

Mycorrhizas of the Dominant Species in Four Plant Communities of Chebaling National Nature Reserve

ZHUANG Xue-ying¹, CHEN Hong-yao¹, HUANG Yong-fang¹, LU Qi-ming², LIN Lin², ZHUANG Yan³

(1 College of Forestry, 2 College of Sciences, 3 College of Resources and Environment,
South China Agric. Univ., Guangzhou 510642, China)

Abstract: Mycorrhizal associations of twenty plant species in four different plant communities of the Chebaling National Nature Reserve were investigated in the summer from 1995 to 1998. Except for two species (*Dicranopteris linearis* and *Diospyros tsangii*), eighteen species examined were associated with either vesicular-arbuscular mycorrhiza (VAM) or ectomycorrhiza (ECM). Four species of Fagaceae and *Pinus massoniana* were consistently associated with ECM while other thirteen species were associated with VAM. The fruiting bodies of ectomycorrhizal fungi were abundant and diverse in intact forest dominated by Fagaceae. Only a few species of macrofungal bodies were found in the pine dominated forest and secondary broad-leaved forest and none were seen in grassland during the study. VAM spore density was generally lower in the grassland than other community types. It is possibly due to degradation in floristic composition and soil fertility.

Key words: Chebaling National Nature Reserve; mycorrhiza, plant communities

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Mycorrhiza is a ubiquitous symbiotic association between plant and fungus. It can improve plant's phosphorus absorption by releasing tightly-bound soil phosphorus, but the beneficial effects of the mycorrhizal fungi may vary with the plants^[1]. Many studies were done on the mycorrhizas of the commercial plants commonly used in forestry^[2,3], but the mycorrhizal associations of many native species involving in natural succession of South China are still unknown. This study aimed to provide the information on the status and distribution of the mycorrhizal associations of the dominant plants from four plant communities at Chebaling National Nature Reserve (CNNR) of Guangdong Province. The role and potential application of mycorrhiza in forest management of South China are discussed.

1 Materials and Methods

1.1 Natural condition of the study site

CNNR (24°41'N, 114°10'E) lies on the southern margin of Nanling Ranges of Guangdong Province. It is

rugged between 330 m and 1 256 m with a total area of 7 545 hm². Mean annual temperature is 19.6 °C with the maximum temperature of 38.4 °C and the minimum temperature of -5.5 °C. Mean annual precipitation is 1 536.6 mm.

1.2 Field survey and sampling

The field sampling was conducted in July during 1995 to 1998. Samples containing plant roots and the soil from the rhizosphere of the sampled plant were taken from the four plant communities—secondary grassland, pine dominated forest and secondary broad-leaved forest, and intact broad-leaved forest (less disturbed). The natural condition and floristic composition of the study sites were briefly described elsewhere^[4].

The root and soil samples of each species were taken from three individuals in each community. A total of ninety-eight root samples and their rhizospheric soil samples were collected from twenty dominant species of four successional stages of vegetation.

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1.3 Examination of root colonization of mycorrhizas

Immediately after field collections, the root samples were washed. The fine roots were cut up into 1-cm segments and fixed in small plastic bottles with FAA (formalin-acetic acid-alcohol solution). The fixed root segments were cleared and stained following Kommanik and McGraw's treatment^[5]. Thirty segments of each sample were applied to assess the colonization of mycorrhizas. Vesicular-arbuscular mycorrhiza (VAM) was identified by the presence of vesicles and/or arbuscles and endomycorrhiza (ECM) was identified by the presence of a typical fungal sheath. Percentage of colonization is calculated as the number of infected root segments over the total number observed.

1.4 Extraction of VAM spores

Wet sieving and decanting method^[6] was used to extract and quantify endogenous spores in the soil. Spores with a diameter greater than 0.046 mm sieve were counted. The total number of spores in the sample was converted to spores per gram of dry soil.

2.1 Mycorrhizal infection of the major plants in different community types

Four species of Fagaceae (*Castanopsis carlesii*, *C. eyrei*, *C. fargesii*, *Lithocarpus glaber*) and *Pinus massoniana* formed ECM while thirteen species were associated with VAM. Only two species (*Dicranopteris linearis* and *Diospyros tsangii*) were not found any structure of mycorrhizal association (Table 1).

2.2 Mycorrhizal fungi in four plant communities

A total of 42 soil-borne macrofungi were seen and collected in the field survey. The major genera and families were shown in Table 2. Of these, nine genera were mentioned to enable develop mycorrhizal associations with the plants^[7]. Ten genera were from the intact forest dominated by Fagaceae species. Only a few species were seen in secondary forest or pine forest and none were seen in the sites of the grassland during the study. Two species were locally common: *Craterellus aureus* in intact forest and *Scleroderma aurantium* in pine forest. Other species were usually rare.

2 Results

Tab. 1 Mycorrhizas and rhizospheric spores of the common species in four communities

Community Type	Species Examined	spores / (spores · g ⁻¹)	Mycorrhiza	
			Infection rates/%	Type ¹⁾
Intact Forest	<i>Castanopsis carlesii</i>	6	52.3	ECM
	<i>Castanopsis eyrei</i>	13	62.0	ECM
	<i>Neolitsea kwangsiensis</i>	5	9.3	VAM
	<i>Symplocos laurina</i>	24	53.3	AM
		7	38.0	AM
Secondary Forest	<i>Adinandra millettii</i>			
	<i>Alniphyllum fortunei</i>	8	18.0	AM
	<i>Bretschneidera sinensis</i>	—	12.0	VAM
	<i>Eleocharis decipiens</i>	8	36.0	AM
	<i>Eurya nitida</i>	8	18.0	VAM
	<i>Liquidambar formosana</i>	29	34.0	VAM
	<i>Lithocarpus glaber</i>	6	77.0	ECM
		27	9.0	ECM
Pine Dominated Forest	<i>Castanopsis fargesii</i>			
	<i>Choerospondias axillaris</i>	11	75.0	VAM
	<i>Dicranopteris linearis</i>	12	0	—
	<i>Diospyros tsangii</i>	5	0	—
	<i>Eurya nitida</i>	—	10.7	VAM
	<i>Liquidambar formosana</i>	29	38.8	VAM
	<i>Machilus chekiangensis</i>	48	13.7	AM
	<i>Pinus massoniana</i>	17	12.0	ECM
	<i>Schima superba</i>	19	20.8	VAM
		4	42.0	AM
Grassland	<i>Imperata cylindrica</i>			
	<i>Miscanthus floridulus</i>	2	50.0	VAM

1) AM = mycorrhiza with only arbuscles, VAM = mycorrhiza with both vesicles and arbuscles, ECM = mycorrhiza with mantle and Hartig net

Endogonaceous spores were commonly found in the rhizosphere of the plants. They were dominated by *Glomus*, but the density varied with the species and

habitats (Table 2). In general, VAM spores were more abundant in the forest communities than in grassland.

Tab. 2 The genera and family of the major macrofungi seen in field survey¹⁾

Family	Genus	Mycorrhiza	Occurrence in the communities			
			IBF	SBF	PF	SG
Amanitaceae	<i>Amanita</i>	Y	+		+	
Boletaceae	<i>Boletus</i>	Y	+			
	<i>Suillus</i>	Y	+			
Cantharellaceae	<i>Craterellus</i>	Y	+	+		
Clavariaceae	<i>Clavaria</i>	N	+			
Coprinaceae	<i>Coprinum</i>	Y	+		+	
Hygrophoraceae	<i>Hygrophorus</i>	Y	+			
Russulaceae	<i>Russula</i>	Y	+			
Sclerodermataceae	<i>Scleroderma</i>	Y			+	+
Strobilomycetaceae	<i>Boletellus</i>	Y		+		
Tricholomataceae	<i>Clitocybe</i>	N	+			
	<i>Collybia</i>	N		+	+	
	<i>Tricholoma</i>	N	+			

1) Type of community: IBF = intact broad-leaved forest; SBF = secondary broad-leaved forest, PF = pine forest; SG = secondary grassland; Mycorrhizal: y = yes, n = no; Distribution: + = rare; ++ = locally common

3 Discussion

3.1 The role of VAM in South China

Many common plantation trees in forestry, such as pines, poplar, and eucalyptus, are associated with ectomycorrhiza and most of agricultural crops are associated with VAM mycorrhiza. Therefore, there is a notion that ECM is important in forestry while VAM is important in agriculture. However, our study and other researches recently done in South China^[8] evidenced that VAM were very common in both native forest and plantations and many native plants involving in early succession could potentially develop VAM. These vesicular-arbuscular mycorrhizal plants play a very important role in natural succession, especially on degraded lands. Therefore, application of vesicular-arbuscular mycorrhizal inoculation has a great potential to promote the forest rehabilitation on degraded lands of South China.

3.2 Diversity of mycorrhizal fungi and forest conservation

Since many ectomycorrhizal fungi are obligated to specific host plants^[9,10], forest conservation is the important basis for high diversity of some ectomycorrhizal fungi. It was evidenced by our field observation that although both the species of Fagaceae and *Pinus*

massoniana could form ECM, the fungal species were different. The dominant ectomycorrhizal fungi in intact broad-leaved forest were abundant and diverse, which included *Boletus*, *Lactarius*, *Craterellus*. The ectomycorrhizal fungi were simple and few in secondary forest. None were seen in grassland which were dominated by endomycorrhizal plants. Therefore, conserving intact old forest or establishing plantations consisting of ectomycorrhizal plants such as Fagaceae is necessary for the development of native mycorrhizal fungi.

The secondary grassland had very low population of endogonaceous spores. It is possibly due to simple floristic composition and lower soil fertility. Some other study elsewhere showed VAM spores were lack or absent in seriously degraded sites, especially in the areas without host plants^[11]. Another possible explanation was that the investigations were done in summer. Based on our study on monthly variations of mycorrhiza and spore density in a plantation of Guangzhou, the endogonaceous spores were generally low in summer and high in autumn (Zhuang et al., in press). Therefore, further studies are required in other seasons to verify it. The present study was working on adult individuals of the plants. Would the status and role of the mycorrhizal associations of these plants change with their ages? The information on the composition of

VAM spores in the soil from different communities was still lack. Further studies on the mycorrhizas of the young seedlings and identification of VAM spores in natural forest are being conducted to supplement more information on this study.

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车八岭国家级自然保护区不同植被群落建群种的菌根

庄雪影¹, 陈红跃¹, 黄永芳¹, 卢其明², 林琳², 庄严³

(1 华南农业大学林学院, 2 华南农业大学理学院, 3 华南农业大学资源环境学院, 广东 广州 510642)

摘要:报道了广东省车八岭国家级自然保护区原生性阔叶林、次生性阔叶林、马尾松林及次生草坡等4种植物群落中20种植物的菌根感染率和土壤中内生菌根菌孢子的分布状况。除了2种植物: 芒萁 (*Dicranopteris linearis*) 和曾氏柿 (*Diospyros tsangii*) 外, 18种植物均可与真菌形成内生型或外生型菌根。其中, 4种壳斗科植物和马尾松 (*Pinus massoniana*) 具有外生菌根, 其它13种植物具有丛生-泡囊型内生菌根。外生菌根菌子实体在以壳斗科植物为优势种的原生性次生林中较多且种类丰富, 在松林和次生阔叶林有少数种类, 但次生草坡群落未见有外生菌根菌子实体。比较不同演替阶段土壤中内生孢子密度, 内生孢子在各种植物群落中普遍存在, 但在次生草坡中通常较少, 这可能与草坡群落植物种类单一及土壤肥力低有关。

关键词: 车八岭国家级自然保护区; 菌根; 植物群落

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