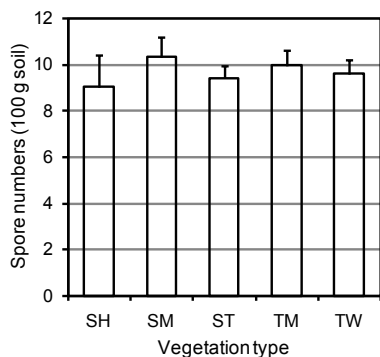


Fig. 5. Average arbuscular mycorrhizal spore numbers in different vegetation types of Velliangiri Hills. SH = Shola forest; SM = southern montane humid grassland; ST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest. The error bars indicate ± 1 SE

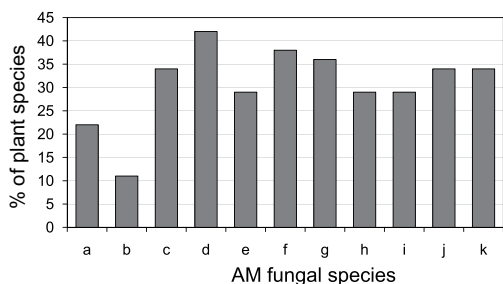


Fig. 6. The spore frequency of arbuscular mycorrhizal (AM) fungal species in rhizosphere of plants in different vegetation types of Velliangiri Hills. AM species code: a = *Acaulospora scrobiculata*, b = *Gigaspora* sp., c = *Glomus aggregatum*, d = *Funneliformis geosporum*, e = *Glomus magnicaulis*, f = *Sclerocystis rubiformis*, g = *Sclerocystis sinuosa*, h = *Sclerocystis taiwaniensis*, i = *Glomus viscosum*, j = *Scutellospora heterogama*, k = *Scutellospora calospora*

The extent of DSE fungal colonisation (%RLDTC) ranged between $< 1\%$ (*Ageratum houstonianum*, *Helichrysum* sp., Asteraceae; *Catunaregam spinosa*, Rubiaceae; *Mukia leiosperma*, Cucurbitaceae; *Oxalis corniculata*, Oxalidaceae; *Scutellaria* sp., Labiatae) and 46.11% (*Mangifera indica*, Anacardiaceae) (Table 3). Eighty-eight percent of the plant species had DSE fungal colonisation levels between 10 and 20%. The percentage root length with DSE fungal hyphae (%RLDH) ranged from $< 1\%$ (*Strobilanthes* sp., Acanthaceae; *Ageratum houstonianum*, Asteraceae; *Catunaregam spinosa*, Rubiaceae; *Mukia leiosperma*, Cucurbitaceae; *Strobilanthes* sp., Acanthaceae; *Vigna unguiculata*, Papilionaceae) to 28.10% (*Cynoglossum zeylanicum*, Boraginaceae). Similarly, the root length with microsclerotia (%RLMi) ranged from $< 1\%$ (*Catunaregam spinosa*, Rubiaceae; *Fimbristylis strigosa*, *Fimbristylis ovata*, Cyperaceae; *Helichrysum* sp., Asteraceae; *Leucas* sp., *Scutellaria* sp., Labiatae; *Oxalis corniculata*, Oxalidaceae, *Vigna unguiculata*, Papilionaceae) to 44% (*Mangifera indica*, Anacardiaceae) (Table 3 and Fig. 2). DSE fungal variables like %RLDH ($X^2_4 = 5.482$), %RLDMi ($X^2_4 = 2.047$) and RLDTTC ($X^2_4 = 0.917$) did not differ

significantly ($P > 0.05$) among forest types, but differed significantly ($P < 0.01$) among species (RLDH, $X^2_{146} = 198.539$; %RLDMi, $X^2_{146} = 194.047$ and %RLDTC, $X^2_{146} = 203.541$). Though, Pearson's correlation analysis indicated the lack of correlation between %RLDTC and %RLTC ($r = 0.149$; $P > 0.05$; $n = 147$), the association was positive as the probability of co-occurrence frequency (p_{gt}) was greater than the observed frequency for these fungal types ($p_{gt} = 0.00076$).

AM fungal spore numbers in different vegetation types

The AM fungal spore numbers in the plant root zones from different vegetations ranged from 2 (*Gynostemma pentaphyllum*, Cucurbitaceae) to 19 spores / 100 g soil (*Conyza leucantha*, Asteraceae) (Table 3). There was no significant difference among various vegetation types on spore numbers ($X^2_4 = 0.183$), however, spore numbers differed significantly among species ($X^2_{146} = 202.675$). Spore numbers were not related to %RLTC ($r = -0.039$; $P > 0.05$; $n = 147$) and average AM fungal spore numbers were higher (10.31 spores / 100 g soil) in the SM (Fig. 5). Eleven AM fungal spore morphotypes were isolated and identified which included one species in *Acaulospora* (*Acaulospora scrobiculata* Trappe), *Funneliformis* [*Funneliformis geosporum* (T. H. Nicolson et Gerd.) C. Walker et A. Schüßler], *Gigaspora* sp., two in *Scutellospora* [*Scutellospora calospora* (T. H. Nicolson et Gerd.) C. Walker et F. E. Sanders and *Scutellospora heterogama* (T. H. Nicolson et Gerd.) C. Walker et F. E. Sanders], three in *Glomus* (*Glomus aggregatum* N. C. Schenck et G. S. Sm, *Glomus viscosum* T. H. Nicolson, *Glomus magnicaule* I. R. Hall) and *Sclerocystis* (*Sclerocystis taiwanensis* C. G. Wu et Z. C. Chen, *Sclerocystis rubiformis* Gerd. et Trappe, *Sclerocystis sinuosa* Gerd. et B. K. Bakshi). Among the different AM spore morphotypes, *F. geosporum* was found associated with maximum number of plant species and *Gigaspora* sp., was found associated with minimum number of plant species (Fig. 6). Spores of *Scutellospora heterogama* were the most frequent (42%) in the SM and TM (Fig. 7). In the ST and SH, *F. geosporum* (50% and 80%) were more frequent. *Sclerocystis rubiformis* and *S. sinuosa* were the most frequent species occurring in TM and TW, respectively. Across vegetation types, *F. geosporum* was the most frequent species occurring in the rhizospheres of 47% of the plant species, whereas spores of *Gigaspora* sp. were infrequent occurring in the rhizospheres of around 13% of the plant species (Fig. 7). Of the 55 AM fungal species pairs that occurred with different plant species 24% were positive and 38% were negative and 38% were random associations (Fig. 8). The species contributing to this high randomness were *Gigaspora* sp., *G. aggregatum*, and *A. scrobiculata*. Around 50% of the associations of *G. magnicaulis* and *G. viscosum* with other AM fungal species were negative (Fig. 8).

Table 3
Extent of arbuscular mycorrhizal (AM), dark septate endophytic (DSE) fungal colonisation, AM spore numbers and AM species associated with angiosperms of Velliangiri Hills

Family / Plant species	AM colonisation (%) ^a					SN ^b	DSE colonisation (%) ^d		
	RLH	RLV	RLA/AC	RLHC	RLTC		AMFS ^c	RLDH	RLDMI
Acanthaceae									
<i>Andrographis lineata</i>	42.58±1.52 ^e	3.20±1.01	16.22±2.50	6.37±2.81	68.37±1.25	7.33±1.45	-	-	-
<i>Justicia beddomei</i>	43.26±2.12	-	4.93±3.98	8.85±2.61	57.05±2.14	11.33±1.86	7.23±3.62	-	7.23±3.62
<i>Justicia tranquebariensis</i>	1.96±0.35	4.51±2.73	12.41 ±1.70	-	18.88±1.84	4.00±0.58	1.01±0.57	-	1.01±0.57
<i>Nilgiranthus asper</i>	38.36±1.21	8.02±2.63	15.95±2.74	12.56±0.44	74.89±2.50	7.33±1.45	3.13±0.32	3.10±0.24	6.24±0.14
<i>Plectocaulis sessilis</i>	1.73±0.07	3.07±1.69	16.30±2.77	-	21.11±1.72	8.67±1.20	-	-	-
<i>Rostellularia japonica</i>	2.64±0.43	12.38±2.20	17.77±3.96	-	32.78±3.02	8.33±0.88	-	-	-
<i>Rangia apiculata</i>	-	0.47±0.47	2.27±0.57	31.42±1.45	34.16±2.12	8.00±0.58	4.19±2.88	-	4.19±2.88
<i>Rangia latior</i>	44.92±1.51	1.72±0.60	11.27±2.93	15.54±2.77	73.45±0.96	10.33±3.48	-	-	-
<i>Strobilanthes asperimus</i>	33.55±1.35	12.21±0.64	16.14±3.59	2.53±1.83	64.42±2.63	11.33±0.88	12.88 ±8.89	-	12.88±8.89
<i>Strobilanthes</i> sp.	2.95±0.88	0.34±0.34	16.55±2.69	-	19.84±3.72	10.00±1.15	0.68±0.34	0.67±0.33	1.35±0.68
Agavaceae									
<i>Sansevieria roxburghiana</i>	7.75±1.01	-	27.92±3.58	18.23±3.39	53.91±1.15	8.44±2.32	5.12±1.15	-	5.12±1.15
Anacardiaceae									
<i>Mangifera indica</i>	-	-	-	17.86±1.01	17.86±1.01	11.33±2.03	1.83±1.03	44.28±10.12	46.11±5.26
Annonaceae									
<i>Goniothalamus</i> sp.	-	-	29.34±3.14	43.78±5.08	73.12±6.20	11.02±2.28	-	-	-
Araceae									
<i>Arisaema leschenaultii</i>	3.36±0.36	5.11±2.60	21.25±2.39	-	29.72±0.86	8.00±1.53	-	-	-
<i>Arisaema tortuosum</i>	30.11±2.79	4.07±0.54	13.39±3.51	13.55±4.08	61.12±2.11	10.33±2.19	-	-	-
Asclepiadaceae									
<i>Cynanchum callitatum</i>	-	7.31±2.85	19.59±0.80	23.72±2.54	50.62±3.75	5.15±2.21	-	-	-

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a				SN ^b	AMFS ^c	DSE colonisation (%) ^d			
	RLH	RLV	RLA/AC	RLHC			RLTC	RLDH	RLDMI	RLDTC
Asteraceae										
<i>Acemella paniculata</i>	3.43±0.23	8.81±1.56	26.91±0.50	-	39.16±2.26	12.67±3.28	b, f, g, i	1.92±0.97	-	1.92±0.97
<i>Ageratum houstonianum</i>	3.23±0.16	2.14±0.08	22.33±1.20	-	27.70±1.22	12.00±1.53	e, f	0.94±0.47	-	0.94±0.47
<i>Anaphalis beddomei</i>	31.23±0.76	5.75±1.15	11.31±1.83	22.33±2.27	70.62±2.28	11.00±0.58	c, d, g, j, k	-	-	-
<i>Anaphalis breusifolia</i>	37.31±0.95	5.63±2.60	5.51±3.08	9.08±1.44	57.54±1.80	3.67±0.67	a	2.46±1.30	4.61±2.32	7.07±3.60
<i>Anaphalis busia</i>	41.05±1.30	3.96±1.98	-	25.01±1.51	70.02±3.20	4.33±0.67	e, f, i	3.68±2.55	-	3.68±2.55
<i>Anaphalis elliptica</i>	2.84±0.17	9.29±0.61	22.04±2.56	-	34.18±2.09	11.00±1.15	d, h, j, k	-	-	-
<i>Anaphalis laonii</i>	33.78±1.09	0.70±0.35	18.16±2.43	15.96±2.54	68.60±4.17	13.67±0.88	e, f, g	-	-	-
<i>Bidens biternata</i>	2.82±0.17	7.58±2.70	24.38±1.05	-	34.78±2.50	14.67±0.88	d, f, h, i, k	1.62±0.83	-	1.62±0.83
<i>Bidens pilosa</i>	22.09±2.72	15.75±2.83	17.91±1.07	7.39±0.89	63.14±2.36	8.33±1.86	d, h, j, k	2.07±1.05	-	2.07±1.05
<i>Bidens</i> sp.	33.00±1.56	0.89±0.46	24.79±0.79	19.34±3.02	78.02±2.86	15.33±3.18	c, e, f, g, i	5.04±2.63	-	5.04±2.63
<i>Chromolaena odorata</i>	2.32±0.33	-	24.70±1.09	-	27.02±1.19	11.00±2.8	d, h, j, k	-	-	-
<i>Conyza japonica</i>	45.08±0.59	1.61±0.81	4.69±2.98	16.19±4.27	67.57±1.22	12.00±1.15	d, h	1.99±1.02	-	1.99±1.02
<i>Conyza leucantha</i>	2.47±0.55	15.32±1.02	16.84±1.74	-	34.63±1.28	19.67±0.88	a, c, d, e, f	-	-	-
<i>Emilia scabra</i>	0.81±0.42	8.12±1.43	18.70±5.76	-	27.63±4.51	6.00±2.08	c, d, g, h, i	-	-	-
<i>Emilia</i> sp.	2.88±0.48	0.25±0.25	19.96±0.90	-	23.09±0.64	14.33±2.33	a, e, f, g, i	-	-	-
<i>Erigeron aegypticus</i>	1.88±0.31	3.49±0.70	22.53±6.68	-	27.92±5.99	13.67±0.67	c, d, j, k	-	-	-
<i>Erigeron bonariensis</i>	42.97±1.31	9.94±1.09	5.19±1.78	9.69±0.50	67.79±3.43	9.33±1.45	c, g, i	1.80±1.31	-	1.80±1.31
<i>Erigeron trilobus</i>	1.15±0.60	11.05±1.68	26.86±0.46	-	39.06±1.39	18.00±0.58	h, j, k	6.97±5.00	-	6.97±5.00
<i>Helichrysum</i> sp.	34.18±0.65	21.52±5.93	11.16±3.25	6.27±1.80	73.13±1.54	17.33±1.45	k, j, h, c, a	-	0.71±0.37	0.71±0.37
Balsaminaceae										
<i>Impatiens jerdoniiae</i>	-	-	-	-	-	3.67±0.88	c, d, g, h, j	-	-	-
<i>Impatiens minor</i>	37.95±1.08	12.02±0.68	19.69±2.92	4.25±0.18	73.92±1.96	2.67±0.88	c, j	-	-	-
Boraginaceae										
<i>Cynoglossum zeylanicum</i>	2.01±0.50	-	15.12±1.62	-	17.13±2.01	4.33±1.20	c, d, g	28.10±12.31	5.00±2.52	33.10±4.82

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^b					SN ^b	AMFS ^c	DSE colonisation (%) ^d						
	RLH	RLV	RLA/AC	RLHC	RLTC			RLDH	RLDMi	RLDTC	RLDTC			
Caesalpiniaceae														
<i>Cassia</i> sp.	3.49±0.95	16.64±2.63	25.26±1.82	-	45.39±1.56	6.67±0.88	c, d, h, j	-	-	-	-	-	-	-
Capparaceae														
<i>Crataeva magna</i>	2.25±1.06	-	30.28±1.25	-	32.53±0.68	12.00±0.68	a, d, e	1.73±0.16	-	-	-	-	1.73±0.16	-
Cannabaceae														
<i>Cannabis sativa</i>	30.11±2.30	14.09±7.05	4.88±3.99	3.61±2.02	52.68±11.80	12.00±1.53	a, g, i	-	-	-	-	-	-	-
Commelinaceae														
<i>Commelina imberbis</i>	33.13±1.51	4.92±2.47	7.92±4.08	22.49±1.64	68.46±3.91	7.00±1.15	c, d	-	-	-	-	-	-	-
<i>Commelina</i> sp.	2.56±0.41	18.63±3.29	22.21±1.49	-	43.39±3.31	11.67±0.88	e, f, g, j, k	-	-	-	-	-	-	-
Cruciferae														
<i>Brassica juncea</i>	-	-	-	-	-	13.33±0.88	c, d, j, k	-	-	-	-	-	-	-
Cucurbitaceae														
<i>Cucumis prothaterum</i>	44.30±1.04	3.53±3.53	-	5.22±1.75	53.05±5.37	7.33±1.20	d, f, g, h, i	14.04±7.83	3.88±1.95	17.92±9.70	-	-	-	-
<i>Gynostemma pentaphyllum</i>	33.19±1.63	15.40±2.51	27.71±2.20	-	76.30±2.51	2.67±0.88	d, e, f, h	-	-	-	-	-	-	-
<i>Gynura</i> sp.	38.37±1.43	5.77±4.16	3.26±1.69	7.92±4.02	55.31±3.56	3.33±1.20	b, g, i	14.06±2.32	13.76±7.74	27.82±9.78	-	-	-	-
<i>Mukia leiosperma</i>	36.51±1.45	-	29.40±1.01	5.84±0.59	71.76±0.50	4.67±0.8	d, j, k	0.75±0.38	-	0.75±0.38	-	-	0.75±0.38	-
<i>Zehneria majusorensis</i>	1.29±0.15	4.71±1.11	22.37±2.73	-	28.37±3.66	4.33±0.88	k	-	4.58±2.38	4.58±2.38	-	-	-	-
<i>Zehneria scabra</i>	-	-	-	-	-	7.00±1.15	h, j	-	-	-	-	-	-	-
Cyperaceae														
<i>Cyperus cyperinus</i>	24.77±3.00	11.55±3.29	-	9.27±4.77	45.59±2.24	14.33±4.10	e, f	-	-	-	-	-	-	-
<i>Cyperus rotundus</i>	-	-	-	-	-	4.00±0.58	j, k	-	-	-	-	-	-	-
<i>Cyperus</i> sp.	30.99±0.62	14.27±3.05	18.91±2.62	8.43±0.26	72.77±0.34	5.00±0.58	a, b, e, f, i	-	-	-	-	-	-	-
<i>Fimbristylis falcata</i>	2.35±0.63	4.78±0.25	17.09±1.55	-	24.22±2.38	14.00±1.15	a, e	5.75±2.89	4.00±1.65	9.75±1.44	-	-	-	-
<i>Fimbristylis ovata</i>	39.84±2.67	6.93±2.87	10.74±4.71	15.74±6.72	73.25±2.25	11.67±0.33	f, g, h, i, k	13.96±1.35	0.89±0.46	14.85±1.70	-	-	-	-

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^b					SN ^b	DSE colonisation (%) ^d			
	RLH	RLV	RLA/AC	RLHC	RLTC		AMFS ^c	RLDH	RLDMI	RLDTC
<i>Fimbristylis strigosa</i>	32.01±1.63	1.87±0.98	9.17±3.12	13.79±1.57	56.84±3.00	17.67±1.45	a, e, i, j	3.95±1.37	0.63±0.33	4.58±1.43
Dioscoreaceae										
<i>Dioscorea oppositifolia</i>	-	6.43±1.84	24.53±2.26	20.40±1.64	51.36±1.84	5.89±3.12	e, g, k	-	-	-
<i>Dioscorea tomentosa</i>	33.04±0.45	5.48±1.64	24.49±0.50	-	63.01±1.73	14.00±1.53	a	4.12±1.12	-	4.12±1.12
Eriocaulaceae										
<i>Eriocaulon</i> sp.	3.40±0.25	7.90±1.97	16.80±0.12	-	28.10±2.05	12.33±0.88	c, d, h, j	3.61±1.83	-	3.61±1.83
Euphorbiaceae										
<i>Acalypha racemosa</i>	3.43±0.23	2.69±2.11	14.69±1.39	-	20.81±2.46	12.00±1.15	b, d, h	-	2.49±0.77	2.49±0.77
<i>Breynia retusa</i>	43.28±1.55	7.76±1.97	1.92±0.43	12.01±1.14	64.97±0.51	9.67±1.20	j, k	-	-	-
<i>Bridelia retusa</i>	-	-	32.87±4.50	39.19±4.53	72.06±4.01	6.15±1.25	a, d	-	-	-
<i>Bridelia stipularis</i>	4.64±1.07	1.13±1.13	54.29±3.11	8.13±2.00	68.20±4.84	5.12±2.12	g, k	-	1.72±0.05	1.72±0.05
<i>Euphorbia indica</i>	3.28±0.15	9.77±0.15	16.23±0.62	-	29.27±0.89	13.00±0.58	e, f, i	-	-	-
<i>Euphorbia tortilis</i>	35.33±1.05	-	15.44±2.88	16.54±1.15	67.31±2.47	7.33±0.88	f, h, j, k	-	-	-
<i>Flueggea leucopyrus</i>	6.97±2.82	14.94±4.31	19.08±0.54	6.85 ±2.56	47.84±3.46	14.22±1.29	c, f, h	-	-	-
<i>Glochidion heyneanum</i>	11.78±4.58	-	27.28±3.05	33.78±4.72	72.84±5.64	9.18±2.25	b, d, k	2.25±0.36	1.25±0.12	3.5±0.48
<i>Mallotus philippensis</i>	5.82±1.49	8.11±0.29	26.68±2.78	35.03±3.23	75.66±2.01	12.58±2.78	a, d, f	4.25±0.56	-	4.25±0.56
<i>Mallotus tetracoccus</i>	10.20±3.10	-	10.9±1.72	31.74±3.10	52.84±1.39	8.19±1.25	d, k	6.12±1.65	-	6.12±1.65
<i>Phyllanthus emblica</i>	3.44±0.24	-	16.97±5.76	-	20.41±5.78	13.33±1.20	c, g, i	-	-	-
<i>Phyllanthus maderaspatensis</i>	1.82±0.32	-	19.06±0.34	-	20.88±0.65	13.30±1.53	c, f, i	-	-	-
<i>Phyllanthus missionis</i>	3.75±0.63	6.44±2.71	18.50±0.29	-	28.68±3.03	9.33±1.20	a, e, f, g, i	-	-	-
<i>Phyllanthus reticulatus</i>	2.73±0.61	7.84±0.17	20.69±0.45	-	31.26±1.11	8.33±0.88	e, f, g, i	4.03±2.10	8.65±4.56	12.68±6.66
<i>Phyllanthus urinaria</i>	39.91±0.33	10.07±2.80	12.35±1.82	10.96±2.56	73.29±2.49	4.67±0.88	a, e	-	-	-
Gentianeaceae										
<i>Exacum</i> sp.	-	-	-	70.49±3.76	70.49±3.76	3.67±0.88	f, g, i	-	-	-
<i>Scoerelia</i> sp.	-	-	-	50.98±2.71	50.98±2.48	12.00±1.15	h, j, k	-	-	-

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a					SN ^b	AMFSC ^c	DSE colonisation (%) ^d				
	RLH	RLV	RLA/AC	RLHC	RLTC			RLDH	RLDMI	RLDTC		
Haloragaceae												
<i>Laurembergia coccinea</i>	33.61±1.24	10.74±4.32	17.97±3.06	6.25±1.31	68.57±2.76	6.00±1.15	c, g, i, j, k	-	-	-	-	-
Juncaceae												
<i>Juncus prismatocarpus</i>	39.87±1.40	9.88±3.13	3.79±2.87	-	53.54±4.39	8.33±0.88	d, h, j, k	-	-	19.25±9.80	19.25±9.80	19.25±9.80
Labiatae												
<i>Leucas marriuboides</i>	3.22±0.21	19.38±0.69	19.15±0.42	-	41.74±0.94	4.33±0.88	a, d, g, j	-	-	-	-	-
<i>Leucas rosmarinifolia</i>	41.74±2.32	11.96±7.11	5.92±0.51	9.95±2.68	69.58±6.47	14.67±0.88	b, e, f, g, i	1.65±0.94	2.24±0.56	2.24±0.56	3.89±1.98	3.89±1.98
<i>Leucas</i> sp.	2.36±0.24	12.20±3.12	17.00±1.51	-	31.57±2.29	11.33±2.03	e, d	1.26±0.66	0.70±0.35	0.70±0.35	1.96±1.01	1.96±1.01
<i>Orthosiphon pallidus</i>	46.01±1.69	0.74±0.37	19.02±1.86	6.33±2.34	72.10±2.45	18.00±1.53	d, c, h, j, k	-	-	-	-	-
<i>Orthosiphon rubicundus</i>	46.04±1.29	5.24±2.69	14.50±2.31	8.09±6.00	73.87±2.67	8.00±1.53	j, k	-	6.44±3.46	6.44±3.46	6.44±3.46	6.44±3.46
<i>Orthosiphon</i> sp.	3.24±0.33	-	15.47±2.08	-	18.71±1.81	12.67±0.88	a, e, f	-	7.83±3.95	7.83±3.95	7.83±3.95	7.83±3.95
<i>Pogostemon</i> sp.	34.73±1.48	9.46±0.73	3.06±1.59	15.93±1.78	63.18±0.74	8.67±0.88	d, h, j, k	9.30±2.26	-	-	9.30±2.26	9.30±2.26
<i>Scutellaria</i> sp.	31.88±1.57	5.66±2.04	13.96±0.88	20.89±0.56	72.38±1.34	8.33±1.45	d, h	-	0.67±0.34	0.67±0.34	0.67±0.34	0.67±0.34
Lauraceae												
<i>Neolitsea scrobiculata</i>	3.52±1.02	-	49.15±5.98	30.28±7.26	82.95±5.79	9.15±1.89	g	-	-	-	-	-
Liliaceae												
<i>Asparagus racemosus</i>	4.12±0.38	12.65±1.65	19.89±0.19	-	36.66±2.10	16.00±0.58	b, d, e, f, k	-	-	-	-	-
<i>Urginea indica</i>	3.58±1.09	10.91±1.58	22.58±2.76	-	37.07±2.89	13.25±1.25	a, c, f, g	-	-	-	-	-
Malvaceae												
<i>Urena lobata</i>	36.66±3.32	13.30±3.24	2.60±1.33	22.09±3.24	74.65±2.42	13.00±1.15	c, d, g, h, i	-	-	-	-	-
<i>Urena</i> sp.	2.77±0.15	5.16±1.44	20.17±0.44	-	28.10±1.09	11.00±1.15	a, e, j, k	-	-	-	-	-
Mimosaceae												
<i>Albizia</i> sp.	15.34±2.35	4.56±0.51	9.00±6.09	20.61±2.91	49.52±3.65	9.12±1.27	d, f	1.62±0.12	-	-	1.62±0.12	1.62±0.12
<i>Pithecolobium dulce</i>	10.39±1.34	-	9.00±0.38	34.74±6.76	54.14±9.06	8.32±2.25	c, k	-	3.12±0.50	3.12±0.50	3.12±0.50	3.12±0.50

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a				SN ^b	AMFS ^c	DSE colonisation (%) ^d		
	RLH	RLV	RLA/AC	RLHC			RLIC	RLDH	RLDMI
Oleaceae									
<i>Jasminum ritchiei</i>	3.42±0.22	0.73±0.37	19.01±0.38	-	23.17±0.56	16.67±1.20	c, e, f, g, i	-	-
Oxalidaceae									
<i>Biophytum longipedunculatum</i>	2.82±0.16	9.66±1.34	16.15±0.17	-	28.63±1.11	11.33±0.88	a, d, f, g, i, j	21.91±3.33	21.91±3.33
<i>Biophytum sensitivum</i>	2.65±0.25	9.32±0.93	19.87±0.00	-	31.84±0.64	5.00±1.15	a, c, g, j	20.96±2.03	20.96±2.03
<i>Oxalis corniculata</i>	37.80±1.28	14.00±4.07	16.45±2.85	4.53±2.89	72.78±2.74	12.00±1.53	c, g, h, k	0.64±0.33	0.64±0.33
Papilionaceae									
<i>Crotalaria clavata</i>	24.47±3.45	10.81±4.46	2.79±2.00	21.11±4.10	59.18±0.81	9.67±1.76	b, e, f, g	-	-
<i>Crotalaria</i> sp.	28.00±2.43	15.35±1.84	13.00±1.97	11.00±0.75	67.36±0.88	12.00±1.53	e, f, i	-	-
<i>Crotalaria verrucosa</i>	3.33±0.27	6.99±2.32	19.28±0.33	-	29.60±2.84	7.67±0.88	d, h, j, k	7.95±4.01	7.95±4.01
<i>Pterocarpus marsupium</i>	12.00±1.23	-	10.53±2.60	34.15±4.69	56.68±8.72	11.02±2.02	b, d, f	-	-
<i>Vigna unguiculata</i>	2.95±0.07	6.31±1.09	13.15±1.53	-	22.41±2.56	7.00±0.58	c, d, h, j	0.64±0.32	0.95±0.55
Plantaginaceae									
<i>Plantago erosa</i>	2.81±0.16	4.16±0.53	7.81±1.23	-	14.78±0.66	13.00±1.53	e, f, i	5.28±2.65	5.28±2.65
<i>Plantago</i> sp.	3.07±0.18	6.94±1.53	12.47±1.61	-	22.48±2.97	8.00±0.58	d, h	-	1.45±0.74
Poaceae									
<i>Arundinella</i> sp.	44.23±0.97	1.86±0.97	7.35±1.59	17.68±1.20	71.12±2.87	15.00±2.89	h	-	-
<i>Brachiaria</i> sp.	25.03±2.40	3.90±1.19	1.89±1.89	4.47±2.09	35.28±4.98	6.67±0.88	c, d, i, j	2.67±1.34	2.67±1.34
<i>Cymbopogon citratus</i>	15.50±2.23	5.58±1.83	10.00±6.18	16.99±4.98	48.07±20.14	15.12±1.23	a, e, f	6.25 ±1.12	2.15±0.25
<i>Cyrtococcum</i> sp.	32.99±1.37	19.05±4.93	19.70±3.61	2.26±0.82	74.01±3.01	15.00±2.89	a, c, d	-	-
<i>Eleusine indica</i>	-	5.04±3.69	-	21.66±1.23	26.69±3.09	19.33±1.20	c, g, h, k	-	-
<i>Heteropogon contortus</i>	42.88±3.13	3.02±1.17	-	3.06±2.12	48.96±5.49	13.67±0.88	b, d, c	7.48±4.14	7.48±1.14
<i>Ischaemum</i> sp.	2.87±0.07	7.21±2.24	18.00±2.00	-	28.09±1.45	11.33±0.88	j, k	1.78±1.10	1.78±1.10

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a					DSE colonisation (%) ^a				
	RLH	RLV	RLA/AC	RLHC	RLTC	SN ^b	AMFS ^c	RLDH	RLDMi	RLDTC
<i>Janseella griffithiana</i>	-	3.41±1.29	-	29.15±4.03	32.56±4.30	8.33±0.88	a, e, f, g, i	1.96±0.98	-	1.96±0.98
<i>Panicum notatum</i>	3.17±0.28	5.00±3.00	18.93±3.14	-	27.11±3.30	5.33±0.33	a, e, f, i	-	-	-
<i>Panicum sparsicomum</i>	46.91±1.11	4.87±0.82	2.37±0.46	10.32±0.41	64.48±1.69	12.67±1.20	e, h, j, k	7.91±1.85	1.58±0.92	9.50±2.77
<i>Polytrias indica</i>	32.39±1.91	0.98±0.04	19.35±0.59	14.98±1.03	67.70±3.11	10.33±0.88	d, h, j, k	-	-	-
<i>Tripogon</i> sp.	-	-	-	-	-	17.33±2.67	d, h, j, k	-	-	-
Polygalaceae										
<i>Polygala</i> sp.	32.27±1.55	5.68±3.97	13.71±1.63	12.33±3.06	64.00±1.89	4.00±0.58	c, d	-	3.37±2.25	3.37±2.25
Polygonaceae										
<i>Persicaria barbata</i>	31.19±0.94	1.69±0.89	0.86±0.45	16.85±3.09	50.60±1.88	13.33±1.20	f, g, i	-	-	-
<i>Persicaria chinense</i>	45.53±1.22	6.34±4.64	1.22±0.62	3.42±1.71	56.51±7.58	14.67±1.45	j, k	11.04±4.15	5.63±3.06	16.67±5.69
<i>Persicaria lanigerum</i>	2.93±0.24	7.00±4.60	19.85±0.43	-	29.78±4.71	8.33±3.53	b, e, f, g, i	-	-	-
Rhamnaceae										
<i>Ziziphus rugosa</i>	43.08±1.25	7.98±1.87	1.40±0.70	12.73±2.95	65.18±0.68	11.67±1.76	c, h, j, k	1.33±0.66	-	1.33±0.66
Rosaceae										
<i>Rubus ellipticus</i>	3.33±0.17	12.25±1.82	20.19±0.41	-	35.77±2.26	14.33±1.20	c, d, g, h, i	-	-	-
Rubiaceae										
<i>Canthium rheedi</i>	1.73±0.07	3.07±1.69	16.30±2.77	-	21.11±1.72	8.67±1.20	d, j, k	-	-	-
<i>Canthium tracaancoricum</i>	-	-	5.00±0.60	66.27±7.63	71.27±6.92	8.56±2.51	a, f	-	-	-
<i>Caturaregam spinosa</i>	20.64±4.64	-	13.00±4.64	43.92±8.09	77.56±3.49	5.25±1.25	c	0.55±0.12	0.25±0.03	0.8±0.19
<i>Knoxia sumatrensis</i>	40.83±0.71	6.48±2.20	22.21±4.00	6.86±2.67	76.38±2.23	5.67±0.88	c, e, h, k	-	-	-
<i>Psychotria dicoccos</i>	6.67±2.91	-	-	50.00±2.91	56.67±2.91	4.25±1.23	a, d, f	-	-	-
Rutaceae										
<i>Clausena heptaphylla</i>	-	-	-	-	-	8.00±2.89	c, f, g, i	-	-	-
<i>Glycosmis</i> sp.	34.47±0.51	0.94±0.52	15.20±2.84	20.04±3.36	70.65±2.85	3.00±0.58	g, i	-	-	-

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a					SN ^b	AMFS ^c	DSE colonisation (%) ^d		
	RLH	RLV	RLA/AC	RLHC	RLTC			RLDH	RLDMi	RLDTC
<i>Toddalia asiatica</i>	1.35±0.84	3.58±1.26	19.58±1.26	-	24.51±2.94	7.00±1.35	b, c, f	3.45±0.75	1.75±0.25	5.2±0.15
Sapindaceae										
<i>Dimocarpus longan</i>	3.53±1.25	6.15±2.35	25.65±1.38	-	35.53±2.58	12.14±1.53	c, e, f	-	-	-
<i>Filicium decipiens</i>	15.25±3.25	-	25.35±1.26	15.25±2.58	55.85±4.28	8.26±2.29	a, d, e	3.25±0.07	-	3.25±0.07
Scrophulariaceae										
<i>Scoparia dulcis</i>	32.29±1.56	4.53±3.00	-	32.11±4.01	68.93±5.24	6.00±0.58	c, d, g, i, j	-	-	-
<i>Torenia hirsuta</i>	34.54±1.11	16.28±1.43	14.17±0.67	3.56±1.35	68.55±1.58	5.33±1.20	j, k	4.65±0.34	5.73±0.60	10.37±0.44
Solanaceae										
<i>Solanum americanum</i>	2.37±0.19	2.34±0.75	20.38±0.14	-	25.09±0.60	7.00±1.15	c, e, f, g, i	-	-	-
<i>Solanum ferrox</i>	31.65±1.03	3.20±1.62	26.56±5.23	6.54±2.37	67.95±0.73	7.33±2.19	a, b, f, g, i	-	5.74±2.95	5.74±2.95
<i>Solanum grandiflorum</i>	30.91±0.61	8.08±1.54	17.73±7.33	1.94±0.16	58.67±6.63	6.00±0.67	e, f	-	-	-
<i>Solanum trilobatum</i>	46.24±2.04	5.95±1.37	4.48±0.80	7.68±1.29	64.35±1.23	10.00±2.89	c, d, e, j, k	5.09±2.54	-	5.09±2.54
<i>Solanum viarum</i>	39.62±3.79	16.00±1.52	8.70±3.63	7.36±2.09	71.69±0.60	3.33±0.88	d, j	-	-	-
Thunbergiaceae										
<i>Thunbergia fragrans</i>	40.01±1.86	5.27±2.70	12.40±4.46	5.70±3.65	63.38±4.89	5.67±1.86	f, g, i	-	14.45±2.28	14.45±2.28
<i>Thunbergia</i> sp.	41.94±1.01	20.42±2.43	3.23±0.97	-	65.60±3.24	10.00±2.89	e, k	3.83±1.25	-	3.83±1.25
Umbelliferae										
<i>Polygopus tuberosus</i>	44.68±0.49	9.62±4.13	5.16±3.16	18.36±5.22	77.82±0.74	3.67±0.88	b, d, h, j	9.77±1.77	-	9.77±1.77
Urticaceae										
<i>Pouzolzia</i> sp.	28.69±4.59	9.98±5.02	3.93±0.68	3.68±0.98	46.28±3.35	11.67±0.88	c, g, k	1.48±0.99	-	1.48±0.99
Verbenaceae										
<i>Lantana camara</i>	2.23±0.37	5.40±0.67	11.60±1.64	-	19.23±1.97	13.33±0.88	c, d	5.61±2.80	-	5.61±2.80
<i>Tectona grandis</i>	5.72±1.07	5.73±1.11	27.39±1.73	17.22±2.99	56.06±18.30	7.44±2.23	c, f, h	5.15±1.25	2.14±0.25	7.29±1.35

Table 3 (continued)

Family / Plant species	AM colonisation (%) ^a					SN ^b	DSE colonisation (%) ^d		
	RLH	RLV	RLA/AC	RLHC	RLTC		RLDH	RLDMI	RLDTC
Vitaceae									
<i>Cayratia auriculata</i>	10.15±2.35	11.00±1.97	25.06±2.73	14.16±2.19	60.05±20.38	7.15±2.25	1.52±0.35	–	1.52±0.35
<i>Tetrastigma</i> sp.	20.91±2.36	–	15.15±2.38	20.73±1.35	56.79±5.30	8.94±2.35	4.15±0.45	–	4.15±0.45

^aRLH = root length with hyphae; RLV = root length with vesicles; RLA/AC = root length with arbuscules/arbusculate coils; RLHC = root length with hyphal coils; RLTC = root length with total colonisation; ^bSN = AM spore numbers / 100 g soil; ^cAMFS = AM fungal species; a = *Acaulospora scrobiculata*, b = *Gigaspora* sp., c = *Glomus aggregatum*, d = *Funnelliformis geosporum*, e = *Glomus magnicaulis*, f = *Sclerocystis rubiformis*, g = *Sclerocystis taiwanensis*, h = *Sclerocystis sinuosa*, i = *Glomus viscosum*, j = *Scutellospora heterogama*, k = *Scutellospora calospora*; ^dRLDH = root length with dark septate fungal endophytic hyphae; RLDMI = root length with microsclerotia; RLDTIC = root length with total colonisation; ^eMean±Standard error

Fig. 7. Percentage occurrence of arbuscular mycorrhizal (AM) fungal spore morphotypes in rhizosphere of different plants in Velliangiri Hills. AM species code: SH = Shola forest; SM = southern montane humid grassland; ST = southern tropical thorn forest; TM = tropical moist deciduous forest; TW = tropical wet evergreen forest

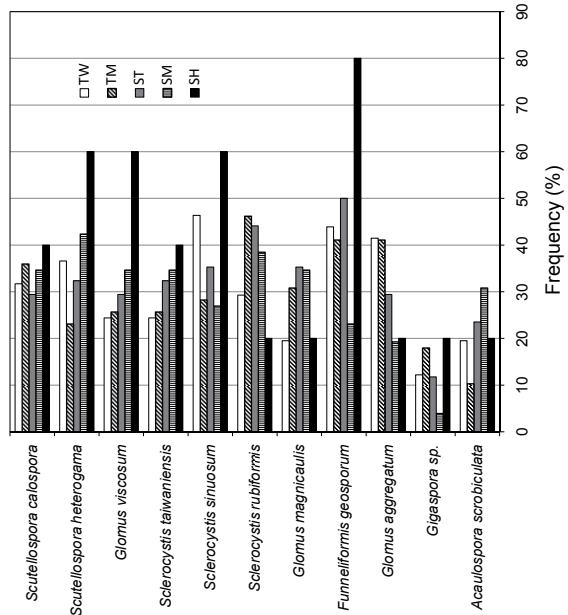
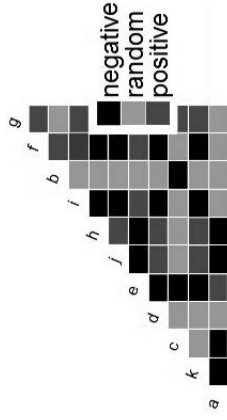


Fig. 8. The heat map showing the arbuscular mycorrhizal fungal species associations as determined by the probabilistic model for Velliangiri Hills. For species code see Figure 6



DISCUSSION

Arbuscular mycorrhizal associations were found in most of the plant taxa examined from different vegetation types of Velliangiri Hills. This concurs with the observations of Wang and Qiu (2006) and Brundrett (2009) who indicated the widespread occurrence of mycorrhizae among vascular plants. Further, AM and DSE fungal associations have been reported to our knowledge in 61 and 42 plant species, respectively, for the first time. High competition for resources and low nutrient status of the soils could have resulted in the high prevalence of AM in plants of different vegetation types. Significant differences both in %RLTC and root length with different AM fungal structures indicate the variation in the dependence of plant species on AM fungi, as a positive correlation between AM fungal colonisation levels and plant-mycorrhizal dependency has been reported in P-deficient soils (Smith *et al.* 2011).

Occurrence of AM and DSE fungi in various vegetation types

Ninety-two percent of plants examined from grasslands were colonised by AM fungi which is almost similar to the findings of Li *et al.* (2004) who also reported AM in 95% of plant species they examined in valley-type savanna in southwest China and 82% (18/22) of the grassland plant species examined by Gai *et al.* (2006) from southern Tibet were mycorrhizal. The presence of AM in 97% of the plant species from the tropical moist deciduous forest is consistent with the findings of Allen *et al.* (1998) who reported AM association in all the plant species they examined from a Mexican tropical deciduous forest.

The plants that lacked mycorrhizae in the present study belonged to Balsaminaceae, Cruciferae, Cucurbitaceae, Cyperaceae and Poaceae. Of these, except Cruciferae, all other families have been reported as mycorrhizal (Brundrett 2009, Muthukumar *et al.* 2004, Wang and Qiu 2006). *Brassica juncea* examined from tropical wet evergreen forest lacked mycorrhizal associations in the present study. Nevertheless, AM characterised by the presence of *Glomus*-type vesicles and hyphae but not arbuscules have been reported in other species of *Brassica* like *Brassica napus* and *Brassica oleracea* (Harley and Harley 1987, Tester *et al.* 1987, Vierheilig *et al.* 2000). A functional association with abundant arbuscules in *Brassica* has never been found so far. The other non-mycorrhizal family Cyperaceae is no longer considered so, but the mycorrhizal status of its members can be greatly influenced by environmental factors (Brundrett 2009, Muthukumar *et al.* 2004). *Cyperus rotundus* has been reported to be both mycorrhizal (Muthukumar and Udaiyan 2002, Muthukumar *et al.* 1997) and non-mycorrhizal (Koske and Gemma 1992) in different studies.

The presence of DSE fungal association in 62% of the plant species in the southern tropical thorn forest corroborates the observations of Fracchia *et al.* (2009) who reported DSE association in 75% of the plant species they examined from Chaco Serrano woodland colonised by DSE fungi. All the plant species harbouring DSE fungi were also mycorrhizal, which is in line with the observations of Fracchia *et al.* (2009), Sathiyadash *et al.* (2010) and Uma *et al.* (2010), where dual colonisation of AM and DSE fungi has been reported. The present studies, as well as the other studies cited above, clearly suggest that DSE fungal associations in various vegetation types exist as a backup system and tend to take over the functions of AM fungi under conditions unfavourable for AM fungi (Jumpponen and Trappe 1998).

AM and DSE fungal association in plant life-forms

The widespread occurrence of AM in herbs of thorn and deciduous forests agrees with findings of Yamato and Iwasaki (2002), where all the herbaceous understory plants examined from Japanese deciduous broad-leaved forests were mycorrhizal. Our findings of high incidence of DSE fungal association in herbs compared to other life-forms examined from different vegetations is in accordance with other studies where high prevalence of DSE association has been reported in herbs (Muthukumar *et al.* 2006, Schmidt *et al.* 2008). Trees examined from the different vegetation types in the present study were invariably colonised by AM fungi similar to the observations of Fracchia *et al.* (2009) and Uma *et al.* (2012), where all the tree species examined from Chaco Serrano woodlands from central Argentina and South India, respectively, were mycorrhizal. A high incidence of mycorrhizae in tree species has also been reported by Onguene and Kuyper (2001) from south Cameroon (74%) and McGuire *et al.* (2008) from central Guyana (94%). Generally, trees have a very sparse root system so to increase the surface for absorption of nutrients trees tend to depend on AM fungi (Phillips and Fahey 2006). This may be the reason for high incidence of AM association of trees in the present study. Shrubs from all the vegetation types examined, except those from tropical moist deciduous forests were mycorrhizal. This is in line with the observations of Fracchia *et al.* (2009), who also reported the presence of AM in all the shrubs they examined from Chaco Serrano woodlands, Argentina. However, Fontenla *et al.* (2001) found only 86% of shrubs in Patagonian steppe, Argentina to be mycorrhizal. In general, the frequent occurrence of AM in plant roots from all the vegetation types shows the inability of non-mycorrhizal plants to compete with mycorrhizal plants in these well-established ecosystems (Smith and Read 2008).

Extent of AM and DSE fungal association

Generally, it is hypothesised that plants with a more efficient root system are less dependent on mycorrhizas than plants with less efficient root system. Nevertheless, this hypothesis was recently rejected by Maherali (2014) and the results of the present study also support this as the calculated frequency of occurrence of AM tended to be almost similar in dicots (96.46%) with sparse root system and monocots (93.93%) with highly efficient fibrous root system. Likewise, mean colonisation levels of dicots (52%) were only slightly higher than those of monocots (48%). This suggests that in highly competitive ecosystems like those studied here even the moderately or low mycorrhizal plant species tend to depend on AM fungi. The extent of DSE fungal colonisation in most of plant species was < 20%, which is in accordance with Rains *et al.* (2003) who also reported low levels of DSE fungal colonisation (25%) in the epiphytic and terrestrial plants they examined from the Costa Rican cloud forest. The lack of correlation between the root length colonised by AM and DSE fungi suggest that these two fungal groups do not significantly influence each other within roots. Moreover, the positive association of these fungal groups as evidenced by the probabilistic model indicates that these fungal types could co-exist in a wide range of plant species and in different ecosystems.

AM fungal morphology in vegetation types

In this study AM morphology dominated by intermediate type is reported for the first time in 64 plant species. The dominance of the intermediate type AM morphology in the present study is consistent with the findings of Uma *et al.* (2010), who observed that 80% (32/40) of the ginger and spiral ginger are intermediate type AM. The presence of the *Arum*-type morphology in only 33% of the tropical wet evergreen forest plant species is consistent with the findings of Matekwor Ahulu *et al.* (2005), where 33% of evergreen species they examined had *Arum*-type AM. But the occurrence of *Paris*-type AM in 67% of the evergreen species of a mixed pine forest of Central Honshu, Japan (Matekwor Ahulu *et al.* 2005) does not agree with the present study where only 8% of the plants from tropical wet evergreen forests formed typical *Paris*-type AM. Instead, the majority of plants from this vegetation type formed intermediate type AM. This suggests that under low light intensity in the evergreen forests, plants tend to grow slowly and favour formation of *Paris*-type colonisation (Brundrett *et al.* 1990). When compared to other forest types (50%) species of the Southern montane humid grassland had *Paris*-type AM. This is in accordance with the findings of Muthukumar *et al.* (2006), who reported *Paris*-type AM in 71% of the plant species they examined from

grasslands of Western Ghats. At high altitudes, plant growth tends to slow down due to various environmental factors, which may favour the formation of *Paris*-type AM in plants at high altitudes (Matekwor Ahulu *et al.* 2005).

AM fungal spore characteristics of the study sites

Spore numbers in present study were low (2 to 19 spores per 100 g soil) compared to 135 to 150 spores per 100 g soil reported by Suchitra *et al.* (2012) for different soil types in Tamilnadu, India and 66 to 1,308 spores per 100 g soil reported by Lakshmipathy *et al.* (2011) from different land use systems in the Nilgiris biosphere reserve of the Western Ghats, southern India. Zangaro *et al.* (2013) also reported a high AM fungal spore numbers ranging from 20 to 150 spores per 150 g soils from soils of an Atlantic forest biome in southern Brazil. The low density of AM fungal spores documented the present study, however, is consistent with the reports from humid tropical forests where spore numbers tend to be low or infrequent (Fischer *et al.* 1994, Janos 1980). The observation of the present and other studies clearly indicates that in vegetation types where root growth occurs throughout the year AM colonisation of new roots can occur through the extraradical hyphae in the soil or the hyphae emerging from mycorrhizal roots. Hence, in such ecosystems, the spore populations may be small despite high root colonisation levels (Muthukumar *et al.* 2003, Zandavalli *et al.* 2008). In this study, spores of AM fungi were present in the rhizospheres of NM plants. In natural vegetations, AM and non-mycorrhizal plants grow in close proximity and the roots of these two often overlap. Therefore, the AM spores in the rhizosphere a plant could be contributed by the coexisting companion AM plants (Muthukumar and Udaiyan 2000a, b).

A total of 11 AM fungal morphospecies were identified, which is similar to the observations of Sathiyadash *et al.* (2010) who also observed spores of 11 AM fungal species in association with South Indian Grasses. However, Muthukumar and Udaiyan (2000a) reported 6–22 morphospecies per site from the Western Ghats region of South India. Arbuscular mycorrhizal fungal spores belonging to *Glomus* dominated species diversity, which is in accordance with the observations that species of *Glomus* dominate tropical soils (Devi *et al.* 2017, D'Souza and Rodrigues 2013, Kumar and Adholeya 2016, Sathiyadash *et al.* 2010, Suchitra *et al.* 2012). The lack of correlation between spore numbers and %RLTC suggests that root colonisation could be initiated by propagules other than spores like AM fungal hyphae in the soil or mycorrhizal roots of the same plant or conspecifics (Smith and Read 2008). An interesting observation made in the present study is the different types of associations among AM fungi. Although, AM fungal community composition and the role of vari-

ous factors influencing it are well known, the interaction between different AM fungal species has been largely ignored (Alguacil *et al.* 2016, Gosling *et al.* 2013). As obligate biotrophs the distribution of AM fungi depends on the host plants (Álvarez-Sánchez *et al.* 2012). Moreover, AM fungi have been shown to possess low host specificity as experimental evidences do indicate that an AM fungus can colonise a wide range of plant species (Álvarez-Sánchez *et al.* 2012). Nevertheless, in the present study most of the AM fungal pairs (72%) had either positive or negative associations. This suggests the existence of certain level of host preference as certain fungi tend to associate with a large number of plant species and sporulate abundantly, while others tend to more restricted in their association and sporulation (Álvarez-Sánchez *et al.* 2012, Vandenkoornhuyse *et al.* 2002).

CONCLUSIONS

Arbuscular mycorrhizal and DSE fungal association were found to be widespread in plant species from different vegetation types in Velliangiri Hills. Moreover, the report of AM and DSE fungal associations in several plants for the first time clearly indicates that many plants in natural vegetations are yet to be examined for their fungal associations. The widespread occurrence of AM and DSE in rare and economically important plant species, emphasises the potential for their exploitation in plant production systems. The number of AM fungal spores and their diversity was less compared to reports from other vegetations worldwide. This study for the first time shows that there could be different types of associations between co-occurring species in AM fungal communities. Further, experimental studies are required to determine the effects of the fungal inoculants in the conservation of these rare and economically important plant species.

*

Acknowledgements – We thank Prof. Christos Mammides, Guangxi Key Laboratory of Forest Ecology and Conservation, College of Forestry, Guangxi University, Daxuedonglu 100, Nanning, 530004, China for his help in probabilistic co-occurrence analysis. We also sincerely thank the anonymous reviewers whose suggestions and critical comments greatly helped in improving an earlier version of this paper.

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