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FULL-LENGTH RESEARCH ARTICLE

Distribution of Arbuscular Mycorrhizae Associated with Coconut and Arecanut Based Cropping Systems

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Abstract Mycorrhizal fungi are widespread in agricultural systems and are especially relevant for organic agriculture. A study was conducted to assess diversity in the arbuscular mycorrhizal (AM) fungi associated with coconut and arecanut intercropping systems of Kasaragod and Thiruvananthapuram districts of Kerala. Mycorrhizal parameters like spore density, root colonization, species richness, and relative occurrence of species were recorded. Coconut cropping system was found to be densely vegetated with diverse AM fungi, *Glomus* spp., *Gigaspora* spp., and *Acaulospora* spp. The diversity of fungal species was found to be maximum in the high density multiple species cropping system plot of CPCRI, Kasaragod with coconut as the main crop and banana, pepper as intercrops and least in farmers' plot of Mogral Puthur, Kasaragod with arecanut as main crop and banana as the intercrop. A total of fourteen AM fungi were identified from coconut and arecanut intercropping systems. *Glomus aggregatum, Funneliformis mosseae*, and *Rhizophagus fasiculatum* were observed in both the cropping systems studied. Among the six edaphic factors analysed, an inverse relationship of mycorrhizal population with soil pH and soil phosphorous was observed. An abundance of P-solubilizers, fluorescent *Pseudomonas* spp., N-fixers, *Bacillus* spp., and *Trichoderma* spp. were observed in the rhizosphere, with *Bacillus* spp. showing the maximum association with AM fungi. The higher AMF colonization in coconut cropping system imply that the AM fungi colonization is primarily dependent on the host plant rather than the climatic/edaphic components of an area.

Keywords Coconut intercropping system · Arecanut intercropping system · AMF · *Glomus* spp. · *Gigaspora* spp. · *Acaulospora* spp.

Introduction

Coconut and arecanut are the important plantation crops grown in the state of Kerala. The plant-microbial relationship can play a very important role in crop performance. Often the relationship is symbiotic. Among the active micro-organisms in the soil there are three main groups that are more or less directly involved in the palm's nutrient supply: nitrogen-fixing bacteria in the rhizosphere, phosphate solubilizing fungi, and arbuscular mycorrhizal fungal association that help in the absorption of phosphorus and other immobile elements. The symbiosis of plant with arbuscular mycorrhizal (AM) fungi is the widest spread symbiosis in natural ecosystems [11]. AM are associations where Glomeromycete fungi produce arbuscules, hyphae, and vesicles within root cortex cells [23]. Studies on microbial interactions in the mycorrhizosphere have focused on exotic populations of beneficial soil micro-organisms, plant growth promoting rhizobacteria [15], and phosphate- solubilizing bacteria [30]. Relationships between native soil microbe communities and AM fungi have received less attention [19] and it is not known whether members of a native soil bacterial flora show preference for native or exotic AM fungi. Different bacterial populations may establish themselves under the influence of different plant-AM fungus combinations [25]. Control of AM fungi over the nature and quantity of root exudates and subsequent competition between

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bacteria and AM fungi for this C source may determine the size and composition of bacterial populations in the rhizosphere [5]. There are also reports on the bacteria associated with AMF spores which have been found in the cytoplasm of AMF spores [2].

AM symbiosis can improve host responses to other environmental limitations, like drought, salinity, pollutants, erosion, and infection by pathogenic fungi [15]. AM fungi in symbiotic association with plants affect the hormone level; increase the level of cytokinins [1] and alter level of gibberellins and abscissic acid.

Arbuscular mycorrhizal associations have been well reported in palms, such as *Cocos nucifera* L. [29], arecanut [3], and, more recently in some tropical palms [10] under natural conditions.

In India, a number of fungi belonging to four genera viz., *Glomus*, *Gigaspora*, *Sclerocystis*, and *Acaulospora* have been found to form mycorrhizal associations with coconut [9]. The occurrence of a mixed population of AM has been commonly recorded from the coconut rhizosphere soils. Research on genotypic dependency of AMF in coconut revealed higher colonization rate in tall varieties compared to dwarf ones [28]. The quantitative and qualitative distribution of AMF also varied in response to a single crop or a combination of intercrops [21]. Present study focused on the distribution of arbuscular mycorrhizae in coconut and arecanut based cropping systems. The main aim of the study was to compare the species richness and diversity of AMF within the cropping systems and also to enumerate the plant beneficial micro-organisms in the rhizosphere of the plants.

Materials and Methods

Study Site and Sampling

Samples were collected from farmers' fields of coconut and arecanut based cropping systems of Kasaragod and Thiruvanathapuram districts to study the mycorrhizal spore load as well as root colonization.

Rhizospheric soil samples as well as root bits were collected to study the mycorrhizal association. Three replications per crop from each cropping system were analysed. Samples were collected from a soil depth of 0–25 cm from the rhizosphere of each crop, and stored in polyethylene bags.

Rhizospheric Edaphic Features

Physico–chemical parameters of the soil samples namely soil pH (Eutech instruments pH tutor), Electrical conductance (Eutech instruments), Organic carbon [32], Soil available phosphorous [4, 17] available potassium [8], and Nitrogen were estimated [12].

Mycorrhizal studies

Isolation of arbuscular mycorhizal spores was done by wet sieving decanting technique [7]. The identification was based on spore color, size, surface ornamentation, and wall structure with reference to the description and pictures provided by International Collection of Vesicular and Arbuscular Mycorrhizal Fungi (http://invam.caf.wvu.edu) and the original species descriptions [24]. Roots were stained for mycorrhizal infection [20]. AMF structures like vesicles and hyphae were recorded. Percentage of root colonization was calculated using the formula.

$$\text{Frequency of root colonization} = \frac{\text{Number of root bits having colonization}}{\text{Number of root bits observed}} \times 100$$

Analysis of Soil Microflora

Rhizospheric soil samples were enumerated for the presence of beneficial microbes. Population estimation was done by plate count method. Soil samples were serially diluted and pour plated on Jenson's agar, Pikovskya's agar, Kings B, Nutrient agar and *Trichoderma*-specific medium for the isolation of N-fixers, P-solubilizers, fluorescent *Pseudomonas* spp., *Bacillus* spp., and *Trichoderma* spp., respectively.

Data analysis

Pearson's correlation analysis was used to relate AMF spore load and frequency of root colonization with edaphic factors under each cropping systems. The statistical analysis was based on significant levels of $P < 0.05$. The relationship between mycorrhizal fungi and soil microflora were also analysed.

The diversity of AM fungi in the cropping systems was assessed based on diversity indices

$$\text{Simpsons index (Ds)} = 1 - \left(\sum \text{ni2} - \text{N}\right)/\text{N}(\text{N} - 1)$$

[26]

$$\text{Shannons index (Hs)} = \text{NC}\ \{(\text{N log 10N}) - \sum \text{ni}/\text{log10ni}\}$$

where, C = 3.32192 9 (constant used in converting log 10 to log 2). "ni" is the number of species in the'ith' species and "N" is the total number of individual [14]

Table 1 Geographical position, crops cultivated, and fertilizer input details of the study sites

Location	Geographical coordinates	Intercrops	Fertilizer input
Coconut cropping system			
HDMSCS, CPCRI, Kasaragod	12°31′32′’N, 74°58′4′’E	Pepper, banana, pineapple	Vermicompost and husk burial
Patena 1, Kasaragod	12°15′0′’N, 75°6′0′’E	Banana	Cow dung
Patena 2, Kasaragod	12°15′18″N, 75°8′13″E	Banana, pepper	Cow dung
Azad Nagar, Kasaragod	12°33′13″N, 74°57′39″E	Banana	Green leaf manure
Neerchal, Kasaragod	12°35′0″N, 75°2′0″E	Banana, pepper	Cow dung
Velanad, Thiruvananthapuram	8°34′0″N, 77°3′0″E	Banana, pepper	Cow dung
Pulippara, Thiruvananthapuram	8°46′4″N, 76°57′9″E	Banana	Cow dung
Arecanut cropping system			
Mogral puthur, Kasaragod	12°33′18.7′’, N74°57′43.08′’E	Banana	Cow dung
Keloth, Kasaragod	12°23′0′’N, 75°6′0′’E	Banana	Cow dung
Neerchal, Kasaragod	12°35′0″N, 75°2′0″E	Banana, pepper, rasna, cardamom	Green leaf manure
Veliyamangalam, Thiruvananthapuram	8°46′4″N, 75°54′9″E	Banana	Green leaf manure
Kumbara, Thiruvananthapuram	8°46′4″N, 75°54′8″E	Banana	Green leaf manure

HDMSCS High Density Multiple Species Cropping System

$$\text{Frequency of occurrence (\%)} = \frac{\text{Number of soil samples possessing spores of a particular species}}{\text{Total number of samples analysed}} \times 100$$

$$\text{Relative abundance (\%)} = \frac{\text{No of spores of particular species}}{\text{Total number of spores}} \times 100$$

Results and Discussion

Coconut and arecanut based cropping systems of two districts of Kerala were studied for their arbuscular mycorrhizal distribution. The details of the sampling site along with its nutrient management practices is furnished in Table 1. The analysis of soil physico- chemical and mycorrhizal parameters are given in Table 2. Arbuscular mycorrhizal abundance were observed in 93 soil samples with a spore load, ranging from 33.83 ± 10.84 to 154.5 ± 7.01 spores/10 g soil. All the plant roots observed were mycorrhizal except in arecanut at Mogral Puthur. Pearson's correlation of mycorrhizal spore load with root colonization and soil edaphic factors is represented in Table 3. Frequency of root colonization was found to be negatively correlated with mycorrhizal spore load in majority of cropping systems studied. Among the six rhizospheric edaphic factors analysed, soil P and soil pH was found to have a negative correlation with spore load. Total organic carbon content and electrical conductance showed insignificant correlation; however spore load at Patena plot was found to be negatively correlated with electrical conductance at $P \leq 0.05$. Total Nitrogen content was found to be negatively correlated with frequency of root colonization with a significant relation at Keloth. Soil K is often reported to have a stimulatory effect on AM fungi variables [18] and a minimum soil K is often prerequisite for mycorrhizal colonization. However, present data showed that mycorrhizal parameters were independent of available potassium.

AM fungi and Beneficial Microflora

Enumeration of rhizospheric soil samples showed an abundance of soil microflora. Relation between AMF and beneficial microflora is represented in Table 4. Earlier works have reported the presence of different functional groups of bacteria such as nitrogen-fixing bacteria [27], plant growth promoting rhizobacteria, phosphate-solubilizing bacteria [13] associated with the rhizosphere of different plants colonized by AMF [25]. Some of the N-fixing, *Bacillus* spp., fluorescent *Pseudomonas* spp., *Trichoderma* spp., and P-solubilizers obtained in this study site are shown in Fig. 1. In coconut cropping system, a significant correlation could not be drawn for the beneficial microflora and AMF population. However, in arecanut cropping system, a negative correlation existed in AMF population with *Trichoderma* spp., fluorescent *Pseudomonas* spp., and nitrogen fixers. A positive correlation was observed for P-solubilizers. Studies have reported an increase in P-solubilizers in arecanut cropping system with increase in intercrops [22].

Colonization and Spore Density

AMF association in the cropping system was assessed by spore density (spore load) in the rhizospheric soil and by

Table 2 Soil edaphic factors and mycorrhizal parameters

Location	pH	OC (%)	N (%)	P (ppm)	K (ppm)	EC (µs)	Spore load10 g^{-1}	F (%)
HDMSCS, CPCRI	5.43 ± 0.3	0.84 ± 0.4	0.14 ± 0.7	41.4 ± 6.7	20.5 ± 9.1	44.15 ± 7.5	56.83 ± 10.83	59.3 ± 5.2
Patena	5.58 ± 0.1	0.52 ± 0.2	0.11 ± 0.1	20.5 ± 0.7	21.6 ± 3. 7	40.14 ± 1.2	40.14 ± 1.15	69.5 ± 14.5
Patena plot 2	5.90 ± 0.1	1.2 ± 0.2	0.16 ± 0.1	54.86 ± 15.7	208.67 ± 27.7	226.6 ± 57.5	48.66 ± 10.16	‘64.2 ± 7.03
Azad Nagar	5.15 ± 0.2	0.64 ± 0.3	0.1 ± 0.2	24.81 ± 1.6	167.16 ± 6.1	84.4 ± 8.9	154.5 ± 7.01	77.2 ± 2.9
Neerchal	5.34 ± 1.8	2.3 ± 0.9	0.28 ± 0.1	32.7 ± 13.8	51.7 ± 21.6	481.3 ± 90.3	60.33 ± 10.33	57.7 ± 9.62
Velanad	4.02 ± 0.1	1.60 ± 4.8	0.085 ± 0.2	91.5 ± 30.5	13.52 ± 0.5	24.98 ± 12.5	59.98 ± 17.66	61.11 ± 18.3
Pulippara	4.76 ± 2.6	2.2 ± 2.0	0.17 ± 0.1	0.17 ± 0.1	17.3 ± 14.8	49.84 ± 11.3	50.33 ± 33.66	56.4 ± 23.3
Mogral Puthur	7.00 ± 1.1	1.12 ± 1.2	0.15 ± 0.3	22.65 ± 10.6	28.32 ± 24.7	118.11 ± 106.7	33.83 ± 10.84	–
Keloth	5.3 ± 0.8	1.61 ± 1.0	0.191 ± 0.2	21.2 ± 28.1	50.5 ± 24.8	109.03 ± 45.1	33.33 ± 34.17	15 ± 0.34
Neerchal	5.29 ± 1.3	0.766 ± 0.9	0.135 ± 0.2	35.18 ± 25.3	23.7 ± 20.5	129.05 ± 47.7	68.33 ± 15.12	57.16 ± 56.46
Veliyamamgalam	4.82 ± 1.5	0.83 ± 1.0	0.08 ± 0.1	0.063 ± 0.1	50.04 ± 24.8	144.73 ± 72.7	44.5 ± 37.5	39 ± 14.85
Kumbara	4.32 ± 1.6	0.99 ± 2.4	0.19 ± 0.1	78.3 ± 68.3	20.3 ± 9.03	93.4 ± 5.1	44.5 ± 37.15	34.5 ± 14.5

HDMSCS high density multiple species cropping system, *OC* organic carbon, *N* Total Nitrogen, *P* available phosphorous, *K* Available potassium, *EC* Electrical conducatance, *F%* Frequency of root colonization

Table 3 Pearsons correlation analysis of mycorrhizal spore load with root colonization and edaphic factors

Location	Soil pH	OC (%)	EC (µs)	N (%)	P (ppm)	K (ppm)	F (%)
Coconut cropping system							
HDMSCS	−0.19	0.462	−0.23	−0.41	−0.39	0.18	−0.27
Patena	−0.56	−0.49	0.03	0.33	−0.26	−0.01	−0.21
Patena plot 2	−0.09	−0.49	0.03	0.33	−0.26	−0.09	−0.22
Azad Nagar	−0.12	0.05	0.22	−0.07	0.19	−0.12	−0.34
Neerchal	−0.51	0.05	0.22	−0.06	0.19	−0.12	−0.23
Velanad	−0.12	0.56	0.55	0.24	0.11	−0.12	0.80
P ulippara	−0.52	−0.10	-0.69*	−0.09	0.48	−0.52*	1.00
Arecanut cropping system							
Mogral Puthur	0.74	−0.21	−0.23	0.66	−0.01	0.74	–
Keloth	−0.58	0.49	0.34	0.08	0.15	−0.58	0.63
Neerchal	0.83	−0.05	0.35	0.04	0.69	0.83	0.10
Veliyamangalam	0.45	0.66	−0.87*	−0.29	−0.40	0.45	−0.76
Kumbara	0.12	−0.4	−0.78	−0.70	0.40	0.12	−0.03

* Significant at $P < 0.05$

root colonization characterized by arbuscules, vesicles and hyphae. Root colonization percentage in coconut cropping system was the maximum at Azad Nagar (77.76 ± 2.96) and least at Patena plot 2 (48.6 ± 10.16). In arecanut cropping system, the maximum spore load was observed in Keloth plot (58.33 ± 15.2). The fungal spore density ranged from 40.4 to 154.5 spores per 10 g in coconut cropping system and a range of 33–44.5 spores per 10 g soil in arecanut cropping system. There are many factors that could affect spore density in a given host rhizosphere. Values for arbuscular mycorrhizal fungal spore density have varied greatly in previous reports [31].

AMF Species Richness and Diversity

Distribution of AM fungal species in coconut and arecanut cropping systems of two different districts of Kerala are represented in the Table 5. Species richness was the maximum at HDMSCS plot. AM fungal diversity varied with difference of sites (Table 5, 6). Most of the spore morphotypes were common to all sites, and few were specific. Altogether 14 AMF species (Fig. 2) were identified from 93 samples analysed. All spores belonged to the Glomineae order, represented by Glomaceae, Claroideoglomeraceae, Diversisporaceae, Acaulosporaceae, and Gigasporaceae families. Simpson's diversity index (Ds) and Shannon's diversity index (Hs) in coconut cropping system was in the range of 0.89–0.98 and 1.9–4.25, respectively. In arecanut cropping system, the index value of "Ds" and "Hs" ranged from 0.81 to 0.93 and 1.39 to 3.44, respectively. The variation in AM fungal diversity in rhizosphere soil of a particular plant in different locations may be due to the influence of adjoining plants [30, 31]. Earlier studies have reported the occurrence of *Glomus* and *Acaulospora* spp. in coconut

Table 4 Correlation analysis of AMF with other rhizosphere microflora

Location	P_solubilizers	Fluorescent *Pseudomonas* spp.	*Trichoderma* spp.	N_2_fixers	*Bacillus* spp.
Coconut cropping system					
HDMSCS	−0.47	0.23	−0.39	0.15	−0.32
Patena plot 1	0.21	−0.05	−0.30	0.81	−0.61
Patena plot 2	0.35	−0.33	0.07	0.33	0.23
Azad Nagar	0.52	0.10	0.73	−0.65	−0.64
Neerchal	−0.59	–	0.13	0.58	0.79
Velanad	−0.60	–	−0.13	0.23	−0.02
Pulippara	−0.16	–	0.16	0.29	0.07
Arecanut cropping system					
Mogral Puthur	−0.58	0.49	0.34	0.08	0.15
Keloth	0.74	−0.22	−0.23	0.66	−0.01
Neerchal	0.83	−0.04	0.35	0.04	0.69
Veliyamangalam	0.45	0.66	−0.87	−0.29	−0.40
Kumbara	0.12	−0.42	−0.78	−0.70	0.40

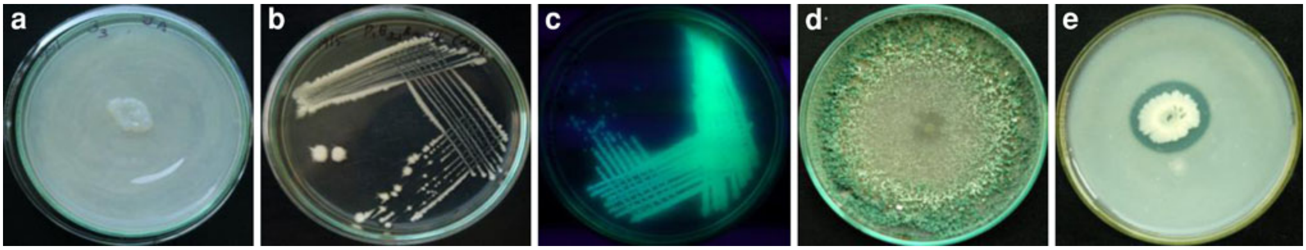

Fig. 1 Rhizosphere microflora. **a** Growth of N-fixer on Nitrogen free media, Banana rhizosphere; ACS,Veliyamangalam. **b** *Bacillus* sp., Banana rhizosphere, CCS, Patena 1. **c** fluorescent *Pseudomonas* sp., Coconut rhizosphere, HDMSCS, CPCRI. **d** *Trichoderma* sp., Arecanut rhizosphere, Kumbara. **e** P-solubilizer, Pepper rhizosphere, ACS, Neerchal

Table 5 Mycorrhizal status in coconut and arecanut cropping sytems

Location	AMF spp.
HDMSCS, CPCRI	*Funneliformis caledonium, Funneliformis mosseae, Rhizophagus fasiculatum, Diverssipora eburneum, Gigaspora decipiens, Gi.giganteae, Acaulospora denticulata, A. scrobiculata*
Patena	*G.macrocarpum, Funneliformis mosseae, Rhizophagus clarus*
Patena plot 2	*G.macrocarpum, Gi.giganteae, A. denticulata, A. Scorbiculata*
Azad Nagar	*Rhizophagus fasiculatum, Rhizophagus clarus, Diverssipora eburneum*
Neerchal	*G. aggregatum, Rhizophagus fasiculatum, Gi.giganteae, A. denticulata, A. Scorbiculata*
Velanad	*Rhizophagus fasiculatum, G. aggregatum*
Pulippara	*G. aggregatum, Funneliformis mosseae*
Mogral Puthur	*Rhizophagus fasiculatum*
Keloth	*G. aggregatum, Funneliformis mosseae*
Neerchal	*G. aggregatum, Claroideoglomus luteum, Funneliformis caledonium, A. Bireticulata*
Veliyamangalam	*Rhizophagus fasiculatum, Claroideoglomus luteum*
Kumbara	*Rhizophagus fasiculatum, G. multicaule*

HDMSCS high density multiple species cropping system

cropping system [29]. Interestingly, species diversity was more in coconut cropping system than in arecanut cropping system. Studies have reported that the host root structure can influence the mycorrhizal morphology. The relative abundance and frequency of occurrence of the fourteen identified AMF species is depicted in Table 7. An increase in number

Table 6 AMF diversity indices in coconut and arecanut based cropping systems

Location	Diversity index		Species richness
	Ds	Hs	
Coconut cropping system			
HDMSCS	0.89	3.30	8
Patena plot 1	0.59	1.91	3
Patena plot2	0.86	2.91	4
Neerchal	0.83	4.56	5
Azadnagar	0.98	2.61	2
Velanad	0.85	2.98	2
Pulippara	0.81	2.41	2
Arecanut cropping system			
Mogral Puthur	0.83	2.49	1
Keloth	0.83	2.48	2
Neerchal	0.91	3.44	5
Veliyamangalam	0.81	1.39	2
Kumbara	0.84	2.50	2

Ds Simpsons diversity index, *Hs* Shannons diversity index

of intercrops increased the AMF diversity, this can be due to the fact that an increase in intercrops over a cropping system increases the microbial yield of a place due to the greater availability of root exudates for microbial survival. Overall, Glomeraceae was the dominant family with a frequency of occurrence of 33.5 % and 38.5 % in coconut and arecanut cropping systems respectively. The reports of earlier workers also revealed that *Glomus* is the dominant genus occurring in Indian soil [16]. Acaulosporaceae dominated next with an occurrence frequency of 14.5 % in coconut and 6.8 % in arecanut cropping systems. AM spp. of the family Gigasporaceae (5.1 %) and Diversisporaceae (2.3 %) were observed only in coconut cropping system, while members of the family Clarideoglomeraceae (1.7 %) were observed only in arecanut cropping system. The relative abundance of the most dominant genus *Funneliformis* was higher in coconut cropping system (51–52.5 %) when compared to its abundance in arecanut cropping system (19.1 %). It was followed by the second most frequented genus *Glomus*, with

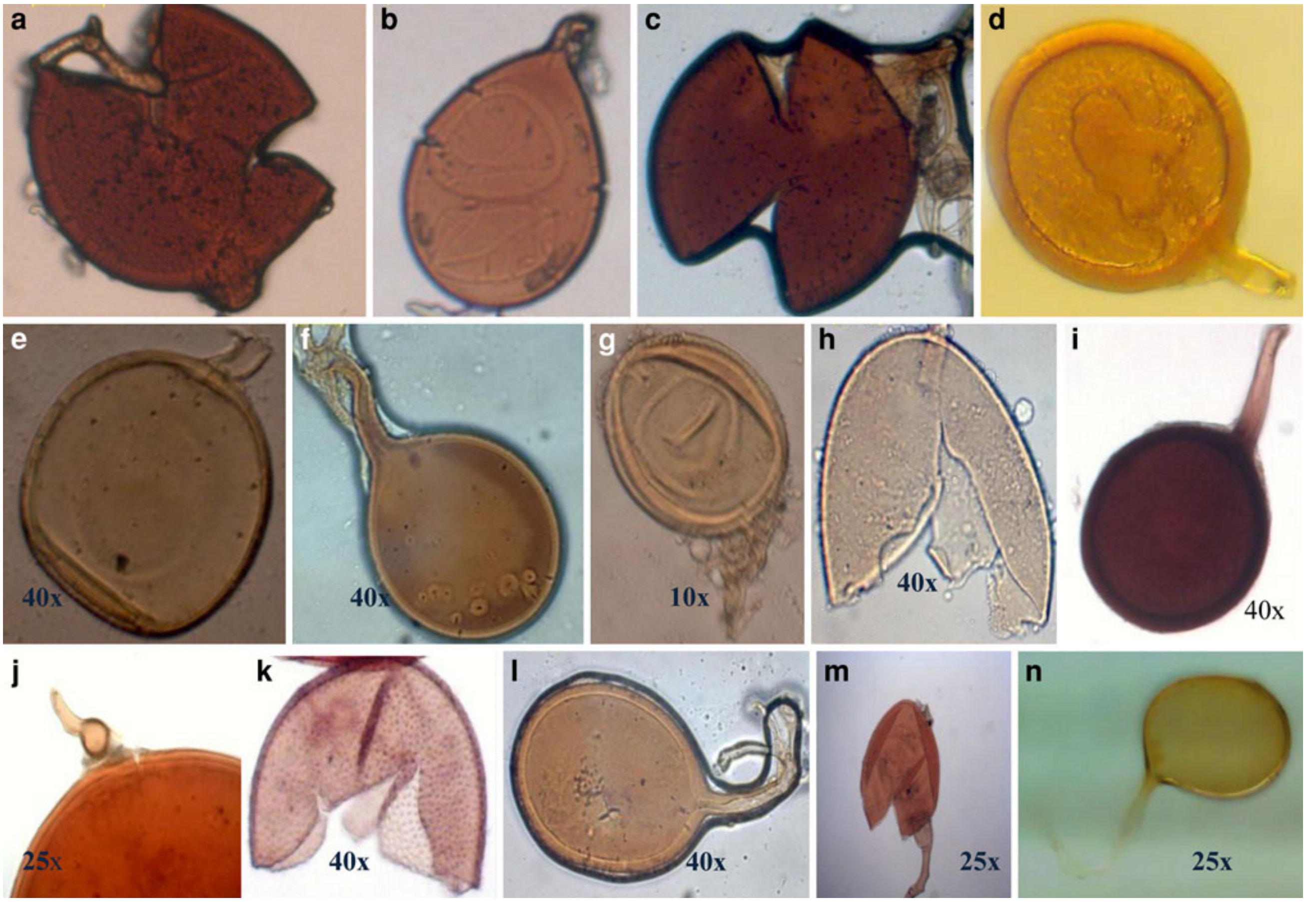

Fig. 2 AMF diversity in coconut and arecanut based cropping systems. **a** *Glomus multicaule,* ACS, Neerchal. **b** *Claroideoglomus, luteum,* ACS, Keloth. **c** *Glomus* sp,ACS, Neerchal. **d** *Glomus* sp., CCS, Velanad. **e** *Glomus* sp., CCS, Azad Nagar. **f** *Funneliformis, caledonium,* Keloth. **g** *Rhizophagus clarus*, CCS, Azad Nagar. **h** *Acaulospora laevis,* CCS, HDMSCS. **I** *Rhizophagus fasiculatum,* CCS, HDMSCS, CPCRI. **J** *Gigaspora giganteae*,HDMSCS, CPCRI. **k** *Acaulospora denticulata,* HDMSCS,CPCRI. **l** *Diverssipora, eburneum,* Azad Nagar. **m** *Gigaspora decipiens*, HDMSCS, CPCRI. **n** *Glomus* sp., CCS, Velanad

Table 7 Distribution of AMF in coconut and arecanut cropping systems

Family/AMF sp.	Frequency of occurrence (%)[a]		Relative abundance (%)[b]	
	CCS	ACS	CCS	ACS
Glomeraceae				
Glomus aggregatum	3	5	24.0	20.03
G. multicaule	0	9.8	0	3.94
G.macrocarpum	8.5	0	29.5	0
Rhizophagus fasiculatum	5.4	5.4	33.68	2.2
Rhizophagus clarus	0	12	0	4.8
Funneliformis caledonium	8.4	0	52.1	0
Funneliformis mosseae	8.2	5	51.2	19.1
Claroideoglomeraceae				
Claroideoglomus luteum	0	1.7	0	7.2
Diversisporaceae				
Diverssipora eburneum	2.3	0	14.5	0
Gigasporaceae				
G.giganteae	2.5	0	3.40	0
G.decipiens	2.6	0	0.325	0
Acaulosporaceae				
Acaulospora denticulata	7.9	6.8	49.1	0.78
A. scrobiculata	5	0	31.5	0
A.laevis	1.6	0	10.5	0

CCS coconut cropping system, *ACS* arecanut cropping system

[a] Number of soil samples possessing spores of a particular species divided by total number of samples analysed ×100

[b] Number of spores of a particular species divided by total number of spores ×100

a relative abundance of 24 % and 20.03 % respectively in coconut and arecanut cropping systems.

Glomus aggregatum (3–5 %), *Funneliformis mosseae* (5–8.2 %), and *Rhizophagus fasiculatum* (5.4 %) were uniformly abundant in both the cropping systems. *Diverssipora eburneum* (2.3 %)**,** *Funneliformis caledonium (*8.4 %), *G.macrocarpum* (8.5 %), *Gi.giganteae* (2.5 %), *Gi.decipiens* (2.3 %), *A.bireticulata* (7.9 %), *A.scorbiculata* (5 %), and *A.laevis* (1.6 %) were found to be associated with coconut cropping system. *Claroideoglomus luteum* (1.7 %), *A.scorbiculata* (6.8 %) *Rhizophagus clarus* (12 %), *Glomus multicaule* (9.8 %) were found to be associated with arecanut cropping system. Our studies were in tandem with other reports which revealed that differences in host plants may alter the spore population at a particular place [6].

Conclusions

AMF colonization studies have been reported in coconut cropping systems, but few works throw light on the mycorrhizal association in arecanut cropping systems. This study also reveals that AM Fungal colonization pattern is inversely related to soil pH and available phosphorous in the soil. Our studies suggest that AMF colonization and species richness is more in coconut cropping systems compared to arecanut cropping systems. It was observed that the spore load and spore diversity were not related and diversity increased with the increase in number of intercrops irrespective of the cropping systems studied. Glomeraceae and Acaulosporaceae families were preponderent in both the cropping systems. However, Gigasporaceae was solely present in coconut cropping system. *Glomus aggregatum*, *Funneliformis mosseae*, and *Rhizophagus fasiculatum* were the uniformly abundant genera in both the cropping systems. Enumeration of the soil microflora revealed that the population of P-solubilizers and AMF spore density were positively correlated in arecanut cropping system, however there was no relationship between soil microflora and AMF species in coconut cropping system.

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References

1. Allen MF (1982) Influence of vesicular-arbuscular mycorrhiza on water movement through *Boutenia gracilis* (HBK) Long ex Steud. New Phytol 91:191–196
2. Bianciotto V, Lumini E, Lanfranco L, Minerdi D, Bonfante P, Perotto S (2000) Detection and identification of bacterial endosymbionts in arbuscular mycorrhizal fungi belonging to family *Gigasporaceae*. Appl Environ Microbiol 66:4503–4509
3. Bopaiah BM (1991) Soil microflora and VA-mycorrhiza in areca based high density multiple species cropping and monocropping systems. J Plant Crops 18(Supplement):224–228
4. Bray RH, Kurtz LT (1945) Determination of total, organic, and available forms of phosphorus in soils. Soil Sci 59:39–45
5. Christensen H, Jakobsen I (1993) Reduction of bacterial growth by a vesicular-arbuscular mycorrhizal fungus in the rhizosphere of cucumber (*Cucumis sativus* L.). Biol Fertil Soils 15:253–258
6. Dodd JC, Koomen Arias I, Hayman DS (1990) The management of populations of vesicular-arbuscular mycorrhizal fungi in acid-infertile soils of a savanna ecosystem. Plant Soil 122:229–240
7. Gerdmann JH, Nicolson TH (1963) Spores of mycorrhizal endogone species extracted from soil by sieving and decanting. Trans British Mycol Soc 46:235–244
8. Hanway JJ, Heidel H (1952) Soil analysis method as used in Iowa state college soil testing laboratory. Iowa state coll agric 57:1–31
9. Harikumar VS, Thomas GV (1991) Effect of fertilizers and irrigation on vesicular arbuscular mycorrhizal association in coconut. Philipp J Coconut Stud 16:20–24
10. John TV St (1988) Prospects for application of vesicular-arbuscular mycorrhizae in the culture of tropical palms. Adv Econ Bot 6:50–55
11. Johnston A (1949) Vesicular-arbuscular mycorrhiza in sea island cotton and other tropical plants. Trop Agr (Trinidad) 26:118–121
12. Kjeldahl J (1883) A new method for the estimation of nitrogen in organic compounds. Z Anal Chem 22:366

13. Linderman RG, Paulitz TC (1990) Mycorrhizal–rhizobacterial interactions. In: Hornby D, Cook RJ, Henis Y, Ko WH, Rovira AD, Schippers B, Scott PR (eds) Biological control of soil-borne plant pathogens. CAB International, Wallingford, pp 261–283
14. Lloyd H, Zar KH, Karr JR (1968) On the calculation of information-theoretical measures of diversity [J]. Am Midl Nat 79:257–272
15. Meyer JR, Linderman RG (1986) Response of subterranean clover to dual inoculation with vesicular-arbuscular mycorrhizal fungi and a plant-growth-promoting bacterium, *Pseudomonas putida*. Soil Biol Biochem 18:185–190
16. Muthukumar T, Udaiyan K (2000) Arbuscular mycorrhiza of plants growing in the Western Ghats region, Southern India. Mycorrhiza 9:297–313
17. Olsen S, Cole C, Watanabe F, Dean L (1954) Estimation of available phosphorus in soils by extraction with sodium bicarbonate. USDA Circular Nr 939, US Gov. Print. Office, Washington, D.C
18. Ouimet R, Camire C, Furlan V (1996) Effect of soil K, Ca and Mg saturation and endomycorrhization on growth and nutrient uptake of sugar maple seedling. Plant Soil 179:207–216
19. Pankhurst CE, Lynch JM (1994) The role of soil biota in sustainable agriculture. In: Pankhurst CE, Doube BM, Gupta VVSR, Grace PR (eds) Soil biota: management in sustainable farming systems. CSIRO Information Sytems, East Melbourne, pp 3–9
20. Philips SJM, Hayman DS (1970) Improved procedure for cleaning roots and staining parasitic and vesicular arbuscular fungi for rapid assessment of infection. Trans British Mycol Soc 55: 158–161
21. Ramesh CR (1984) Root infection and population density of VA mycorrhizal fungi in a coconut based multistoreyed cropping system. Proc Plantation Crops Symposium V (PLACROSYM), pp 548–554
22. Rawther TS, Abraham KJ, Achuthan Nair M, Jayasankar NP (1980) Microbial profiles of arecanut soils under mixed cropping with special reference to arecanut yellow leaf disease. Proc Plantation Crops Symposium II (PLACROSYM), pp 71–75
23. Sanders FE, Sheikh NA (1983) The development of vesicular arbuscular mycorrhizal infection in plant root systems. Plant Soil 71:223–246
24. Schübler A, Schwarzott D, Walker C (2001) A new fungal phylum, the Glomeromycota: phylogeny and evolution. Mycol Res 105:1413–1421
25. Secilia J, Bagyaraj DJ (1987) Bacteria and actinomycetes associated with pot culture of vesicular arbuscular mycorrhizas. Can J Bot 33:1069–1107
26. Simpson EH (1949) Measurement of diversity. Nature 163:688
27. Smith KP, Goodman RM (1999) Host variation of interactions with beneficial plant associated microbes. Annu Rev Phytopathol 37:473–491
28. Thomas GV, Ghai SK (1987) Genotype dependent variation in vesicular-arbuscular mycorrhizal colonization of coconut seedlings. Proc Indian Acad Sci Plant Sci 97:289–294
29. Thomas GV, Rajagopal V, Bopaiah BM (1993) VA-Mycorrhizal associations in relation to drought tolerance in coconut. J Plant Crops 21:98–103
30. Toro M, Nedialkova K, Azcon R, Barea JM (1996) Establishment of two rock phosphate-solubilizing bacteria in the rhizosphere of mycorrhizal onion plants and their effect on plant growth in a microcosm. In: Azcon-Aguilar C, Barea JM (eds) Mycorrhizas in integrated systems from genes to plant development. European Commission, Directorate-General XII, Science, Research and Development, Brussels, pp 665–668
31. Walker C, Mize CW, McNabb HS (1982) Populations of endogonaceous fungi at two locations in central Iowa. Can J Bot 60:2518–2529
32. Walkley A, Black IA (1934) An examination of degtjareff method for determining soil organic matter and a proposed modification of the chromic acid titration method. Soil Sci 37:29–37