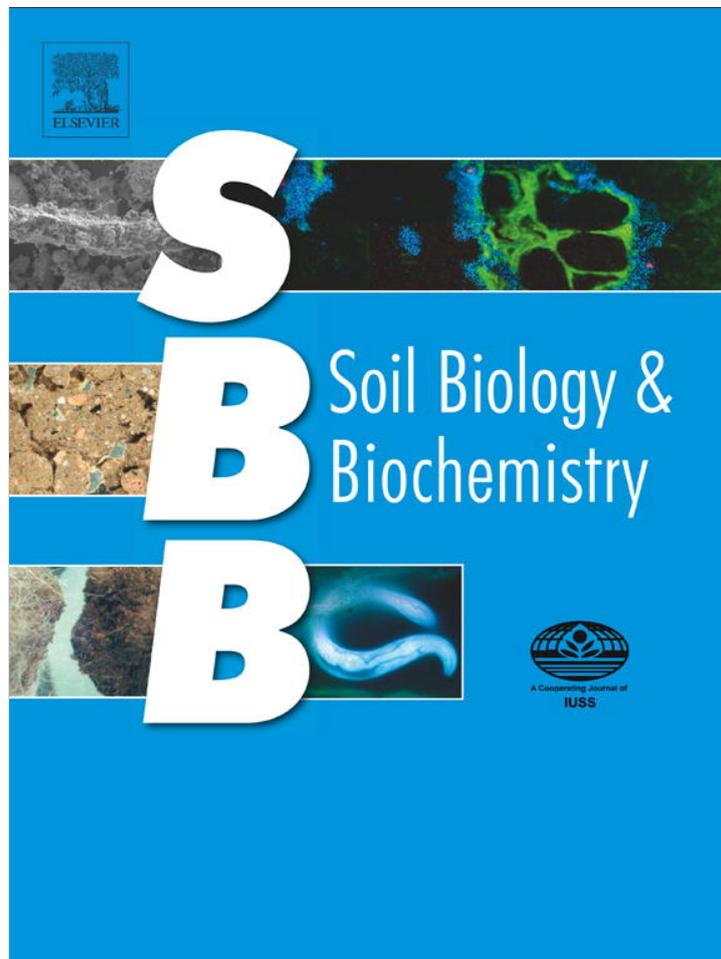


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Ectomycorrhizal diversity enhances growth and nitrogen fixation of *Acacia mangium* seedlings

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ABSTRACT

Increasing interest has been given so far to the role of mycorrhizal symbiosis on plant diversity and ecosystem productivity. However much remains unknown about the effect of ectomycorrhizal fungal diversity on plant growth and rhizobial symbiosis. The purpose of this study is to investigate the influence of ectomycorrhizal diversity on root nodulation and plant nutrient uptake during plant growth. A gradient of ectomycorrhizal diversity was created (ranged from one to six fungal isolates) on Australian Acacia (*Acacia mangium*) seedlings grown on a phosphate-deficient soil in controlled conditions. The results clearly show (i) an enhancement of *A. mangium* growth due to ectomycorrhizal fungal inoculation, (ii) as well as significant effects of increasing ectomycorrhizal diversity and soil ectomycorrhizal mycelium density on whole plant biomass and plant nutrient uptake. They also reveal an effect of ectomycorrhizal diversity effect on the functioning of the nitrogen-fixing symbiosis. These results emphasize the need to manage soil ectomycorrhizal potential (abundance and diversity of ectomycorrhizal mycelium) in forest management practices in order to optimize N₂ fixation and seedling growth, leading thus to dramatic improvements in outplanting performances with fast-growing tree legumes on various reforestation sites, more particularly in tropical and Mediterranean areas.

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1. Introduction

The nature of relationships between biodiversity and plant productivity has aroused general interest but the majority of experimental studies have primarily focused on aboveground plant diversity (Daft, 1991; Tilman et al., 1996; Hooper and Vitousek, 1997, 1998; Wardle et al., 2000). The crucial role of belowground microbial communities in terrestrial ecosystem functioning (van der Heijden et al., 2008), such as nutrient uptake (Sprent, 2001), carbon cycling (Högberg et al., 2001), nitrogen cycling (Kowalchuk and Stephen, 2001), and soil formation (Rillig and Mummey, 2006) has only been recently investigated. Mycorrhizal fungi form an important component of the sustainable soil–plant–system (Bruno

et al., 2003; Finlay, 2008) forming symbiotic relationships with about 80% of terrestrial plant species (Smith and Read, 2008) and mainly enhancing plant nutrient uptake, especially of phosphorus (Smith and Read, 2008). The benefits of mycorrhizal symbiosis to the host plant not only result from a close relationship between the fungal symbiont and plant species but also from the interactions between soil bacterial and fungal communities (Garbaye, 1991; Founoune et al., 2002a,b; Frey-Klett et al., 2005; André et al., 2005). It is well known for instance that mycorrhizal symbiosis can dramatically increase rhizobial symbiosis (nodulation and N₂ fixation) (André et al., 2005).

Deciphering the relationships between mycorrhizal symbiosis, plant diversity and ecosystem productivity is of major interest. van der Heijden et al. (1998, 2002, 2003) demonstrated that species composition and species richness of arbuscular mycorrhizal communities are essential factors in determining the plant composition and the ecosystem variability and productivity. The

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other major form of mycorrhizas, the ectomycorrhizas, is also considered as an important ecological factor influencing plant community dynamics since the vegetation with which they are associated is unlikely to survive without ectomycorrhizal symbionts (Smith and Read, 2008). Ectomycorrhizal fungi affect trees and shrubs, gymnosperms (Pinaceae) and angiosperms, and usually this symbiosis results from the association of Homobasidiomycetes with about 20 families of mainly woody plants. It has been reported that a relatively high diversity of ectomycorrhizal fungi (estimated 5000–6000 species worldwide, mainly Basidiomycetes and Ascomycetes) contracted symbiotic relationships with these woody species (Molina et al., 1992; Allen et al., 1995; Valentine et al., 2004). On a root system and within a few centimeters may coexist more than 5–10 different ectomycorrhizal fungal species (Allen et al., 1995). However, few studies have been performed to test the influence of multiple ectomycorrhizal fungal inoculations on plant growth (Baxter and Dighton, 2001, 2005). For instance, it has been reported that the growth of Douglas fir seedlings inoculated with two ectomycorrhizal species was larger than that recorded with plants inoculated with a single fungal species (Parlade and Alvarez, 1993). Jonsson et al. (2001) have investigated the influence of ectomycorrhizal diversity on the growth of *Betula pendula*. They reported that the tree species growth was higher when seedlings were inoculated with eight ectomycorrhizal fungi compared to the plants inoculated with single fungal species. All these data suggest that ectomycorrhizal diversity plays a significant role in the host development. However, these experiments remain very scarce. They have been performed with only a few tree species such as *Pinus radiata* (Chu-Chou and Grace, 1985), *Pinus patula* (Reddy and Natarajan, 1997), and *B. pendula* (Jonsson et al., 2001). It is well known that many N₂-fixing trees are especially dependent on mycorrhizas to take up nutrients other than N required for plant growth and efficient N₂ fixation (Smith and Read, 2008). However the influence of ectomycorrhizal diversity on growth response and on the rhizobial symbiosis development of fast-growing leguminous trees remains largely unknown.

It has been shown in controlled glasshouse conditions that mycorrhizal symbiosis can significantly increase the growth of Australian *Acacia* which are frequently used in agroforestry plantations to rehabilitate degraded soils in the tropics (Duponnois et al., 2000; Duponnois and Plenchette, 2003). The *Acacia* species are able to grow on low-N soils thanks to their capacity to form root symbiosis with rhizobial bacteria. As other tree genera native from Australia (i.e. *Casuarina* and *Eucalyptus*), they can be associated with either ectomycorrhizal and/or arbuscular mycorrhizal fungi (Ducouso, 1991). The sustainability of the mycorrhizal promoting effect has also been assessed in field conditions (Duponnois et al., 2005, 2007). However, these experiments have been mainly

conducted with plants mycorrhized with a single efficient fungal species.

The aim of this study was to investigate the influence of ectomycorrhizal diversity on *Acacia mangium* plant growth, root nodulation by a strain of *Bradyrhizobium* sp. as well as plant nutrient uptake by creating a gradient of ectomycorrhizal fungal diversity (ranged from one to six fungal isolates). We hypothesized that the influence of ectomycorrhizal fungal diversity on plant performance and root nodulation was not an additive positive effect of each fungal isolate but result from complex interactions between the ectomycorrhizal symbionts, the bradyrhizobial strain and the host plant.

2. Materials and methods

2.1. Plant species

Seeds of *A. mangium* Willd collected in the Bayotte Forest (Casamance, Sénégal) were surface sterilized with 95% concentrated sulfuric acid for 60 min. Then, the acid solution was removed and the seeds were rinsed for 12 h four times with sterile distilled water. Surface-sterilized seeds were then aseptically sown in Petri dishes filled with 1% (w/v) agar and germinated in the dark at 25 °C for 4 days. The seedlings were used when taproots were 1–2 cm long.

2.2. Fungal inocula and rhizobia

The origins of the ectomycorrhizal fungi are indicated in Table 1. The fungal strains were maintained in Petri dishes on Modified Melin-Norkrans (MMN) agar medium at 25 °C in the dark. Fungal inoculum was grown in vermiculite–peat moss (4:1, v/v) moistened to field capacity with 450 mL MMN per liter of vermiculite (Duponnois and Garbaye, 1991). The inoculum was incubated at 28 °C in the dark for 6–8 weeks until the substrate was fully colonized. The rhizobial strain *Bradyrhizobium* sp. Aust 13C was isolated from nodules collected in natural stands of *A. mangium* in Australia (Galiana et al., 1990, 1994). The strain was cultured in glass flasks containing liquid yeast extract-mannitol medium at 28 °C on an orbital shaker (Vincent, 1970).

2.3. Glasshouse experiments

2.3.1. Experiment 1: relationships between fungal inoculum density, plant growth and nodulation parameters

The aim of these experiments was to determine the relationships between the abundance of ectomycorrhizal propagules in the soil and the growth response of the host plant. To obtain a scale of inoculum density, the disinfected soil was mixed with 0, 1.25, 2.5, 5

Table 1
Origins of the six ectomycorrhizal isolates tested in the present study.

Species and herbarium ID	Host tree	Origin	Collectors
<i>Pisolithus albus</i> IR100 (Martin et al., 2002)	<i>Acacia mangium</i>	Casamance, Senegal	R. Duponnois & A.M. Bâ ^a
<i>Scleroderma dictyosporum</i> pat. IR109	<i>Azelia africana</i>	Houet, Burkina Faso	A.M. Bâ ^a
<i>S. verrucosum</i> Bull. (Pers.) sensu Grev. IR500	<i>Uapaca somon</i>	Comoé, Burkina Faso	K. Sanon ^b
<i>Scleroderma</i> sp1 IR409	<i>Uapaca guineensis</i>	Houet, Burkina Faso	K. Sanon ^b
<i>Scleroderma</i> sp1 IR406	<i>Uapaca guineensis</i>	Houet, Burkina Faso	K. Sanon ^b
<i>Scleroderma</i> sp. SC2	<i>Uapaca bojeri</i>	Arivonimamo, Madagascar	H. Ramanankierana ^c

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and 10% (v/v) fungal inoculum, and for each inoculum rate, the amount of peat–vermiculite mixture added to the cultural substrate was adjusted to 10% (v/v) with moistened (MMN medium) vermiculite–peat mixture (4:1; v/v) without fungal mycelium.

For each soil fungal strain and each inoculum density, *Acacia* seedlings were individually grown in 0.25 L pots filled with a sandy soil mixed with the required volume of fungal inoculum. The soil was collected from a stand of *Acacia holosericeae* located east of Dakar. After sampling it was crushed, passed through a 2 mm sieve, autoclaved for 60 min at 120 °C to eliminate the native microbiota and stored for a week in a dry room to avoid any soil toxicity. After autoclaving, soil physico-chemical characteristics were as follows: pH (H₂O) 5.3; clay (%) 3.6; fine silt (%) 0.0; coarse silt (%) 0.8; fine sand (%) 55.5; coarse sand (%) 39.4; carbon (%) 0.17; nitrogen (%) 0.02; total phosphorus 39 mg kg⁻¹; soluble phosphorus (Olsen) 4.8 mg kg⁻¹. The pots were arranged in a randomized complete block design with five replicates per treatment. The plants were placed in a glasshouse (28 °C day, 18 °C night, 10-h photoperiod) and watered regularly with distilled water. After one week of plantation, the young seedlings were inoculated with 5 mL of late log-phase *Bradyrhizobium* strain Aust 13C (10⁷ CFU mL⁻¹ approximately).

After 4 months of culturing, the height of the plants and the oven-dried weight (1 week at 65 °C) of shoot were recorded. Then the root systems were gently washed in tap water. Root nodules were counted. The root systems of individual seedlings were cut into 1-cm root pieces. The percentage of ectomycorrhizal root tips [colonization index = (number of ectomycorrhizal root tips/total number of root pieces) × 100] was assessed under a stereomicroscope (magnification ×40) on a random sample of at least 100 root tips per plant. Then root dry weight (1 week at 65 °C) was determined for each plant.

2.3.2. Experiment 2: ectomycorrhizal diversity effect on the growth and nodulation of *A. mangium* seedlings

The cultural conditions of *A. mangium* seedlings and the experimental design were the same as described above (see experiment 1). The ectomycorrhizal species combination treatments provided a diversity gradient from one to six species with all the species previously tested in monoculture (Table 1). This experimental design allowed comparing the effect of the multiple fungal species with that recorded with each of the fungal species in monoculture. It also allowed avoiding the “sampling effect” (Huston, 1997; Wardle, 1999). For the single fungal species treatments, the soil was mixed with 10% (v/v) fungal inoculum or 10% moistened (MMN medium) vermiculite–peat mixture (4:1; v/v) for the control treatment. For the other ectomycorrhizal diversity treatments, the soil was mixed using an additive design where the amount of fungal inoculum was the same across treatments as indicated in Table 2. All the pots were inoculated with *Bradyrhizobium* sp. strain Aust 13C as described above.

After 4 months of plantation, the seedlings were harvested and the growth parameters (height, shoot biomass, root biomass) were measured. The ectomycorrhizal colonization index was determined as described above. Root nodules were counted and surface sterilized by immersion in 0.1% (w/v) HgCl₂ for 30 s, washed in sterile water and then in 96% ethanol for 2–3 min to finally be rinsed in sterile water and stored at –80 °C in 20% glycerol (v/v) for further analyses. Dried ground plant tissues were ashed at 500 °C, digested in 2 mL of HCl (6 N) and 10 mL of HNO₃ (N), then analyzed by colorimetry for phosphorus (John, 1970). For nitrogen (Kjeldhal) determination, dried ground plant tissues were digested in 15 mL H₂SO₄ (36 N) containing 50 g L⁻¹ of salicylic acid.

Table 2

Fungal species combinations and fungal inoculum rates used in the ectomycorrhizal diversity experiment.

Treatment	Species richness	Inoculation rates of each ectomycorrhizal strains (%)					
		IR100 ^a	IR109 ^b	IR500 ^c	IR409 ^d	IR406 ^e	SC2 ^f
A	0	0	0	0	0	0	0
B	1	10	0	0	0	0	0
C	2	5	5	0	0	0	0
D	3	3.3	3.3	3.3	0	0	0
E	4	2.5	2.5	2.5	2.5	0	0
F	5	2	2	2	2	2	0
G	6	1.66	1.66	1.66	1.66	1.66	1.66

^a *Pisolithus albus* IR100.

^b *Scleroderma dictyosporum* pat. IR109.

^c *S. verrucosum* Bull. (Pers.) sensu Grev. IR500.

^d *Scleroderma* sp1 IR409.

^e *Scleroderma* sp1 IR406.

^f *Scleroderma* sp. SC2.

2.4. Assessment of *Bradyrhizobium* sp. strain Aust 13C root colonization

PCR and Southern hybridization methods were used for studying the distribution of *Bradyrhizobium* sp. Aust 13C in each treatment.

2.4.1. DNA extraction

Twenty nodules were randomly collected in each treatment and crushed in a drop of sterile distilled water. For the DNA extraction, 150 µL of 2 × CTAB/PVPP buffer (0.2 M Tris–HCl, pH 8; 0.04 M EDTA; pH 8; 2.8 M NaCl; 4% (w/v) CTAB; 2% (w/v) PVPP) were added to 300 µL of crushed nodule. The homogenate was incubated at 65 °C for 60 min and centrifuged for 10 min at 11,000 g to remove cell debris. Supernatant was taken and an equal volume (300 µL) of phenol–chloroform–isoamyl alcohol (25:24:1; v/v/v) was added. The samples were homogenized and centrifuged for 15 min at 13,000 g. The aqueous phase containing nucleic acids was transferred in a new tube and 300 µL of chloroform–isoamyl alcohol (24:1; v/v) was added, then centrifuged for 15 min at 13,000 g. DNA was finally precipitated overnight at –20 °C in a solution containing 0.1 volume of sodium acetate and 2.5 volumes of absolute ethanol. The samples were centrifuged for 30 min at 13,000 g at 4 °C. The resulting DNA pellet was washed with 70% (v/v) ethanol by centrifugation for 15 min at 13,000 g at 4 °C, vacuum dried, and solubilized in 20 µL of ultrapure water. The DNA purity and quantity were assessed by spectrophotometry.

2.4.2. Probe design

A strain-specific DNA oligonucleotide probe targeting the ITS 16S–23S rDNA of the strain Aust 13C was designed and its theoretical specificity was evaluated by alignment against the GenBank database by using the algorithm BLAST (Altschul et al., 1997). The probe 5′-CGTTGTTTCATCGCGGCTCATCG-3′ has been synthesized and labeled by with 5′, 3′ and internal Dig-labeling (Eurogentec, Seraing, Belgium). The hybridization conditions have been determined empirically by probe hybridization on strain DNA with a hybridization temperature of 52 °C.

2.4.3. Slide preparation by “dot blotting”

The DNA extracted from nodules randomly collected in each treatment was denatured by incubation at 100 °C for 10 min and cooled in ice for 10 min before dotting to 0.45 µm Biotodyne Plus nylon membrane (PALL, Saint-Germain-en-Laye, France) at a rate of 1 µg per dot with Dot blotting Fisher Bioblock Scientific system. The DNA was fixed on filter for 30 min at 80 °C.

2.4.4. Probe hybridization

Filters were pre-incubated in a hybridization buffer (750 mM NaCl, 75 mM Sodium Citrate, 1% w/v blocking reagent, 0.1% w/v N-laurylsarkosine sodium salt, 0.02% w/v SDS) for 2 h at 68 °C. The hybridization step was performed overnight at 52 °C in the hybridization buffer containing 2.5 pmole L⁻¹ of probe.

2.4.5. Anti-DIG recognition and signal detection

Filters were washed at hybridization temperature twice for 5 min in a first washing solution (2 × SSC, 300 mM NaCl, 30 mM citrate de sodium, 0.1% w/v SDS) and twice for 5 min in a second washing solution (0.1 × SSC, 15 mM NaCl, 1.5 mM Sodium Citrate, 0.1% w/v SDS). Filters were then incubated in a washing buffer (150 mM NaCl, 100 mM Tris–HCl, pH 7.5) for 1 min at room temperature (RT) and transferred in blocking solution (150 mM NaCl, 100 mM Tris–HCl, pH 7.5, 0.5% blocking powder [Roche Diagnostics, Meylan, France]) for 30 min at RT. Stock anti-DIG-labeled alkaline phosphatase (Roche Diagnostics) was diluted 5000 times in washing buffer (150 mM NaCl, 100 mM Tris–HCl, pH 7.5) and each filter was then incubated with 10 mL of diluted anti-DiG-labeled alkaline phosphatase solution for 30 min, and washed twice in washing buffer for 15 min. The signal was detected by using CDP-Star Chemiluminescence substrate (Roche Diagnostics) in 0.13 mM detection buffer (100 mM NaCl, 100 mM Tris–HCl, pH 9.5) per 100 cm² filter and incubated in plastic bags for 5 min in the dark. Positive signal were detected by imprint on Lumi-film chemiluminescent detection film (Roche Diagnostics) after a 10 min exposition.

2.5. Statistical analysis

Plant growth measurements were treated with one-way analysis of variance and means were compared with the Newman–Keuls multiple range test ($P < 0.05$). The fungal colonization indexes were transformed by arcsin (sqrtx) before statistical analysis. The numbers of *Bradyrhizobium* sp. strain Aust 13C nodules along the root systems in each treatment were compared with 2 × 2 contingency tables and chi-square test (χ^2 -test) and Yates correction for small numbers.

Data from experiment 1 (fungal monoculture treatment) were analyzed with Principal Component Analysis (PCA). The data table used in this PCA had 174 rows and seven columns. The 174 rows corresponded to the five replicates of the four different inoculum densities, plus nine controls, for each of the six fungal species. The seven columns were the plant growth and nodulation parameters.

Data from experiment 2 (multiple fungal isolate treatment) were projected as additional elements in the PCA of the first experiment. The projection of supplementary data as additional elements in a PCA is useful to assess the position of these supplementary data with respect to the original data set. The projection of additional elements does not modify the results of the PCA. It simply gives row scores that can be used to display these new elements on the factor map. Here, this technique allowed us to compare the effects of single and multiple fungal inoculations on plant growth parameters. PCA and additional elements computations were done with the ade4 package for the R software (Thioulouse and Dray, 2007; R Development Core Team, 2010).

3. Results

3.1. Experiment 1: relationships between fungal inoculum density, plant growth and nodulation parameters

A. mangium seedlings were colonized by all the fungal isolates. For all the tested ectomycorrhizal strains, inoculation with

increased ectomycorrhizal rates significantly increased shoot, root and total biomasses, ectomycorrhizal colonization and the total number of nodules per plant as well as phosphorus and nitrogen foliar contents (Table 3).

3.2. Experiment 2: effect of ectomycorrhizal diversity on plant growth and root nodulation

All *A. mangium* seedlings inoculated with a single strain of ectomycorrhizal fungus were mycorrhized after 4 month culturing (Table 4). Ectomycorrhizal colonization ranged from 35% (*Scleroderma dictyosporum* IR109) to 79.4% (*Scleroderma* sp. IR406) (Table 4). All single fungal isolate inoculations significantly enhanced plant growth (height, shoot and root biomasses) as well as foliar mineral (N and P) contents (Table 4). For total biomass, the highest promoting effect was recorded with *Scleroderma* sp. SC2 (+78.6%). The strongest fungal effect on plant growth parameters was obtained with *Scleroderma* sp. SC2 and the weakest with *Scleroderma* sp. IR406 (Table 4). A similar pattern was observed for root infection by *Bradyrhizobium* Aust 13C (Table 4). All the fungal strains have

Table 3

Regression analysis between the rate of ectomycorrhizal inoculation and plant growth, ectomycorrhizal colonization and rhizobial nodulation of *A. mangium* seedlings for each fungal strain after a 4-month plantation (Experiment 1).

Fungal strains	Parameters	Equation	r	P
IR100	Shoot biomass	y = 53.2 + 41.4x	0.90	<0.0001
	Root biomass	y = 19.1 + 11.8x	0.80	<0.0001
	Total biomass	y = 72.2 + 53.2x	0.89	<0.0001
	Ectomycorrhizal colonization	y = 12.1 + 4.3x	0.67	<0.0001
	Number of nodules per plant	y = -1.04 + 1.97x	0.95	<0.0001
	Shoot N content	y = 0.03 + 0.001x	0.92	<0.0001
	Shoot P content	y = 35.8 + 16.7x	0.97	<0.0001
IR109	Shoot biomass	y = 57.9 + 38.4x	0.84	<0.0001
	Root biomass	y = 22.8 + 8.6x	0.86	<0.0001
	Total biomass	y = 80.7 + 47.1x	0.86	<0.0001
	Ectomycorrhizal colonization	y = 12.2 + 4.3x	0.74	<0.0001
	Number of nodules per plant	y = 0.19 + 2.3x	0.94	<0.0001
	Shoot N content	y = 0.004 + 0.001x	0.87	<0.0001
	Shoot P content	y = 40.2 + 19.6x	0.95	<0.0001
IR500	Shoot biomass	y = 44.1 + 48.1x	0.86	<0.0001
	Root biomass	y = 14.4 + 17.5x	0.85	<0.0001
	Total biomass	y = 58.4 + 65.5x	0.86	<0.0001
	Ectomycorrhizal colonization	y = 5.5 + 3.6x	0.81	<0.0001
	Number of nodules per plant	y = -0.51 + 2.2x	0.95	<0.0001
	Shoot N content	y = 0.004 + 0.001x	0.92	<0.0001
	Shoot P content	y = 32.5 + 33.5x	0.97	<0.0001
IR409	Shoot biomass	y = 22.6 + 75.3x	0.79	<0.0001
	Root biomass	y = 15.6 + 20.1x	0.76	<0.0001
	Total biomass	y = 38.2 + 95.5x	0.80	<0.0001
	Ectomycorrhizal colonization	y = 7.1 + 3.4x	0.59	0.0006
	Number of nodules per plant	y = -0.88 + 1.1x	0.80	<0.0001
	Shoot N content	y = 0.03 + 0.002x	0.46	0.0126
	Shoot P content	y = 45.1 + 25.3x	0.96	<0.0001
IR406	Shoot biomass	y = 57.1 + 37.7x	0.92	<0.0001
	Root biomass	y = 25.5 + 6.8x	0.82	<0.0001
	Total biomass	y = 82.6 + 44.5x	0.92	<0.0001
	Ectomycorrhizal colonization	y = 0.59 + 5.1x	0.93	<0.0001
	Number of nodules per plant	y = -0.67 + 1.4x	0.85	<0.0001
	Shoot N content	y = 0.004 + 4.10 ⁴ x	0.77	<0.0001
	Shoot P content	y = 47.4 + 14.2x	0.94	<0.0001
SC2	Shoot biomass	y = 48.5 + 44.6x	0.88	<0.0001
	Root biomass	y = 26.3 + 9.6x	0.59	0.0008
	Total biomass	y = 74.8 + 54.2x	0.86	<0.0001
	Ectomycorrhizal colonization	y = 7.2 + 5.7x	0.83	<0.0001
	Number of nodules per plant	y = 2.6 + 5.5x	0.91	<0.0001
	Shoot N content	y = 0.003 + 0.001x	0.93	<0.0001
	Shoot P content	y = 56.9 + 46.3x	0.96	<0.0001

Table 4
Effect of ectomycorrhizal isolate inoculation on mycorrhiza formation, rhizobial development, shoot mineral contents and growth of *A. mangium* after 4 months of plantation.

	Ectomycorrhizal strains						
	Control	IR100	IR109	IR500	IR409	IR406	SC2
Height (cm)	8.6 (0.6) ^a a ^b	11.3 (0.55) bc	11.3 (0.84) bc	12.9 (1.11) c	13.1 (0.93) cd	10.3 (0.46) b	15.6 (0.90) d
Shoot biomass (mg dry weight)	160 (46) a	487 (27) bc	385 (47) b	717 (107) cd	508 (54) c	318 (36) b	808 (83) d
Root biomass (mg dry weight)	60 (12) a	150 (23) b	123 (15) b	197 (17) bc	163 (17) b	117 (9) b	220 (33) c
Total biomass (mg dry weight)	220 (45) a	637 (44) c	508 (62) bc	913 (122) cd	670 (70) c	435 (45) b	1028 (114) d
Shoot P content (µg per plant)	44.2 (12.6) a	209.2 (11.5) b	236.8 (28.9) b	375.3 (56.1) bc	295.4 (31.3) bc	183.5 (20.7) b	509.7 (52.1) c
Shoot N content (mg per plant)	3 (0.001) a	10 (0.001) c	9 (0.001) bc	15 (0.002) d	11 (0.001) cd	7 (0.001) b	14 (0.001) d
Ectomycorrhizal colonization (%)	0 a	71.1 (6.1) c	35.0 (4.2) b	68.3 (4.4) c	42.8 (13.7) b	79.4 (4.4) c	46.6 (5.6) b
Number of nodules per plant	7.3 (0.3) a	18.8 (2.5) b	21.2 (3.5) b	21.3 (4.9) bc	11.1 (4.8) ab	13.8 (4.5) a	56.8 (12.7) c

^a Standard error of the mean.

^b Data in the same line followed by the same letter are not significantly different according to the Newman–Keuls test ($P < 0.05$).

significantly stimulated the root nodulation of *A. mangium* by *Bradyrhizobium* sp. Aust 13C (Table 4). The highest number of nodules per plant was recorded with *Scleroderma* sp. SC2 whereas the lowest was measured with *Scleroderma* sp. IR409 (Table 4).

Significant effects of increasing ectomycorrhizal diversity were obtained on whole plant biomass, plant nutrient acquisition and root nodulation (Table 5, Fig. 1). However no significant relationship was observed between ectomycorrhizal colonization and the increase of ectomycorrhizal diversity, whole plant biomass, nutrient acquisition and root nodulation (Table 5).

Although ectomycorrhizal inoculation (single and multiple fungal isolate inoculations) had significantly enhanced root nodulation with *Bradyrhizobium* sp. Aust 13C, the frequencies of Aust 13C nodules decreased from one to six fungal isolates (Fig. 2).

The PCA of the single fungal strain experiment data (black dots and ellipses) and the multiple fungal strain experiment data (color dots and ellipses) is shown in Fig. 3. In the single fungal strain experiment, black ellipses represented the dispersion of the samples inoculated with one of the six fungal species. Each ellipse summarized the five replicates (black dots) for the four inoculum rates and the nine controls (not inoculated). The PCA correlation circle (top left) showed that the first PCA axis (horizontal) was highly correlated with the plant biomass parameters, and that the second axis was correlated with the nodulation parameters.

For the multiple fungal strain experiment, color ellipses represent the dispersion of the samples inoculated with increasing ectomycorrhizal diversity. Each ellipse summarized the four replicates (color dots) for the different number of inoculated fungal strains (from zero species to six species). The plant biomass and notably the nodulation parameters were much higher in samples inoculated with multiple fungal strains and this increase was related to the number of inoculated ectomycorrhizal fungi. Treatments with two and three fungal isolates seemed to have a similar effect, and the effect of four to six isolates treatments was also

comparable. It is worth noticing that the dispersion of plant growth and nodulation parameters for the four replicates also increased with the number of fungal species inoculated (Fig. 3).

4. Discussion

Several experimental studies have demonstrated that plant diversity, plant productivity and ecosystem functioning can be greatly enhanced by plant species richness (Tilman et al., 1996; Hector et al., 1999), symbiotic bacteria (van der Heijden et al., 2006) and mycorrhizal fungi (Grime, 1997; van der Heijden et al., 1998; Clay and Holah, 1999; Rudgers et al., 2004).

However, the data resulting from these studies are subjected to debates (Huston, 1997; van der Heijden et al., 1999; Wardle, 1999; Hector et al., 2000; Huston et al., 2000) since the “diversity effect” could result from a “sampling effect” or from a resource use complementary. In the present study, this “sampling effect” could very likely be the result of a fungal species that induced a large growth effect in all or most of the plant species included in the experiment (van der Heijden et al., 1999). However, the relationships between the ectomycorrhizal diversity and the enhancement of plant biomass and nodulation parameters after a 4 month cultivation of *A. mangium* cannot be explained by a “sampling effect” because (i) only one plant species has been used and (ii) the presence of the most effective fungal species (*Scleroderma* sp. SC2) identified in experiment 1 cannot explain the enhancement of *A. mangium* growth in samples inoculated with a gradient of ectomycorrhizal diversity. These experimental designs followed the recommendations addressed by Garnier et al. (1997) and Huston et al. (2000) to unambiguously differentiate the effects of diversity from those related to the sampling effect.

The present study clearly shows (i) a strong enhancement of *A. mangium* growth due to ectomycorrhizal fungal inoculation, (ii) significant effects of ectomycorrhizal density and diversity on

Table 5
Effect of ectomycorrhizal diversity on growth variables, shoot mineral contents, rhizobial development and ectomycorrhizal colonization in *A. mangium* plants after 4 months of plantation.

	Treatments						
	Control ^a	IR100	C	D	E	F	G
Height (cm)	8.6 (0.6) ^b a ^c	11.3 (0.55) b	16.2 (0.57) b	15.3 (0.53) b	19.6 (0.43) c	21.2 (0.42) d	17.4 (0.74) b
Shoot biomass (mg dry weight)	160 (45) a	487 (27) b	902 (163) cd	805 (85) c	1175 (176) cd	1227 (45) d	1137 (105) cd
Root biomass (mg dry weight)	60 (12) a	150 (23) b	282 (41) c	220 (25) bc	280 (50) c	330 (44) c	297 (38) c
Total biomass (mg dry weight)	220 (55) a	637 (44) b	1185 (204) cd	1025 (110) c	1455 (215) c	1557 (85) d	1435 (132) d
Shoot P content (µg per plant)	44.2 (12.6) a	209.1 (11.5) b	565.9 (102.1) c	648.8 (68.6) c	1108.9 (166) d	1283.9 (47.1) d	1074.9 (99.5) d
Shoot N content (mg per plant)	3.3 (0.96) a	10.5 (0.58) b	18.5 (3.34) c	18.3 (1.93) c	25.1 (3.74) cd	29.2 (1.07) d	25.5 (2.35) d
Ectomycorrhizal colonization (%)	0	71.0 (6) ab	74.4 (3.4) b	75.1 (0.5) b	68.8 (1.8) a	76.9 (2.6) b	78.4 (1.4) b
Number of nodules per plant	7.3 (0.3) a	18.8 (2.5) b	39.2 (1.1) cd	33.2 (4.1) c	89.0 (23.1) de	132.5 (20.9) e	91.5 (13.8) e

^a See Table 2.

^b Standard error of the mean.

^c Data in the same line followed by the same letter are not significantly different according to the Newman–Keuls test ($P < 0.05$).

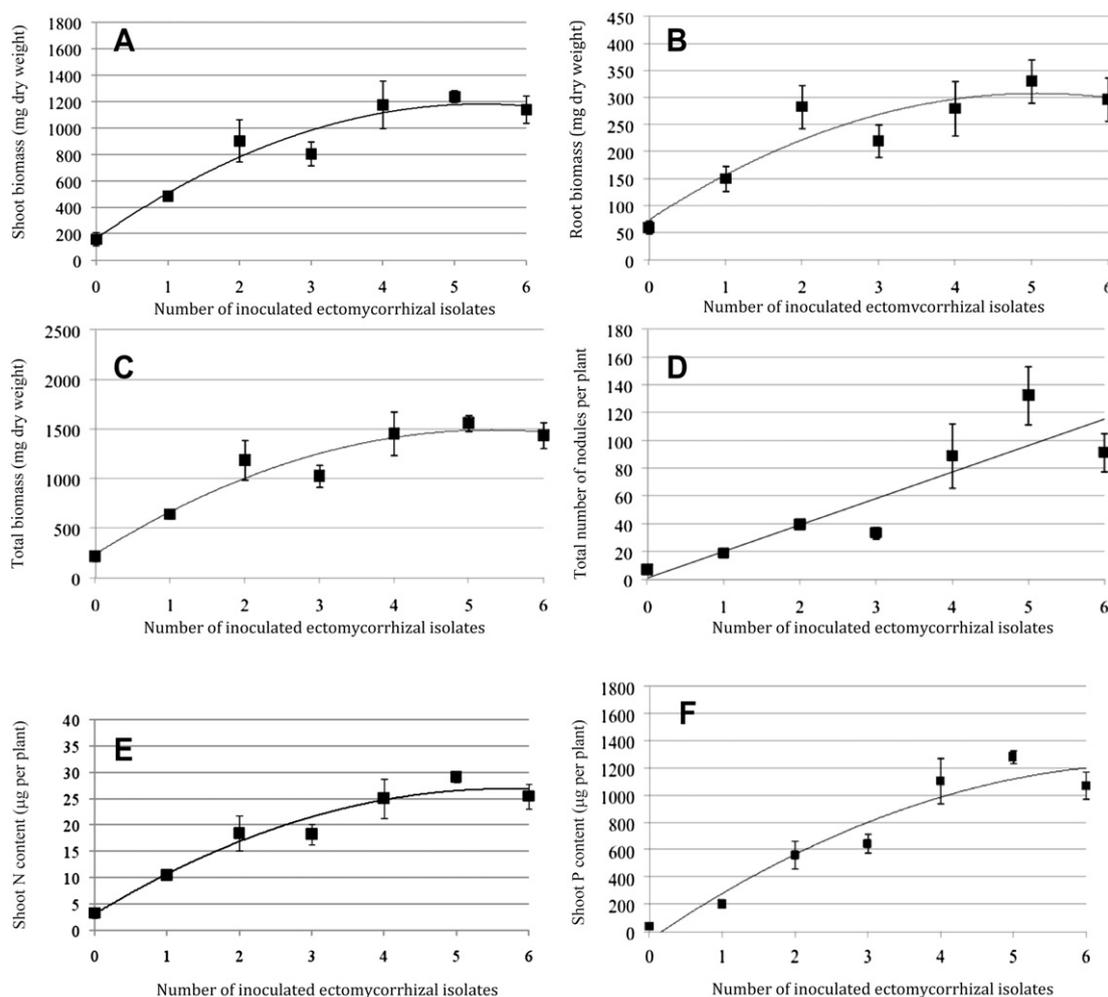


Fig. 1. Relationships between plant growth variables, rhizobial development, mycorrhizal formation and ectomycorrhizal fungal diversity. A: Shoot biomass ($y = -35.23x^2 + 378.6x + 164.6$; $r = 0.85$; $P < 0.0001$). B: Root biomass ($y = -9.09x^2 + 92.4x + 72.8$; $r = 0.74$; $P < 0.0001$). C: Total biomass ($y = -44.27x^2 + 470.5x + 238$; $r = 0.84$; $P < 0.0001$). D: Number of nodules per plant ($y = 19.1x + 1.34$; $r = 0.77$; $P < 0.0001$). E: Shoot N content (mg per plant) ($y = -0.73x^2 + 8.32x + 3.18$; $r = 0.88$; $P < 0.0001$). F: Shoot P content (µg per plant) ($y = -25.6x^2 + 362.5x - 53.8$; $r = 0.96$). Squares represent means (± standard error of the mean).

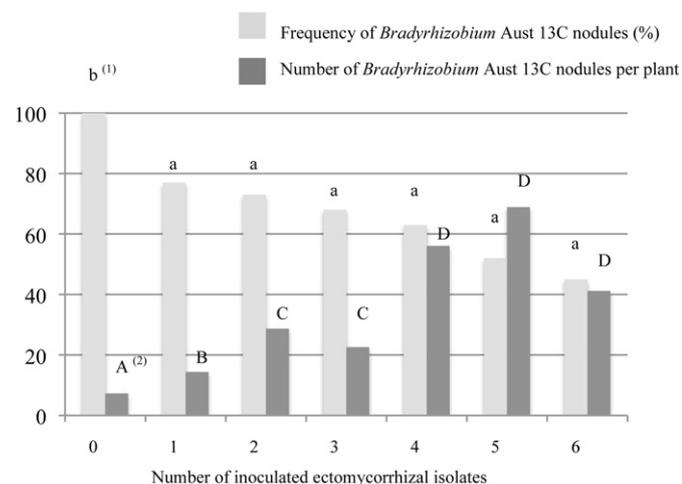


Fig. 2. Frequencies and enumeration of *Bradyrhizobium* Aust 13C nodules in each treatment assessed by PCR-amplified 16S–23S rDNA spacer region and Southern hybridization methods. ⁽¹⁾ Data indexed by the same lowercase letter are not significantly different according to the χ^2 test ($P < 0.05$). ⁽²⁾ Data indexed by the same uppercase letter are not significantly different according to the Newman–Keuls test ($P < 0.05$).

whole plant biomass and plant nutrient acquisition and (iii) an ectomycorrhizal diversity effect on the functioning of the nitrogen-fixing symbiosis.

It is well known that many N_2 -fixing trees and shrubs are especially dependent on mycorrhizas to uptake mineral nutrients and to ensure an efficient N_2 fixation (Cornet and Diem, 1982; Duponnois et al., 2001; Duponnois and Plenchette, 2003). It has been already reported that *A. mangium* was effectively colonized by ectomycorrhizal fungi (Duponnois and Bâ, 1999; Duponnois et al., 2002). Our results also showed that different ectomycorrhizal strains differ in their effect on plant growth and more particularly on plant nutrient acquisition (Chapin, 1980; Smith and Read, 2008). These data are in accordance with other studies performed on *B. pendula* inoculated with eight ectomycorrhizal fungi and from which it has been concluded that ectomycorrhizal fungi were important determinants of seedling root morphology and nutrient foraging ability (Jonsson et al., 2001).

It has been clearly demonstrated that the mycorrhizal effect on plant growth was dependent on the abundance of infective ectomycorrhizal propagules in soil (Garbaye et al., 1988). Our results are in accordance with these authors since the intensity of root colonization by the ectomycorrhizal fungi, the plant response, the rhizobial nodulation and the nutrient acquisition are positively correlated to the ectomycorrhizal inoculum densities in soil.

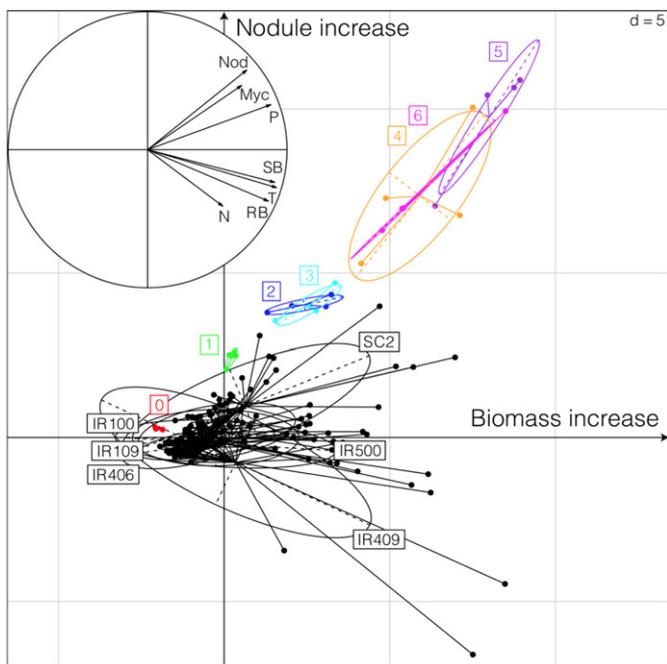


Fig. 3. Comparative effects of single fungal isolate treatments (black dots and ellipses) with multiple fungal isolate treatments (color dots and ellipses) on plant growth parameters and nodulation process analyzed with Principal Component Analysis (PCA). The multiple fungal isolate treatments were projected as additional elements in the PCA computed on the single fungal isolate treatments. The correlation circle of the seven variables is given in the upper-left corner of the figure. The code for variables is as follows. SB: shoot biomass, RB: root biomass, T: total biomass, N: nitrogen rate in plant tissues, Nod: number of nodules per plant, Myc: mycorrhization rate, P: phosphorus rate in plant tissues. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Numerous studies have also reported that mycorrhizas could dramatically increase root nodulation (Founoune et al., 2002a,b,c; Duponnois et al., 2002; Duponnois and Planchette, 2003). It has been suggested that the mycorrhizal symbiosis enhanced nodulation and N_2 fixation by enabling plant P uptake (Cornet and Diem, 1982; André et al., 2005) or by improving root growth that facilitated rhizobial colonization and infection. It is also well known that mycorrhizas modify root functions (in particular, root exudation) and, therefore, could influence the microbial community structure (commonly named the “mycorrhizosphere effect”) (Katznelson et al., 1962; Linderman, 1988; Frey-Klett et al., 2005). Specific relationships occur between mycorrhizal fungi and mycorrhizosphere microflora (Garbaye, 1991; Garbaye and Bowen, 1989; Marshner et al., 2001; Frey-Klett et al., 2005). Moreover, the extraradical mycelium of ectomycorrhizal fungi could also influence the chemical composition and pH of the surrounding soil by excreting chemical substances (Frey et al., 1997; Caravaca et al., 2002). Frey-Klett et al. (2005) have proposed that the ectomycorrhizal symbiosis could be considered as a microbial complex where the fungal symbiosis has a direct effect on plant growth (nutritional and hormonal mechanisms). They further argued that the fungal symbiosis has an indirect positive effect *via* a selective pressure on bacterial communities resulting, for instance, in a higher abundance of Plant Growth Promoting Rhizobacteria (PGPR). In the current study, all these physical and chemical modifications could increase the development of the inoculated bradyrhizobial strain and, consequently, improve the nodulation process. However, these hypotheses are not limited to the environment of the host plant/ectomycorrhizal fungus symbiosis. More specific relationships could be involved during the development of the tripartite

symbiosis, at the physiological and molecular level (van Rhijn et al., 1997; Bliilou et al., 1999; Parniske, 2000). All these experimental studies have been undertaken with single fungal strain inoculations and our study showed that these interactive effects between rhizobia and ectomycorrhizal fungi depend on the amount and diversity of ectomycorrhizal mycelium.

The *Bradyrhizobium* sp. strain Aust 13C has been previously tested in field trials to determine the effect of selected *Bradyrhizobium* strains on the growth of *A. mangium* (Galiana et al., 1990, 1994). Nineteen months after tree transplantation, Aust 13C provided a stimulating effect on tree growth and was predominant in nodules collected from *A. mangium* root systems (Galiana et al., 1994). Using PCR and Southern hybridization methods, our data confirmed the Aust 13C high competitive ability against indigenous N_2 -fixing bacteria and its persistence in soil. However, Aust 13C frequencies decreased with an increasing mycorrhizal fungal diversity. About seven Aust 13C nodules have been recorded in the control treatment whereas 66 Aust 13C nodules have been numbered in the mycorrhizal treatment performed with five ectomycorrhizal isolates. This result suggests that the persistence in soil of this bradyrhizobial strain and its nodulation process are promoted with an increasing ectomycorrhizal fungal diversity.

In conclusion, our results provide evidence that mycorrhizal diversity has a great impact on plant growth and biological nitrogen-fixing symbiosis. They also underline the necessity to manage ectomycorrhizal symbiosis and/or to associate tree seedlings with multiple mycorrhizal symbionts in order to conserve an efficient abundance and diversity of ectomycorrhizal propagules in plantation soils. These management practices would optimize forest plantation performance by promoting the efficiency of nitrogen-fixing symbiosis for legume tree species and depleting the transplant shock, a critical step in successful plantation programs. It is now unquestionable that seedlings inoculated with multiple fungal isolates show better growth parameters as well as better nutrient acquisition than those associated with a single isolate.

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