1 Micro-community associated with ectomycorrhizal *Russula* symbiosis and
 2 sporocarp-producing *Russula* in Fagaceae dominant nature areas in southern China
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15 **ABSTRACT** *Russula griseocarnosa*, an ectomycorrhizal (ECM) fungus, is a
 16 species of precious wild edible mushrooms with very high market value in southern
 17 China. Its yield is affected by many factors including the tree species and
 18 environmental conditions such as soil microbiome, humidity. How the microbiome
 19 promotes the ECM fungus symbiosis with Fagaceae plants and
 20 sporocarp-producing has never been studied. In this study, we collected rhizosphere
 21 samples from Fujian province, the microbiota in the root and mycorrhizal
 22 rhizosphere were identified by Illumina MiSeq high-throughput sequencing. First,
 23 we compared three types of fungal communities: root tips infected with ECM
 24 *Russula* (type 1), tips with *Russula* sporocarp (type 2) and tips without ECM (type
 25 3). Our results showed that the fungal richness was negatively correlated with
 26 *Russula*. *Russula*, *Tomentella* and *Lactarius* were common in Fagaceae ECM roots.
 27 As to the mycorrhizal interactions, *Boletus* may be considered as an indicator
 28 species for sporocarp-producing *Russula*, and *Acremonium*, *Cladophialophora* were
 29 associated with *Russula* symbiosis. Second, we analyzed the fungal and bacterial

communities in rhizosphere soils from the corresponding to previously three types (type 1, 2, 3). *Dacryobolus* and *Acidocella* may be considered as an indicator species for sporocarp-producing *Russula*. Fungi *Tomentella*, *Saitozyma*, *Elaphomyces* and bacteria *Acidicaldus*, *Bryobacter*, *Sorangium* and *Acidobacterium* occurred more frequently in the ECM *Russula* rhizosphere. Furthermore, the indicators *Elaphomyces*, *Tomentella*, *Sorangium* had a positive correlation with *Russula* symbiosis by network analyses. Overall, our results suggest a relationship between micro-community and ECM *Russula* formation and *Russula* sporocarp, which may provide new strategies for improving *Russula* symbiosis rate and sporocarp production.

KEYWORDS micro-Community, *Russula*, ectomycorrhizae, Fagaceae

IMPORTANCE *Russula* (Russulaceae, Russulales, Agaricomycetes, Basidiomycota) species are ectomycorrhizal (ECM) fungi that form symbiotic associations with host roots. Approximately 750 *Russula* species have been reported in worldwide (1). *Russula* taxa showed high diversity, strong habitat preference and some preference for soil horizons (2)(Jo'zsef Geml 2010). Li M(3)(2010)identified that *Russula* emerge at least three divergent lineages based on the genetic diversity and geographic differentiation in southern China , and *R. griseocarnosa* belongs to one of the lineages. *R. griseocarnosa* is described from southern China, including Guangdong, Yunnan, and Fujian Provinces (4). *R. griseocarnosa* sporocarp, which is popularly commercially as food and medicine, is uncultivable and collected from the natural habitat. To date, there is little knowledge about the controlled production of *Russula* and its micro-community.

Several biotic factors affect ectomycorrhizal fungal communities: plant host species (5, 6) , plantation age (7), asymptomatic ectomycorrhiza endophytes (8), ectomycorrhizal propagules in the soil(9) and the traits of the dispersal propagules of ECM fungi (10). The common ectomycorrhizal *Russula* sp. was associated with seven host genera: *Pleioblastus chino*, *Quercus serrata*, *Symplocos prunifolia*, *Ilex pedunculosa*, *Prunus jamasakura*, *Gamblea innovans*, and *Lyonia ovalifolia*(11, 12). *R. griseocarnosa* grows in forests with Fagaceae in southern China (13). ECM

60 fungal communities strongly vary during long-term ecosystem development, even
 61 within the same hosts (14). Some *Russula* spp. was reported to be dominant
 62 colonizers of mature roots of pines (15)(Horton & Bruns, 2001) but did not
 63 colonize bioassay seedlings (16). ‘Early stage’ and ‘late stage’ mycorrhizal fungi of
 64 birch appeared distinction (7). Gebhardt also found that Ectomycorrhiza
 65 communities of *Quercus rubra* of different age performed specificity with low
 66 similarity between the chronosequence stands site (17) . Some fungal root
 67 endophytes prefer ECM formed by particular species of ectomycorrhizal fungi (8,
 68 18), potentially representing a second level of root endophyte selection. Dark
 69 septate endophytes are considered to be ubiquitous, colonizing mycorrhizal(19).
 70 ECM propagule communities in soil may diverge from those root-colonizing ECM
 71 communities and affect persistence of symbiotic relationship between mycorrhiza
 72 and available host roots by competitive networks(20). ECM propagules in soil are
 73 less frequent and diverse in early primary succession and become more frequent
 74 and diverse along forest development, due mainly to the accumulation of dormant
 75 spores of *Rhizopogon* spp. and sclerotia of *Cenococcum* spp(20). Simultaneously
 76 dispersal ability across ECM species correlated well with the composition of
 77 communities associated with host (21). *Russula* naturally propagate by
 78 short-distance spore dispersal rather than vegetative growth of dikaryophytic
 79 mycelia or long-distance spore dispersal(22). In all, the *Russula* ECM community
 80 may be affected by symbiotic structures and root endophytes in the roots,
 81 mycorrhizal extraradical mycelia, spores in the soil , as well as its dispersal ability.

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83 Mycorrhizal interactions are usually classified on the basis of the features of the
 84 symbiotic interfaces(23). The ECM community colonizing root tips was strongly
 85 structured by competitive interactions or ecological processes generating a similar
 86 spatial pattern, rather than neutral processes. The ECM *Cortinarius* sp. and
 87 *Lactarius rufus* competed for root tips(24). Both *Cenococcum geophilum* and
 88 *Clavulina cinerea* as mycorrhizas and as extramatrical mycelium (EMM) in a *Pinus*
 89 *resinosa* plantation showed a negative correlation(25). Hortal suggests that

interspecific competition between *Lactarius deliciosus* (inoculated fungi) and *Rhizopogon roseolus* (indigenous fungi) occurs in the root system for ectomycorrhiza formation in available roots, rather than in the extramatrical mycelium phase (26). However, associations among *Suillus bovinus* and *Gomphidius roseus* occur within ectomycorrhizal roots (27). There are also a number of notable examples of associations between sporocarps of different species, such as between *Boletus parasiticus* and *S. citrinum*, *Asterophora parasitica* and *Lactarius*, and between *Claudopus parasiticus* and *Cantharellus cibarius* (28). However, mycorrhizal interaction studies of *Russula* are limited in the literature.

Similar to the rhizosphere, mycorrhizosphere is the feet of fruiting bodies or the root of ectomycorrhizal fungi. Mycorrhizosphere may constitute a hot spot(29), in which microorganisms were affected(30-32).The mycosphere effect was prominent, though previous studies have failed to demonstrate significant differences between bacterial communities associated with roots colonized by *Suillus variegatus* and *T. submollis*, *Lactarius* sp. and *Tomentella* sp.(33) or by *C. geophilum* and *Russula* sp. (34). It has also been established that mycorrhizal networks have different microbial communities compared with bulk soil by stimulating some families such as *Bradyrhizobiaceae*, *Burkholderiaceae*, and *Pseudomonadaceae* (35). Bacterial activity is stimulated by the provision of easily available nutrition such as carbonaceous compounds (30).The mycosphere effect might exert strong influences on the bacterial community of soil(36), in which bacterial activity is stimulated by trehalose, which is degraded by hyphosphere and derived from fungi (37, 38). Andersson(39)(2003)., who used phospholipid fatty acid profiles to characterize bacterial communities, has demonstrated that basidiomycete wood-decomposing fungi are able to influence bacterial community structure. Bacteria adapted to the mycospheres of three or more or just one fungal species was defined as specific selective bacterial(40). The specific members of the Sphingomonadaceae family selected were at the bases of the fruiting bodies of the ectomycorrhizal fungi *Laccaria proxima* and *Russula exalbicans* in comparison to the adjacent bulk soil,

major of which did not cluster with known bacteria from the database (36, 41). On the other hand, some mycorrhiza-associated bacteria have been shown to produce compounds that are antagonistic to plant pathogens (42). Meanwhile, “mycorrhiza helper bacteria” (MHB) appeared to positively influence the development and function of ectomycorrhiza (43), but the effects varied with different species combinations (44, 45). *Ralstonia* sp. and *Bacillus subtilis* can promote *Suillus granulatus*-infected *Pinus thunbergii* (34). *Bacillus subtilis* helped the growth of *Cenococcum geophilum* Fr and promoted *Suillus granulatus* infection (34) but inhibited *Rhizopogon* sp. infection (45). Apart from bacterial , ectomycorrhizal symbionts strong also selected ascomycete communities and other ECMs(31) (32).Högberg (2002)(46) demonstrated that the EMM is at least 30% of the microbial biomass in boreal forest soils. ECM fungi competed with saprotrophic fungi in soil by the EMM(47). *Tuber rufum* and some members of *Boletales* are typically restricted to productive truffle plots. On the other hand, *Hebeloma*, *Laccaria* and *Russula* species are mostly associated with unproductive truffle plots, Ectomycorrhizae belonging to *Thelephoraceae* are frequently found in mature truffle orchards but do not seem to affect sporocarp production (32). Ascomycetes associated with ectomycorrhizas: molecular diversity and ecology with particular reference to the Helotiales had been reported (48).However, the rhizosphere, mycosphere effect of *Russula griseocarnosa* has not been recorded in the literature.

Regarding the relationship between the amount of soil EMM with ectomycorrhizae and sporocarps, different mycorrhizas have different conclusions . Zampieri et al.(2010)(49) showed that the mycelium of *Tuber magnatum* was more widespread than was inferred from the distribution of its fruiting bodies and ectomycorrhizae. Zhou et al. (2001) (50)demonstrated that the development of *Suillus grevillei* sporocarps is correlated with amount of EMM and ectomycorrhizae of *S. grevillei* in a narrow area. The *Tuber melanosporum* EMM biomass detected in the soil from the natural truffle ground was significantly greater than that of other plant orchards analyzed, and the lowest amount of *T. melanosporum* mycelium maintained a

150 sporocarp production in plant orchards (51). However, Some ECMs are consistent
151 in ectomycorrhizae but inconsistent in sporocarps. De la Varga et al. (52)(2012)
152 quantified *B. edulis* extraradical mycelium in a Scots pine forest and found a
153 positive correlation between the amount of mycelia and the presence of *Boletus*
154 *edulis* mycorrhizae, but not with the productivity of fruiting bodies. However, the
155 relationship between the amount of *Russula* with ectomycorrhizae and sporocarps is
156 scarce in the literature.

157 The relation between the productivity of fruiting bodies and ECM symbiosis is still
158 unclear. Some ectomycorrhizal species produce abundant ectomycorrhizal root tips
159 but few or no fruiting bodies, while other ectomycorrhizal fungi form abundant
160 fruiting bodies but a low number of ectomycorrhizal root tips. Guidot et al.
161 (53)(2001) found a spatial congruence of above- and belowground distribution for
162 *H. cylindrosporum* . However, De la Varga et al.(52) (2012) found that the presence
163 of mycorrhizae of the *B. edulis* symbiotic rate was not consistent with the
164 production of fruiting bodies. There are also *Russula* species difference between the
165 above-ground *Russula* sporocarp and underground *Russula* mycorrhizal(2) .
166 Geml(2010) (2)observed that 15 and 45 of the 50 *Russula* phylogroups species were
167 found in sporocarp and soil clone sequences, respectively. Given the long delay
168 between the establishment of the plantation and the formation of sporocarps, short-
169 and medium-term control of the survival and persistence of fungal symbionts in
170 plantations have to still be evaluated by the assessment of vegetative structures as
171 the ectomycorrhizas or extraradical mycelium.

172 Microbial community affected mycorrhizal fungal function (for example, symbiosis
173 establishment capacity, sporocarp production), and the reciprocal effects are vice
174 versa. The microorganisms associated with mycorrhizal fungi may either have
175 positive or negative impacts on fungal spore germination, growth, nutrient
176 acquisition and plant colonization (43, 54). *Tuber indicum* altered the
177 ectomycorrhizosphere and endoectomycosphere microbiome and metabolic profiles
178 of the host tree *Quercus aliena* (55). *Tuber borchii* shapes the
179 ectomycorrhizosphere microbial communities of *Corylus avellana*(56). Therefore,

we speculate that detecting the communities of *Russula* can tracked ECM persistence throughout the entire biological cycle, which will help to control ectomycorrhiza formation and sporocarp production. In this study, to understand the communities of the targeted *Russula griseocarnosa* and to find the possible indicator microbes of successful *Russula griseocarnosa* plantations, we identified the *Russula* ectomycorrhizal fungal communities inhabiting different life cycle stages based on MiSeq sequencing of ribosomal internal transcribed spacer (ITS) sequences of root DNA and mycosphere communities based on MiSeq sequencing of the 16S V3-V4 as well as ribosomal internal transcribed spacer (ITS) sequences of mycosphere soil DNA.

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This study is the first attempt to analyze ectomycorrhizal communities of *Russula* using MiSeq sequencing metagenomics DNA of *Russula* root and the Mycorrhizal rhizosphere soil in *Russula* at different stages. We think that *Russula* shapes the ectomycorrhizosphere microbial communities of Fagaceae (*Quercus glauca* and *Castanopsis hainanensis*).

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197 **RESULTS**

Comparing microbiomes among types of the ECM fungus *Russula*. ECM *Russula* was first identified by combining morph typing with Sanger sequencing DNA sequences . We analyzed internal transcribed spacer (ITS) rDNA sequences of ECM root tips and ECM rhizosphere soil samples using phylogenetic methods, operational taxonomic unit (OTU) delimitations and ordinations to compare species composition in various types of ECM *Russula*.

In the ECM metagenome, we found a positive correlation between the concentration of *Russula* DNA and the presence of *Russula* mycorrhizae in the mycorrhizal rhizosphere and ECM root (Tab 1). To analyze whether distinctive communities are selected by *Russula* ectomycorrhizal fungi, the fungi of ECM root microbiomes were compared and divided into three types. *Russula* that could be detected by Sanger sequencing with a DNA concentration above 10% of total ECM

genomic DNA, as determined by MiSeq sequencing, were classified as type 1. *Russula* sporocarps that could be collected from the ground and the extended hyphae of which could be connected between roots of the host and sporocarp within 50 cm, with *Russula* detected by Sanger sequencing, were classified as type 2. *Russula* that were not detected by Sanger sequencing or with a DNA concentration below 5% of the total ECM genomic DNA, as determined by MiSeq sequencing, were classified as type 3. Therefore, the samples of ECM tip and rhizosphere samplings were divided into three types: *Russula*-infected (type 1), sporocarp-producing *Russula* (type 2), and *Russula*-uninfected (type 3) (Tab 1). Relative *Russula* OUT abundance is significant difference in ECM *Russula* symbiosis root and in ECM *Russula* rhizosphere, respectively (Tab 1, Fig. 1A). Type 2 is the most abundant, type 1 is the second, and type 3 is the least. Interestingly, in type 3, the amount of *Russula* in the soil is higher than in the root. This may indicate that in the natural growth area of *Russula*, there are a large number of *Russula* propagules in the soil.

TABLE 1 Relative *Russula* OUT abundance in three types and Alpha diversity analysis of fungi and bacterial of three types of ECM *Russula* roots or *Russula* rhizosphere soil in natural *Russula* growth areas

Type	Relative abundance of <i>Russula</i> OUT (%) in ECM	Chao1 richness of Fungi Community of <i>Russula</i> root	Shannon of Fungi Community of <i>Russula</i> root	Relative abundance of <i>Russula</i> OUT (%) in ECM	Chao1 richness of Fungi Community of <i>Russula</i> rhizosphere	Shannon of Fungi Community of <i>Russula</i> rhizosphere	Chao1 richness of Bacterial Community of ECM	Shannon of Bacterial Community of ECM
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	ula			la	rhizos		la	spher
	root			rhizos	phere		rhizos	e
				phere			phere	
Russula	28.74	663.12±	4.04±	20.22	901.3	4.52±	1010.	7.54±
–infected	±			±	8±		28±	
(type1)		171.655	1.007			0.53a		0.10b
	19.31	b	b	4.59B	32.30		17.29	
	B^{1,2}				a		b	
Russula	66.66	170.44±	2.20±	39.23	756.8	4.56±	945.8	7.49±
sporocarp	±	24.68c	0.19	±	7±		1±	
producing			c			0.99a		0.049
(type2)	12.92			7.58C	52.18		25.08	b
	C				b		b	
Russula-n	1.44±	782.20±	4.55±	5.61±	874.1	4.47±	1099.	7.94±
o-infected					9±		52±	0.13a
(type3)	1.02	102.345	0.921	1.71A		0.95a		
	A	a	a		41.16		13.14	
					a		a	

229 1. mean±standard deviation ; type1 has 4 repeats, type2 has 2 repeats and type3 has
230 3 repeats.

231 2. Analysis of variance by one-way analysis of variance In each column: different
232 words indicate differences, uppercase letters indicate extremely significant
233 differences (P <0.01); and lowercase letters indicate significant differences (P
234 <0.05)

235 **Fungal diversity analysis and analysis of indicator species associated with**
236 **ECM *Russula* roots.** In total, 1346 fungal operational taxonomic units (OTUs)
237 were distinguished in roots. Among the three types, the Chao1 diversity index and
238 Shannon diversity index decreased in sporocarp-producing *Russula* type (type 2)

239 and *Russula*-infected type (type 1) compared to the *Russula*-uninfected (type 3)
 240 (Tab 1). The result shows that species richness shifted in the composition of the
 241 ECM community associated with *Russula*. The fungal community composition and
 242 the abundance of the main fungi (over 0.05% fungi in roots genome) were different
 243 in the three *Russula* types roots (Fig. 1A, Tab 1). The result shows that *Russula* is
 244 dominates in fruiting bodies (type 2) and infected samples (type 1) though *Russula*
 245 in three type samples.

246 Based on the top 20 fungi of each sample, we first obtained the common species of
 247 three types after intersecting each type with the Venny mapping tool: 14 species
 248 were in type 2, 5 in type 2 and 3 in type 3 (Tab S1). Then, we intersected the
 249 common types of three types with the Venny mapping tool. At the genus level, the
 250 three types shared 3 common genera: *Russula*, *Tomentella* and *Lactarius* (Tab S2,
 251 Fig. 1B). These results showed that these are common fungi in Fagaceae ECM roots.
 252 Types 1 and 2 shared 2 common genera: *Acremonium* and *Cladophialophora*, in
 253 addition to the abovementioned three common ECM (Tab S2, Fig. 1B). Second, We
 254 take a collection of three types genera respectively, subsequently we intersected the
 255 collection of three types by the Venny mapping tool (Fig. 1C): 24 species in type 2,
 256 46 in type 1 and 41 in type 3, and 5 genera were exclusively in type 2 collection.
 257 We take the intersection of the unique collection (9 genera) and union (5 genera) in
 258 type 2, and found only one species *Boletus* (Fig. 1D, Tab. 2). Analyze fungi
 259 composition differences of three types roots by PCoA based on the top 20 fungal
 260 genera, we found that the control (type 3) belonged to quadrant IV, type 1 belonged
 261 to quadrant I or II, and type 2 belonged to quadrant III (Fig. 1F). The results show
 262 that the fungal community of sporocarp-producing *Russula* was completely
 263 different from that of *Russula*-uninfected. The *Russula*-infected type was in the
 264 transitional phase. We suggest the *Russula* infection contributed 31.3% and others
 265 elements host contributed 20.5% of the differences, respectively. *Boletus* was the
 266 only ECM with the emergence of *Russula* fruit bodies. In all, *Boletus* may be
 267 considered an indicator species in the *Russula* sporocarp-producing fungal
 268 community, and *Acremonium* and *Cladophialophora* may be considered indicator

species in *Russula* symbiosis fungal communities (Tab. 2). Analyze the different effects of ECM species by PCoA based on the top 20 fungal genera, we found *Tomentella*, *Xylogone*, and *Lactarius* belonged to I, II, while others belonged to quadrant III,V (Fig. 1E). The *Russula* infection contributed 55% and others elements contributed 24% of the differences, respectively. Combining these two factors, it shows *Russula* and *Elaphomyces* can be divided into one categories, while *Xylogone* can be divided into another category functionally. So we assume that *Elaphomyces* are benefit for *Russula* symbiosis while *Tomentella*, *Xylogone*, and *Lactarius* has the function of competing hosts.

Fig. 1 Diversity analysis of fungi of three types of *Russula* symbiosis roots in natural *Russula* growth areas

A: The main fungi genus composition and abundance in type2 *Russula* symbiosis root and the corresponding genus are in the other two types

B: The Venny mapping of the common genus of the top 20 fungi genus in three types

Russula symbiosis root

C: The Venny mapping of the collection genus of the top 20 fungi genus in three

329 types *Russula* symbiosis root
 330 D: The Venny mapping of the common genus and the collection genus of the top 20
 331 fungi genus in type2 *Russula* symbiosis root
 332 E : Analysis of ECM role difference of three types *Russula* symbiosis root on top 20
 333 fungi genus of ECM *Russula* by PCoA
 334 F :Analysis of composition difference of three types *Russula* symbiosis root on top
 335 20 fungi genus of ECM *Russula* by PCoA
 336 In Eand F: The scales of the horizontal and vertical axes are relative distances and
 337 have no practical significance. The contribution rate is the degree of interpretation,
 338 and the hypothetical factors can be evaluated and verified.
 339 In A,Eand F :In the sample name, the first letter M indicates mycorrhizal root ; first
 340 second F stands for fungi; the third letter different treatment :S indicates
 341 sporocarp(type2), E indicates ECM ectomycorrhizal(type1) , K indicates
 342 control(type3) respectively; the fourth number indicates the different biological
 343 repetitions of different treatment .

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345 **Fungal diversity analysis and analysis of indicator species associated with**
 346 **ECM *Russula* rhizosphere soil.** In total, 1829 fungal operational taxonomic units
 347 (OTUs) were distinguished in rhizosphere soil. Interactions with native
 348 ectomycorrhizal fungi present in the soil play a key role in the higher diversity of
 349 fungal taxa .Compared to type 1 and 3, the Chao1 diversity index decreased in
 350 types 2 ; while there were no significant differences between types 1 and 3 (Tab. 1).
 351 But, the Shannon diversity index showed no significant differences in three types
 352 (Tab. 1). The fungal community composition and

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Fig. 2 Diversity analysis of fungi of three types *Russula* mycorrhizal rhizosphere in natural *Russula* growth areas

A: The top 20 fungi genus composition and abundance in type2 *Russula* symbiosis mycorrhizal rhizosphere and the corresponding genus are in the other two types in at Fujian, China

In the sample name, the first letter S indicates mycorrhizal root soil ; first second F stands for fungi; the third letter different treatment :S indicates sporocarp, E indicates ECM ectomycorrhizal , K indicates control respectively; the fourth number indicates the different biological repetitions of different treatment .

B: The Venny mapping of the common genus of the top 20 fungi genus in three types *Russula* symbiosis Mycorrhizal rhizosphere

C: The Venny mapping of the collection genus of the top 20 fungi genus in three types *Russula* symbiosis Mycorrhizal rhizosphere

D: The Venny mapping of the common genus and the collection genus of the top 20 fungi genus in type2 *Russula* symbiosis Mycorrhizal rhizosphere

E : Analysis of ECM role difference of three types *Russula* symbiosis mycorrhizal rhizosphere on top 20 fungi genus of ECM *Russula* by PCoA

F : Analysis of composition difference of three types *Russula* symbiosis mycorrhizal rhizosphere on top 20 fungi genus of ECM *Russula* by PCoA

In E and F: the scales of the horizontal and vertical axes are relative distances and have no practical significance. The contribution rate is the degree of interpretation,

419 and the hypothetical factors can be evaluated and verified.

420 the abundance of the main fungi (over 0.05% fungi in soil genome)were different

421 in the three *Russula* types rhizosphere soil (Fig. 1A,Tab 1).Compared to the

422 root ,The result shows that *Russula* is also dominates in fruiting bodies (type 2) and

423 infected samples(type 1) though *Russula* in three type samples(Fig. 1A,Fig. 2A).

424 However,compared to the root ,the genera variety increased (Fig. 1A,Fig. 2A).

425 The community composition of the top 20 fungi in the three *Russula* rhizosphere

426 soil types was analyzed (Tab. S2). We first obtained the common species of three

427 types after intersecting each type using the Venny mapping tool: 12 species in type

428 2, 7 species in type 1 and 7 species in type 3 (Fig. 2B). Then, we intersected the

429 common types of the three types with the Venny mapping tool. At the genus level,

430 the three types shared 4 common genera: *Russula*, *Mortierella*, *Penicillium* and

431 *Trichoderma*; and *Russula* also had a large frequency in types 1 and 2 (Fig. 2B).

432 This showed that 4 genera are common fungi in Fagaceae-dominant rhizosphere

433 soil. Types 1 and 2 shared 3 common genera: *Elaphomyces*, *Tomentella* and

434 *Saitozyma* ,in addition to the abovementioned 4 common genera(Fig. 2B). Second,

435 we take a collection of three types genera respectively, subsequently intersected the

436 collection of three types by the Venny mapping tool (Fig. 2C): 26 species in type 2,

437 40 in type 1 and 36 in type 3; 4 genera were included exclusively in the type 2

438 collection. We take the intersection of the unique collection (4 genera) and union (4

439 genera) in type 2, and found *Dacryobolus* unique belonged to type 2 (Fig. 2D, Tab.

440 2). The top 20 fungal genera in the sporocarp-producing *Russula* root rhizosphere

441 with types 3 or types 1 were compared. The result shows that *Russula* EMM is

442 dominates in fruiting bodies (type 2) and infected samples (type 1) though *Russula*

443 in three type samples. *Elaphomyces* also dominated in types 1 and 2, but nearly did

444 not exist in the control, type 3 (Fig. 2D). In all, *Dacryobolus* may be considered an

445 indicator species of sporocarp-producing *Russula* in the *Russula* rhizosphere.

446 *Elaphomyces*, and *Tomentella* may be considered indicator species for *Russula*

447 symbiosis in the rhizosphere (Tab. 2). Analyze three types of fungi composition

448 differences of top 20 genera by PCoA in *Russula* rhizosphere soil based on the top

20 fungal genera, we found that type 2 belonged to quadrant II and type 1 belonged to quadrants I, III and IV, while type 3 belonged to quadrants III and IV, down the horizontal axis (Fig. 2E). The host and *Russula*-infection contributed 29.3% and 25.0%, respectively. Furthermore, analyzing the different effects of fungi species by PCoA, we found *Russula* and *Elaphomyces* belonged to quadrant IV, *Mortierella* and *Tomentella* belonged to quadrant I, *Trichoderma*, *Penicillium*, *Geminibasidium* and *Saitozyma* belonged to quadrant II, while others belonged to quadrant III (Fig. 2E). The *Russula* infection contributed 49.4% and others elements host contributed 19.4% of the differences, respectively. Combining these two factors, we assume that *Elaphomyces* in soil are benefit for *Russula* symbiosis.

Bacterial diversity analysis and analysis of indicator species associated with ECM *Russula* rhizosphere soil. In total, 1494 bacterial operational taxonomic units (OTUs) were distinguished in this study. Compared to type 3, the Chao1 diversity index decreased in types 1 and 2 (Tab. 1). There were significant differences between type 3 and the other two types. However, there were no significant differences between types 1 and 2. The Shannon diversity index showed the same tendency as the Chao1 diversity index (Tab. 1). The bacterial community composition and the abundance of the main bacterial (the over 0.05% bacteria in soil genome) were analyzed (Fig. 3A). About 40-60% of the species in the sample cannot be identified by Illumina MiSeq high-throughput sequencing and the remaining bacterial genera in the sporocarp-producing *Russula* root rhizosphere soil were showed for the three types (Fig. 3A). Compared to the fungi of the root and rhizosphere soil, the bacterial genera variety still increased (Fig. 1A, 2A, 3A).

The community composition of the top 20 f bacteria in the three *Russula* rhizosphere soil types was analyzed (Tab. S3). We first obtained the common species of the three types after intersecting each type with the Venny mapping tool: 18 species in type 2, 14 in type 1 and 12 in type 3 (Fig. 3B). Then, we intersected the common types of the three types with the Venny mapping tool. At the genus level, the three types shared 10 common genera: *Acidibacter*, *Candidatus*,

479 *Rhizomicrobium*, *Acidotherrmus*, *Variibacter*, *Burkholderia*, *Roseiarcus*,
480 *Bradyrhizobium*, *Candidatus* and *Granulicella*. (Fig. 3B). This showed that 10
481 genera are common bacteria in Fagaceae-dominant rhizosphere soil. Types 1 and 2
482 shared 4 common genera: *Bryobacter*, *Sorangium*, *Acidicaldus*, and
483 *Acidobacterium* „in addition to the abovementioned 10 common genera(Fig. 3B).
484 Second, we obtained the collection of the various types: 20 species in type 2, 27 in
485 type 1 and 26 in type 3 (Fig. 3C,Tab S3). Then, the unique genera were analyzed of
486 the unique collection (4 genera) and union (3 genera) in type 2 by the Venny
487 mapping tool, and 2 genera *Acidocella* and *Edaphobacter* were found (Fig. 3D). In
488 all, *Acidocella* ,*Edaphobacter* may be considered indicator species for
489 sporocarp-producing *Russula*, and *Bryobacter*, *Sorangium*, *Acidicaldus*, and
490 *Acidobacterium* can be considered indicator species for *Russula* symbiosis in the
491 bacterial community (Tab. 2). By PCoA based on the top 20 fungal genera, we
492 found that type 2 belonged to quadrant III , left of the vertical axis. Except for one
493 sample, other samples of type 1 belonged to quadrants II or III, left of the vertical
494 axis . Type 3 belonged to the right of the vertical axis (Fig. 3F). We assume that the
495 *Russula* infection and host contributed 47.3% and 21.4%, respectively(Fig. 3F).
496 Analyze the different effects of bacteria species by PCoA , we found *Acidocella*,
497 *Sorangium*, *Haliangium* , *Telmatospirillum* , *Edaphobacter* , *Acidobacterium* ,
498 *Sphingomonas*, *Candidatus_Koribacter* , *Roseiarcus* , *Granulicella* and *Acidicaldus*
499 belonged to quadrant II, III , while the others belonged to quadrant I, IV (Fig. 3E).
500 It shows 11 gengus in quadrant II, III can be divided into one categories by role. All
501 indicator species for sporocarp-producing *Russula* or *Russula* symbiosis in the same
502 categories but *Bryobacter*. We assume that the *Russula* infection contributed
503 80.9% and others elements contributed 10.5% respectively. Combined with
504 indicator species analysis, we assume that 11 bacterial gengus beneficial to the
505 symbiosis of *Russula*.

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Fig. 3 Diversity analysis of bacterial of three types *Russula* Mycorrhizal rhizosphere in natural *Russula* growth areas

A: The top 20 bacterial genus composition and abundance in type2 *Russula* symbiosis mycorrhizal rhizosphere and the corresponding genus are in the other two types in natural *Russula* growth areas , Fujian, China

569 In the sample name, the first letter s indicates mycorrhizal root soil; first second b
570 stands for bacteria; the third letter different treatment :S indicates sporocarp, E
571 indicates ECM ectomycorrhizal , K indicates control respectively; the fourth
572 number indicates the different biological repetitions of different treatment .
573 B: The Venny mapping of the common genus of the top 20 bacterial genus in three
574 types *Russula* symbiosis Mycorrhizal rhizosphere
575 C: The Venny mapping of the collection genus of the top 20 bacterial genus in three
576 types *Russula* symbiosis Mycorrhizal rhizosphere
577 D: The Venny mapping of the common genus and the collection genus of the top
578 20 bacterial genus in type2 *Russula* symbiosis Mycorrhizal rhizosphere
579 E: Analysis of 20 bacterial genus role difference of three types *Russula* symbiosis
580 mycorrhizal rhizosphere on top 20 bacterial genus of ECM *Russula* by PCoA
581 F : Analysis of composition difference of three types *Russula* symbiosis
582 mycorrhizal rhizosphere on top 20 bacterial genus of ECM *Russula* by PCoA
583 In E and F: The scales of the horizontal and vertical axes are relative distances and
584 have no practical significance. The contribution rate is the degree of interpretation,
585 and the hypothetical factors can be evaluated and verified.

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587 **Table 2** Indicator species of fungi and bacterial community of *Russula*
588 Mycorrhizal based on the top 20 genus

Common species in three types		Common species in type1 and type2, Excluding those that are common to all three types	species included exclusively in Type 2,compareing to collecting Type 1,3; and belong to Common in type2
Fungi of ECM	<i>Tomentella</i> , <i>Lactarius</i> , <i>Russula</i>	<i>Acremonium</i> , <i>Cladophialophora</i>	<i>Boletus</i>

Russula			
root			
Fungi of	<i>Russula</i> , <i>Mortierella</i>	<i>Elaphomyces</i> ,	<i>Dacryobolus</i>
Russula	<i>a</i> , <i>Penicillium</i>	<i>Tomentella</i>	
Mycorrhizal	<i>Trichoderma</i>		
rhizosphere			
e			
Bacterial	<i>Acidibacter</i> ,	<i>Bryobacter</i> , <i>Sorangium</i> ,	<i>Acidocella</i> ,
of Russula	<i>Acidothymus</i> ,	<i>Acidicaldus</i> ,	<i>Edaphobacter</i>
Mycorrhizal	<i>Candidatus_Solibacter</i>	<i>Acidobacterium</i>	
rhizosphere	<i>Rhizomicrobium</i> ,		
e	<i>Variibacter</i> ,		
	<i>Burkholderia-Paraburkholderia</i> , <i>Rosei</i>		
	<i>arcus</i> ,		
	<i>Bradyrhizobium</i> ,		
	<i>Candidatus_Koribacter</i> ,		
	<i>Granulicella</i>		

589 Type2:Russula sporocarp producing; type1 :Russula –infected;
590 type3 :Russula-no-infected; If one species is with one type and without the other
591 type, then the species is assumed as the indicator of the type based on the top 20
592 genus.

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594 Interaction of fungi and bacteria with ECM *Russula* root and mycorrhizal 595 rhizosphere

596 By network net, we analyzed the interaction of the top 20 fungal OTUs of *Russula*
597 rhizosphere soil and ECM *Russula* root, including 7 *Russula* OTUs(MSFH OTU_1,

MSFH OTU_3, MSFH OTU_4, MSFH OTU_16, MSFH OTU_21, MSFH OTU_24 and SMFH OTU_1639) (Table S7), five indicator species (MSFH OTU_19 *Elaphomyces*, MSFH OTU_9 *Tomentella*_sp, MSFH OTU_655 *Tomentella*_sp, MSFH OTU_6 *Elaphomyces*, and MSFH OTU_5 *Tomentella*_sp). *Russula*, which interacted with other species in positive ways, was the representative and contributed to the main ECM in the community. For example, the interaction result predicted that many fungi had a positive correlation with *Russula* (Fig.4A, Table S4), MSFH OTU_19 (*Elaphomyces*) and MSFH OTU_5 (*Tomentella*_sp) with the *Russula rosea*; MSFH OTU_21, MSFH OTU_655 (*Tomentella*_sp) and MSFH OTU_5 with *Russula* sp. In all, *Elaphomyces*_sp, *Tomentella*_sp have a positive correlation with *Russula*, combining the previous results that *Elaphomyces* and *Tomentella* were considered indicator species for *Russula* symbiosis in the *Russula* rhizosphere based on the top 20 genera (Tab. 2). Therefore, we further assume that the indicators *Elaphomyces* and *Tomentella* have a positive correlation with *Russula* symbiosis.that

Fig. 4 Interaction of indicator species with the top 20 fungi and bacterial OTUs in

community of *Russula* mycorrhizal

A: Interaction of fungi in *Russula* ECM root and *Russula* mycorrhizal rhizosphere

B: Interaction of bacterial in *Russula* mycorrhizal rhizosphere

In A and B: The size of the dots represents the abundance, the color of the dots represents the phylum (In A : Orange represents p__Ascomycota, blue represents p__Basidiomycota, gray represents p__Mortierellomycota; in B: gray represents p__Proteobacteria, Orange represents p__Acidobacteria, blue represents p__Actinobacteria), the thickness of the lines represents the magnitude of the correlation, and the red line indicates a positive correlation, the blue color indicates a negative correlation.

Meanwhile, we analyzed the relationship of the top 20 bacterial OTUs in *Russula* rhizosphere soil by Network net. Only 15 bacterial OTUs were included in the network net (Fig. 4B, Table S5). Among the top 15 bacterial OTUs, there is 1 OTUs SBH OTU_70 *Sorangium* belonging to indicator species. The network net suggested that SBH OTU_70 was positive with SBH OTU_16 (Acidobacteriaceae), 24(Caulobacteraceae), 27(Solibacteraceae), 69(Solibacteraceae). Another indicator species *Acidobacterium* was't within network net . Therefore, we further assumed that *Sorangium* and other OTUs (Acidobacteriaceae, Caulobacteraceae, Solibacteraceae) have a positive correlation with *Russula* .

DISCUSSION

The complete exclusion of other species by any single species could be prevented by either fluctuation in the environment, by seasonal root production or by the presence of microbiome competitive networks, the situation in which no single species is competitively superior to all other species. So, we usually obtain 1 ECM species or 2 ECM species by Sanger sequencing of the root sample with basidiomycete-specific primers. The introduction of high-throughput sequencing techniques, metagenomics or environmental genomics has provided new information on ECM fungal communities by 'barcodes' of ITS regions in several biomes/ecosystems, e.g., truffle grounds (57) and ECM roots in the Svalbard(58). In this study, we found that *Russula* cannot successfully infect roots if the amount

of *Russula* in the mycorrhizal rhizosphere is less than 10% by MiSeq sequencing (Table 1, part data not shown). Although ECM fungi infection have been detected in nonproductive plots, the amount was not sufficient to shift from vegetative growth to fruit body. *Russula* can form a fruiting body, only when *Russula* infection could be detected by Sanger sequencing of ECM roots, contemporary the relative abundance of its DNA was greater than 60% by MiSeq sequencing. Compared to control, we found significantly more *Russula* DNA in *Russula* sporocarps rhizosphere soil or *Russula* symbiosis rhizosphere soil, above 15% amount of the metagenomics of rhizosphere soil. Zampieri et al.(2012) (49) detected significantly more *T. melanosporum* DNA in truffle productive plots of soil. Zhou et al. (2001) (50) also demonstrated that the development of *S.grevillei* sporocarps is correlated with that of extraradical mycelia, which are distributed in a narrow area. So , we suggest that to the type 2(sporocarps-producing) ,there is congruence of the above-sporocarps and belowground root or mycorrhizospheres soil DNA for *Russula*. However, interestingly, in type 3(uninfected), the amount of *Russula* in the soil is higher than in the root. This may indicate that in the natural growth area of *Russula*, there are a large number of *Russula* propagules in the soil. Whether the *Russula* propagules naturally in the soil of the natural growth area can colonize to the host or not depends on other factors.

Fewer species were detected in *Russula* productive root than in nonproductive root, which is consistent with French *truffle* grounds. *T. melanosporum* grounds also have shown a reduced fungal biodiversity, a reduced presence of both ECM Basidiomycota (57). Truffle-colonization reduced the abundance of some fungal genera surrounding the host tree, such as *Acremonium* (55) . *Russula* fruiting body decreased the Chao richness bacterial index and Shannon diversity of bacterial index in rhizosphere soil. Simultaneously, *Russula* fruiting body decreased the Chao richness fungi index but no effect on Shannon diversity of fungi index in rhizosphere soil. Warmin (2009)(40) found bacteria adapted to the mycospheres of three or more or just one ECM fungal species was defined as specific selective bacterial. So, we suggest the diversity decreased phenomenon may be related with

688 the *Russula* sporocarp selection effect, especially to rhizosphere soil bacterial.

689 Temperate forests are generally dominated by Fagaceae, and species in these plant

690 families form mycorrhizae with various phylogenetic clades of ectomycorrhizal

691 fungi(8, 11, 59). Members of the *helotialean* group have recently been identified as

692 the dominant species in the roots of Fagaceae trees in the temperate and subtropical

693 forests of Japan (60, 61). In our study, we found that 3 ECM, *Russula*, *Tomentella*,

694 and *Lactarius*, are the main members in the natural Fagaceae (*Quercus glauca* and

695 *Castanopsis hainanensis*)-dominant *Russula* ground in all the types. This result is

696 consistent with the preference of *Russula* and *Lactarius* for the Fagaceae host. In

697 *Castanopsis*-dominant forest in Japan (62), there are ECM fungi such as *Amanita*

698 (*Amanitaceae*), *Boletus* (*Boletaceae*), *Tylopilus* (*Boletaceae*), *Cortinarius*

699 (*Cortinariaceae*), *Inocybe* (*Inocybaceae*), *Lactarius* (*Russulaceae*), and *Russula*

700 (*Russulaceae*). The dominant ECM lineages of *Quercus liaotungensis* were

701 *Tomentella*, *Thelephora*, *Cenococcum*, *Russula*, *Lactarius* and *Inocybe*(63). The

702 ectomycorrhizal *Russula*, *Lactarius*, *Cortinarius*, *Tomentella*, *Amanita*, *Boletus* and

703 *Cenococcum* were dominant in the *Quercus serrate* plot (11). *R. vinosa* grows in

704 tropical and subtropical evergreen forests in southern China dominated by trees of

705 *Castanopsis* spp., and *R. griseocarnosa* grows in forests with Fagaceae (13). Given

706 commercially harvested truffles can establish ectomycorrhizal relationships with

707 different woody host species, and many different combinations of truffle and host

708 species mycorrhizal seedlings are produced in nurseries (64). Our study shows that

709 *Russula* inoculation may establish satisfactory ectomycorrhizal relationships with

710 two indigenous tree species, *Quercus glauca* and *Castanopsis hainanensis*.

711

712 Healthy ECM can support a wide variety of organisms, including a diverse array of

713 fungi other than the dominant ectomycorrhizal symbiont. Some pathogenic fungi,

714 including *Ilyonectria* and *Podospora*, and other competitive mycorrhizal fungi,

715 such as *Hymenochaete*, had significantly lower abundance in the *T.*

716 *borchii*-inoculated root and *Trechispora* and *Humicola*, which were more abundant

717 in the *T. borchii*-inoculated root. There are some notable examples of associations

among *suilloid* fungi and members of the Gomphidiaceae occur within ectomycorrhizal roots (27). Olsson considered *Gomphidius roseus* acted as a parasite of *Suillus bovinus*, the former never occurs without the latter(27) , Based on MiSeq sequencing analysis of the top 20 ectomycorrhizal fungi in *Russula* root, we found *Acremonium*; *Cladophialophora* are associated with ECM *Russula*-Fagaceae roots, and *Boletus* was in association with sporocarp-producing *Russula*. Meanwhile, based on the top 20 genera in *Russula* rhizosphere soil, we found that *Elaphomyces*, and *Tomentella* in association with *Russula* symbiosis; *Dacryobolus* were associated with sporocarp-producing *Russula*. The result will help to find and develop PGPF for *Russula* symbiosis or sporocarp-producing.

Many studies have addressed the role of soil bacteria in establishing the symbiotic relationship between plants and mycorrhizal fungi (43, 65). We found differences in fungal genus among the three ECM *Russula* types in rhizosphere soil (Table S 3, Table 2).The interactions of bacteria with the dense hyphal network underneath fungal fruiting bodies have also been addressed (44, 66). Differences in bacterial communities associated with the mycorrhizospheres of *Suillus bovinus*- and *Paxillus involutus*-colonized plants were detected early (67, 68). Frey et al.(1997)(69) reported that specific *Pseudomonas fluorescens* prefer *Laccaria laccata*. *P.fluorescens* and *Burkholderia terrae* are exclusively found in the mycosphere soil of *Laccaria proxima* (30, 40). Boersma(2009)(36) found that the mycospheres of basidiomycetous fungi indeed exerted a universal selective effect on the *Pseudomonas* community (i.e., *Pseudomonas poae*, *P. lini*, *P. umsongensis*, *P. corrugata*, *P. antarctica* and *Rahnella aquatilis*); as well as species-specific selective (i.e. *P. viridiflava* and candidatus *Xiphinematobacter americani*). For the selection of the bacteria family *Sphingomonadaceae* by the mycorrhizal fungi *L. proxima* and *R. exalbicans*, the mycosphere effect was most prominent in the latter (36). The mycosphere-isolated bacterium *Burkholderia terrae* has been shown to protect its fungal host *Lyophyllum* sp. from several antifungal agents, such as metabolites produced by *P. fluorescens*, as well as from the antifungal agent

cycloheximide (70). Some studies have concentrated on mycorrhization helper bacteria (MHB) in facilitating mycorrhizal colonization of roots in forest nursery environments(43, 71). Rich in bacteria in the mycorrhizal roots, mycorrhizosphere soil and peridium of desert truffles may be used to increase the survival and mycorrhization in the desert truffle plant production system at a semi-industrial scale(72) . The associated bacteria of *Truffle brûlés* are *Pseudomonas* and *Flavobacteriaceae* (73). To achieve successful reforestation, PGPR and MHB were screened to improve the establishment of *Lactarius deliciosus*-Pinus sp. symbiosis(74). In our study, *Acidocella* , *Bryobacter*, *Sorangium*, *Acidicaldus*, *Edaphobacter* and *Acidobacterium* were indicator species for *Russula* symbiosis in the bacterial community. we also found ECM universal selective *Sphingomonadaceae* work with *Russula* species-specific selective *Acidocella* ,*Sorangium*, *Acidicaldus*, *Edaphobacter* and *Acidobacterium* in the soil bacterial community of *Russula* symbiosis (Fig. 3E).Further, by network analysis, *Acidobacteriaceae*, *Sorangium* and *Acidobacteria* had a positive correlation with *Russula*. There may be further instruction to provide a wide collection of these bacterial associates of *Russula* and to develop *Russula* MHB or Fagaceae PGPR.

Only a few edible ectomycorrhizal fungal species, such as black truffles or saffron milk caps, can be produced in manufactured orchards. To date, *Russula* fruit bodies are uncultivable. Five *Russula* were used to inoculate *Shorea parvifolia* seeding successfully (75) , and one *Russula* was used to inoculate *Quercus garryana* seeding successfully(76) . Our results will provide instruction to specifically isolate the fungi or beneficial rhizosphere microbes associated with ECM *Russula* from the root or mycorrhizal rhizosphere. Next , we will further need to isolate and culture the microbial communities of the *Russula* root or mycorrhizospheres soil in three types, which will supplement our research findings. The inoculation of these microbes can stimulate establishment and will help to enhance plant growth and promote a change in infected frequency.

Conclusion. The amount of *Russula* DNA is positively correlated with fruiting body and *Russula* mycorrhizae based on the metagenomics of *Russula* root and soil. Fewer fungi species were detected in *Russula*- infected and *Russula* sporocarp root. Fewer bacteria and fungi species were detected in *Russula*- infected and in *Russula* sporocarp rhizosphere soil. *Boletus* is considered as indicator species in *Russula*-Fagaceae root (*Quercus glauca* and *Castanopsis hainanensis*) for sporocarp-producing *Russula*. The *Russula* sporocarp rhizosphere fungi *Dacryobolus* and *Russula* sporocarp rhizosphere bacteria *Acidocella* is considered as indicator species for sporocarp-producing *Russula*. On the other hand, a number of taxa within *Acremonium* and *Cladophialophora* were identified in Fagaceae root in *Russula* symbiosis. The *Russula* mycorrhizal rhizosphere fungi *Tomentella*, and *Elaphomyces* and the *Russula* mycorrhizal rhizosphere bacteria *Acidocella*, *Bryobacter*, *Sorangium* and *Acidobacterium* occurred more frequently in association with the ECM genus *Russula*. Understanding the ectomycorrhizal fungal communities inhabiting natural *Russula* growth areas may give us clues about the dynamics of the targeted *Russula* and the possibility of identifying mycorrhizal fungal species that are good indicators of successful *Russula* semicultivation. This research may provide novel targeted strategies to improve the establishment of *Russula*-Fagaceae sp. symbiosis and improve *Russula* ascospore productivity and sustainability.

MATERIALS AND METHODS

Sampling . Our study was conducted in areas of *Russula* growth in Jianou, Fujian province, China, in which species of the genus *Russula* are well represented. The dominant trees of the areas are *Quercus glauca* and *Castanopsis hainanensis*. The herb layer is composed of *Podophyllum peltatum*, *Panax stipuleanatus* and *Saxifraga stolonifera*. Fine roots were excavated 2-3 m from the trunk of an adult *Russula* symbiotic tree(Fig. S1A). In addition, another type of fine roots that was clearly connected to *Russula* sporocarp by extraradical mycelia was collected(Fig. S1B,C). We collected three 15-30 cm fine-root segments (containing 100-200 root tips) at a depth of 20 cm (77) . Roots from a single tree were pooled into a single

808 plastic bag. More than 200 cm³ of rhizosphere soil was collected around the root
809 samples for analyses. All root and soil samples were stored in a cooler containing
810 several ice bags and transported to our laboratory within 24 h for subsequent
811 analysis.

812 **DNA extraction, amplification, and sequencing.** The collected root samples were
813 washed carefully with tap water. Root tips were preserved in a plastic centrifuge
814 tube at -20°C before DNA extraction. DNA samples were pulverized using liquid
815 nitrogen. Total genomic DNA was extracted from ECM root tips using a modified
816 cetyltrimethylammonium bromide method, which was modified according to Wang
817 et al. (63)(2017). Total genomic DNA of corresponding rhizosphere soil was
818 extracted using a Fast DNA SPIN Kit (MP Bio) for soil according to the kit
819 operation steps.

820 First, the entire range of fungal ITS sequences was amplified from roots using the
821 ECM Basidiomycetes-specific high-coverage primer polymerase chain reaction
822 (PCR) with the primer pair ITS-1F (CTTGGTCATTTAGACGAAGTAA) and
823 ITS-4B (CAGGAGACTTGTACACGGTCCAG) (M. Gardes, 1993), and
824 traditional Sanger sequencing was performed. The sequences were BLAST against
825 the UNITE database/NCBI database (<http://www.ncbi.nlm.nih.gov>), and taxonomy
826 was assigned to species or genera using sequence similarity criteria of ≥97% for
827 species and 90–97% for genera. Furthermore, DNA of root tips identified as
828 *Russula* and the corresponding *Russula* symbiosis rhizosphere soil were subjected
829 to Illumina MiSeq high-throughput sequencing of ITS sequences to investigate their
830 associated microbiomes, while DNA of root tips with no mycorrhiza was used as a
831 control. The MiSeq sequences were edited, manually corrected in BioEdit 7.0.8 and
832 clustered into species-level operational taxonomic units (OTUs) at 97% sequence
833 similarity for species delimitation using PlutoF (<http://unite.ut.ee>) in UNITE(80). If
834 no match was found in the PlutoF system, any resulting OTU assignments were
835 individually checked by BLAST against the UNITE database/NCBI database
836 (<http://www.ncbi.nlm.nih.gov>).

837 To identify the fungi composition, we analyzed 18S ITS1-ITS4 DNA sequences of

ECM rhizosphere root and soil samples using phylogenetic methods, operational taxonomic unit (OTU) delimitations and ordinations to compare species composition in various types of ECM *Russula*. To identify the bacterial composition, we analyzed 16S V3-V4 DNA sequences of ECM rhizosphere soil samples using phylogenetic methods, operational taxonomic unit (OTU) delimitations and ordinations to compare species composition in various types of ECM *Russula*.

Statistical analyses. Chao1 (species richness index) and Shannon (microbial diversity index) indices were analyzed by 97% OTU similarity. ECM fungal richness and the microbial diversity index of each *Russula* root tip and the corresponding rhizosphere soil of *Russula* symbiosis were calculated using the vegan package and compared by one-way ANOVA. PCoA analyses were based on any distance other than the Euclidean distance using abundance and presence-absence data of the top 20 genera in three types. Differences in community composition among *Russula*-infected samples were visualized by PCoA (79).

Micro-Community diversity analysis and indicator species analysis. Taxonomic analyses were generated based on the community species abundance (each was above 0.05% of all reads) using Microsoft Excel. The main fungal genus patterns were determined by taxonomic analysis at different ECM *Russula* mycorrhizal roots. The main fungal and bacterial genus patterns were also observed in the *Russula* mycorrhizal rhizosphere. To assess *Russula* preference, aspects indicator species analysis was carried out by comparing the top 20 genera of three types of root micro-communities. Indicator species of the community of the top 20 genera based on the species presence in the *Russula* sample and absence in the no-*Russula* sample were analyzed by Venny drawing tools (<https://bioinfogp.cnb.csic.es/tools/venny/index.html>).

Network analyses. The relationships of *Russula* and other fungi in the *Russula* community were analyzed by Spearman correlation of the absolute top 20 most abundant in all the samples using the igraph, psych software package. Network nets

constructed on the interrelationship result with $P > 0.05$ or $|R| < 0.4$ were filtered. The relationships of bacteria in the *Russula* mycorrhizal rhizosphere were also analyzed by Spearman's correlation.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at

SUPPLEMENTAL FILE 1, TIFF file, 0.48 MB.

SUPPLEMENTAL FILE 1, PDF file, 0.22 MB.

SUPPLEMENTAL FILE 1, PDF file, 0.22 MB.

SUPPLEMENTAL FILE 1, PDF file, 0.22 MB.

SUPPLEMENTAL FILE 1, PDF file, 0.17 MB.

SUPPLEMENTAL FILE 1, PDF file, 0.13 MB.

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Type	Relative Russula OUT abundance (%) in ECM Russula a root	Chao1ric hness of Fungi Communi ty of ECM Russula root1	Shanno n of Fungi Commu nity of ECM Russula root	Relative Russula OUT abunda nce (%) in ECM Russula rhizosp here	Chao1 richness of Fungi Commu nity of ECM Russula rhizosp here	Shanno n of Fungi Commu nity of ECM Russula rhizosp here	Chao1 richness of Bacteria l Commu nity of ECM Russula Rhizosp here	Shannon of Bacteria l Commu nity of ECM Russula Rhizosp here
Russula – infected (type1)	28.74 ± 19.31B _{1,2}	663.12 ± 171.655b	4.04 ± 1.007b	20.22 ± 4.59B	901.38 ± 32.30a	4.52 ± 0.53a	1010.28 ± 17.29b	7.54 ± 0.10b
Russula sporocarp producing (type2)	66.66 ± 12.92C	170.44 ± 24.68c	2.20 ± 0.19 c	39.23 ± 7.58C	756.87 ± 52.18b	4.56 ± 0.99a	945.81 ± 25.08b	7.49 ± 0.049b
Russula-no-in fected (type3)	1.44 ± 1.02A	782.20 ± 102.345a	4.55 ± 0.921a	5.61 ± 1.71A	874.19 ± 41.16a	4.47 ± 0.95a	1099.52 ± 13.14a	7.94 ± 0.13a

Common species in three types			Common species in type1 and type2, Excluding those that are common to all three types	species included exclusively in Type 2, comparing to collecting Type 1,3; and belong to Common in type2
Fungi of ECM Russula root	<i>Tomentella, Lactarius, Russula</i>		<i>Acremonium, Cladophialophora</i>	<i>Boletus</i>
Fungi of Russula Mycorrhizal rhizosphere	<i>Russula, Mortierella, Trichoderma</i>	<i>Penicillium</i>	<i>Elaphomyces, Tomentella,</i>	<i>Dacryobolus</i>
Bacterial of Russula Mycorrhizal rhizosphere	<i>Acidibacter, Candidatus_Solibacter, Variibacter, Burkholderia-Paraburkholderia, Roseiarcus, Bradyrhizobium, Candidatus_Koribacter, Granulicella</i>	<i>Acidothermus, Rhizomicrobium,</i>	<i>Bryobacter, Sorangium, Acidicaldus, Acidobacterium</i>	<i>Acidocella</i>

	TYPE2		TYPE1		TYPE3				
sample name	MFS1 ^A	MFS2	MFE1	MFE2	MFE3	MFE4	MFK1	MFK2	MFK3
Total number of genus in Inters section	15		6				4		
Total number of genus in Collection	24		46				41		
1	g__Russula	g__Russula	g__Russula	g__unidentif	g__unidenti	g__Russula	g__Tomente	g__unidentif	g__unidentifi
2	g__Tomente	g__Tomente	g__Microidi	g__Russula	g__Russula	g__unidentifi	g__unident	g__Tomentell	g__Trechispor
3	g__Boletus	g__unident	g__Cladophi	g__Elaphom	g__Sebacina	g__Elaphomyce	g__Sporide	g__Lactarius	g__Tomentella
4	g__unident	g__Lactari	g__unidenti	g__Hydnum	g__Hemilecc	g__Pseudoprob	g__Lactari	g__Russula	g__Pseudoprob
5	g__Lactari	g__Boletus	g__Cytospor	g__Clitocy	g__Elaphomy	g__Tomentella	g__Russula	g__Rhizoderm	g__Xylogone

	us		a	bula	ces			ea	
6	g__Hymenos cyphus	g__Hymenos cyphus	g__Cortinar ius	g__Tomete lla	g__Trechisp ora	g__Cladophial ophora	g__Talarom yces	g__Phialea	g__Sebacina
7	g__Clitocy bula	g__Cortina rius	g__Archaeor hizomyces	g__Lauriom yces	g__Psathyre lla	g__Lactarius	g__Sebacin a	g__Trichoder ma	g__Lactarius
8	g__Xylogon e	g__Acremon ium	g__Phellinu s	g__Cladoph ialophora	g__Lactariu s	g__Mortierell a	g__Cladoph ialophora	g__Cladophia lophora	g__Talaromyce s
9	g__Acremon ium	g__Phellod on	g__Mortiere lla	g__Myriost oma	g__Tomentel la	g__Fusarium	g__Penicil lium	g__Thozetell a	g__Calvatia
10	g__Cladoph ialophora	g__Xylogon e	g__Penicill ium	g__Phellod on	g__Lasiosph aeria	g__Acremonium	g__Deconic a	g__Rhodovero naea	g__Cephalothe ca
11	g__Cortina rius	g__Cladoph ialophora	g__Acremoni um	g__Xylogon e	g__Xylogone	g__Rasamsonia	g__Coprine llus	g__Chaetosph aeria	g__Lysurus
12	g__Elaphom yces	g__Clitocy bula	g__Lactariu s	g__Rhodove ronaea	g__Mortiere lla	g__Sordaria	g__Trichod erma	g__Gliocepha lotrichum	g__Hemileccin um
13	g__Phellod on	g__Thozete lla	g__Rhodover onaea	g__Acremon ium	g__Cladophi alophora	g__Sporidesmi um	g__Inocybe	g__Chalara	g__Pezoloma
14	g__Thozete lla	g__Elaphom yces	g__Fusarium	g__Cortina rius	g__Oidioden dron	g__Hyaloscyph a	g__Mortier ella	g__Mortierel la	g__Cytospora
15	g__Chaetos phaeria	g__Kazachs tania	g__Cryptosp oriopsis	g__Oidiode ndron	g__Hydnum	g__Nectria	g__Cercoph ora	g__Oidiodend ron	g__Russula
16	g__Penicil lium	g__Issatch enkia	g__Rhizoder mea	g__Lactari us	g__Operculo myces	g__Trichoderm a	g__Xylogon e	g__Chloridiu m	g__Oidiodendr on
17	g__Phialea	g__Phialea	g__Dactylel lina	g__Clavuli na	g__Trichode rma	g__Clathrus	g__Clathru s	g__Cortinari us	g__Thozetella
18	g__Inocybe	g__Chaetos	g__Myrmecri	g__Rhizode	g__Acremoni	g__Antrodiell	g__Dendroc	g__Hymenoscy	g__Genolevuri

		phaeria	dium	rmea	um	a	lathra	phus	a
19	g__Colleto trichum	g__Thielav ia	g__Xylogone	g__Sebacin a	g__Clitopil us	g__Colletotri chum	g__Fusariu m	g__Sporidesm ium	g__Penicilliu m
20	g__Myrmecr idium	g__Rhodove ronaea	g__Tomentel la	g__Opercul omyces	g__Pezoloma	g__Talaromyce s	g__Elaphom yces	g__Calonectr ia	g__Chaetomium

	TYPE2		TYPE1		TYPE3				
sample name	SFS1	SFS2	SFE1	SFE2	SFE3	SFE4	SFK1	SFK2	SFK3
Total number of genus in Inters	12		7				7		
ection									
Total number of genus in Collec	26		40				36		
tion									
1	g_Russula	g_Russula	g_Mortierella	g_Elaphomyces	g_Russula	g_Russula	g_Archaeorhizomyces	g_unidentified	g_unidentified
2	g_Elaphomyces	g_Elaphomyces	g_unidentified	g_Russula	g_unidentified	g_Elaphomyces	g_Penicillium	g_Tomentella	g_Mortierella
3	g_unidentified	g_unidentified	g_Russula	g_unidentified	g_Trichoderma	g_Mortierella	g_unidentified	g_Rhodoveronaea	g_Geminibasidium
4	g_Clitocybula	g_Tomentella	g_Geminibasidium	g_Archaeorhizomyces	g_Tomentella	g_unidentified	g_Russula	g_Lactarius	g_Tomentella
5	g_Tomentella	g_Lactarius	g_Tomentella	g_Clitocybula	g_Mortierella	g_Pseudopro	g_Pseudopro	g_Russula	g_Russula

	la	us	lla	la	ella	boscispora	boscispora		
6	g_Lactarius	g_Clitocybula	g_Elaphomyces	g_Tomentella	g_Elaphomyces	g_Trichoderma	g_Rhodoveroniaea	g_Archaeorhizomyces	g_Penicillium
7	g_Archaeorhizomyces	g_Sporidesmium	g_Penicillium	g_Rhodoveroniaea	g_Lactarius	g_Tomentella	g_Myrmecridium	g_Cortinari	g_Saitozyma
8	g_Mortierella	g_Lasiosphaeria	g_Clitocybula	g_Trechispora	g_Penicillium	g_Penicillium	g_Trechispora	g_Corticium	g_Trichoderma
9	g_Penicillium	g_Mortierella	g_Trichoderma	g_Acremonium	g_Saitozyma	g_Sebacina	g_Cladophialophora	g_Mortierella	g_Clavulina
10	g_Cladophialophora	g_Inocybe	g_Saitozyma	g_Mortierella	g_Umbelopsis	g_Lactarius	g_Aspergillus	g_Saitozyma	g_Pseudoprocaryota
11	g_Cortinari	g_Saitozyma	g_Bifiguratus	g_Microdochium	g_Sporidesmium	g_Chloridium	g_Oidiodendron	g_Microdochium	g_Bifiguratus
12	g_Saitozyma	g_Cladophialophora	g_Lactarius	g_Cookeina	g_Geminibasidium	g_Amplistroma	g_Trichoderma	g_Sympodiella	g_Sebacina
13	g_Coralloidiomyces	g_Penicillium	g_Cladophialophora	g_Cladophialophora	g_Sebacina	g_Fusarium	g_Chloridium	g_Trichoderma	g_Talaromyces
14	g_Rhodoveroniaea	g_Trichoderma	g_Chaetomium	g_Trichoderma	g_Lasiosphaeria	g_Microdochium	g_Chaetomium	g_Penicillium	g_Clitopilus
15	g_Dacryobolus	g_Thanatephorus	g_Hypomyces	g_Pseudoprocaryota	g_Inocybe	g_Antrodia	g_Mortierella	g_Chaetomium	g_Chaetomium
16	g_Trichoderma	g_Microdochium	g_Umbelopsis	g_Penicillium	g_Bionectria	g_Bifiguratus	g_Lactarius	g_Cladophialophora	g_Umbelopsis
17	g_Acremonium	g_Dacryobolus	g_Coralloidiomyces	g_Myrmecridium	g_Cladophialophora	g_Clitopilus	g_Acremonium	g_Clitopilus	g_Sordaria
18	g_Botryobas	g_Acremonium	g_Xylogon	g_Saitozyma	g_Chlorid	g_Sordaria	g_Chaetosphaeria	g_Oidiodendron	g_Oidiodendron

	sidium	ium	e		ium		aeria	dron	ron
19	g__Clitopil us	g__Chaetom ium	g__Sebacin a	g__Hydnum	g__Chaetom ium	g__Nectria	g__Fusarium	g__Clavulin opsis	g__Cladophia lophora
20	g__Arachnop eziza	g__Talarom yces	g__Chaetos phaeria	g__Chaetomiu m	g__Staphyl otrichum	g__Acremoniu m	g__Amplistro ma	g__Xylogone	g__Xylogone

	TYPE2		TYPE1		TYPE3				
sample name	SBS1	SBS2	SBE1	SBE2	SBE3	SBE4	SBK1	SBK2	SBK3
Total number of genus in Intersection	18		14				12		
Total number of genus in Collection	20		27				26		
1	g__unidentified	g__unidentified	g__unidentified	g__unidentified	g__unidentified	g__unidentified	g__unidentified	g__unidentified	g__unidentified
2	g__Acidibacter	g__Acidibacter	g__Candidatus_Solibacter	g__Acidibacter	g__Candidatus_Solibacter	g__Candidatus_Solibacter	g__Candidatus_Solibacter	g__Candidatus_Solibacter	g__Rhodanobacter
3	g__Candidatus_Solibacter	g__Acidotherrmus	g__Acidibacter	g__Burkholderia-Paraburkholderia	g__Variibacter	g__Variibacter	g__Variibacter	g__Sorangium	g__Acidotherrmus
4	g__Rhizomicrobium	g__Candidatus_Solibacter	g__Rhizomicrobium	g__Acidotherrmus	g__Burkholderia-Paraburkholderia	g__Acidotherrmus	g__Bradyrhizobium	g__Acidibacter	g__Variibacter

5	g__Bryobacter	g__Rhizomicrobium	g__Bryobacter	g__Candidatus_Solibacter	g__Acidibacter	g__Bradyrhizobium	g__Acidibacter	g__Acidothermus	g__Acidibacter
6	g__Acidothermus	g__Bryobacter	g__Acidothermus	g__Bradyrhizobium	g__Bradyrhizobium	g__Bryobacter	g__Acidothermus	g__Bryobacter	g__Burkholderia-Paraburkholderia
7	g__Variibacter	g__Variibacter	g__Variibacter	g__Variibacter	g__Rhizomicrobium	g__Acidibacter	g__Rhizomicrobium	g__Rhizomicrobium	g__Bradyrhizobium
8	g__Sorangium	g__Bradyrhizobium	g__Sorangium	g__Bryobacter	g__Bryobacter	g__Burkholderia-Paraburkholderia	g__Bryobacter	g__Variibacter	g__Candidatus_Solibacter
9	g__Hallangium	g__Burkholderia-Paraburkholderia	g__Candidatus_Koribacter	g__Rhizomicrobium	g__Acidothermus	g__Rhizomicrobium	g__Sorangium	g__Burkholderia-Paraburkholderia	g__Rhizomicrobium
10	g__Burkholderia-Paraburkholderia	g__Roseiarcus	g__Granulicella	g__Roseiarcus	g__H16	g__Candidatus_Koribacter	g__Burkholderia-Paraburkholderia	g__Granulicella	g__Bryobacter
11	g__Roseiarcus	g__Sorangium	g__Burkholderia-Paraburkholderia	g__Sorangium	g__Candidatus_Xiphinematobacter	g__Sorangium	g__Reyranelia	g__Mucilaginibacter	g__Granulicella
12	g__Sp	g__Candidatus	g__Roseiarcus	g__Granulicell	g__Acidobacter	g__Granulic	g__H16	g__Candidatus	g__Candidatus

	hingo monas	s_Koribacter		a erium		ella		us_Koribact er	us_Xiphinem atobacter
13	g__Br adyrh izobi um	g__Granulic ella	g__Acidobac terium	g__Candidat us_Xiphinem atobacter	g__Sphingom onas	g__Roseiarc us	g__Roseiarc us	g__Bradyrhi zobium	g__Dyella
14	g__Ca ndida tus_K oriba cter	g__Telmatos pirillum	g__Bradyrhi zobium	g__Mycobact erium	g__Candidat us_Koribact er	g__H16	g__Candidat us_Koribact er	g__Roseiarc us	g__Candidat us_Koribact er
15	g__Ac idoce lla	g__Acidical dus	g__Haliangi um	g__Candidat us_Koribact er	g__Granulic ella	g__Candidat us_Xiphinem atobacter	g__Haliangi um	g__Acidobac terium	g__Acidical dus
16	g__Ac idica ldus	g__Haliangi um	g__Mucilagi nibacter	g__Acidical dus	g__Sorangi um	g__Haliangi um	g__Acidical dus	g__Haliangi um	g__Acidobac terium
17	g__Gr anuli cella	g__Sphingom onas	g__Telmatos pirillum	g__Leptothr ix	g__Roseiarc us	g__Acidical dus	g__Granulic ella	g__Bdellovi brio	g__Sphingom onas
18	g__Te lmato spiri llum	g__Acidobac terium	g__Inquilin us	g__H16	g__Acidical dus	g__Luedeman nella	g__Rhizobi um	g__Sphingom onas	g__Roseiarc us
19	g__Ed aphob	g__Acidocel la	g__Bdellovi brio	g__Acidobac terium	g__Mycobact erium	g__Acidobac terium	g__Sphingom onas	g__H16	g__Mycobact erium

	acter								
20	g__Ac idoba cteri um	g__Bdellovi brio	g__Acidical dus	g__Haliangi um	g__Dyella	g__Gemmatim onas	g__Candidat us_Xiphinem atobacter	g__Dyella	g__H16

Group	MSF	MSF	MSF	MSF	MSF	MSF	MSF	MSF	MSFO	MSF	MSF	MSF	MSF	MSF	MSFOT	MSF	MSF	MSF	MSF	MSF
	OTU_19	OTU_9	OTU_65	OTU_24	OTU_16	OTU_18	OTU_17	OTU_23	TU_43	OTU_16	OTU_11	OTU_7	OTU_14	OTU_21	U_2	OTU_6	OTU_4	OTU_3	OTU_5	OTU_1
			5							39										
	s_E laph omyc es_s p ¹	s__ Tom ent ell a_s p	s__ Tom ent ell a_s p	s__Ru ssula _cyan oxant ha	s__ Rus sul a_s p	s__ Tre chi spo ra_ sp	s__ Hel oti ale s_s p	g__ Cli toc ybu la	s__S orda riom ycet es_s p	s__ Rus sul a_s p	o__C haet osph aeri ales ;	s__Mi croid ium_p hylla nthi	g__ Mor tie rel la	s__ Rus sul a_s p	f__Ar chaeo rhizo mycet aceae	g__ Ela pho myc es	s__ Rus sul a_s p	s__R ussu la_o dora ta	s__ Tom ent ell a_s p	s__ Rus sul a_r ose a
S F K 1 2	0.0	0.0	0.0	0.0	0.0	0.0	11.0	0.0	0.0	486.0	0.0	28.0	16.0	0.0	10107.0	0.0	0.0	929.0	0.0	0.0
S F K 2	5.0	92.0	144.0	71.0	53.0	2.0	89.0	272.0	30.0	21.0	3.0	0.0	436.0	94.0	0.0	102.0	29.0	47.0	246.0	659.0
S F K 3	0.0	5.0	1387.0	1181.0	25.0	3.0	47.0	3.0	192.0	14.0	0.0	0.0	867.0	48.0	0.0	19.0	14.0	23.0	98.0	4.0

S F E 1	1.0	6.0	113.0	5.0	30.0	2.0	96.0	7.0	29.0	43.0	225.0	1.0	32.0	56.0	0.0	28.0	35.0	1734.0	236.0	10.0
S F E 2	3.0	11.0	16.0	1.0	22.0	0.0	134.0	895.0	1.0	167.0	0.0	0.0	13.0	50.0	0.0	5968.0	2.0	468.0	833.0	56.0
S F E 3	6.0	2.0	33.0	13.0	1637.0	4.0	67.0	40.0	13.0	22.0	0.0	0.0	442.0	2694.0	0.0	622.0	22.0	72.0	801.0	3.0
S F E 4	3164.0	3.0	18.0	3326.0	0.0	0.0	31.0	5.0	1.0	20.0	16.0	0.0	1302.0	2.0	0.0	366.0	130.0	36.0	284.0	8.0
S F S 1	2.0	754.0	2.0	4.0	0.0	0.0	19.0	2971.0	0.0	7.0	0.0	0.0	22.0	2.0	0.0	79.0	1.0	29.0	10.0	6631.0
S F S 2	1.0	6.0	55.0	8.0	3104.0	1.0	100.0	7.0	13.0	12.0	2.0	0.0	50.0	4806.0	0.0	26.0	16.0	32.0	1604.0	3.0

M F K 1	1.0	7.0	16.0	8.0	90.0	4.0	1382.0	16.0	14.0	8.0	0.0	0.0	48.0	115.0	0.0	36.0	11.0	21.0	10091.0	4.0
M F K 2	13.0	1.0	1782.0	23.0	0.0	0.0	238.0	39.0	2.0	2.0	5116.0	3.0	53.0	2.0	0.0	4.0	61.0	20.0	32.0	6.0
M F K 3	0.0	1.0	885.0	136.0	0.0	4740.0	8.0	12.0	3231.0	0.0	0.0	14.0	10.0	0.0	0.0	0.0	2.0	0.0	2.0	4.0
M F E 1	0.0	0.0	0.0	0.0	0.0	0.0	98.0	0.0	0.0	3551.0	0.0	6136.0	58.0	0.0	48.0	0.0	0.0	6651.0	1.0	0.0
M F E 2	1.0	2.0	10.0	1.0	3.0	8.0	1024.0	741.0	42.0	713.0	0.0	22.0	9.0	3.0	0.0	3740.0	32.0	2773.0	630.0	68.0
M F E 3	2.0	0.0	14.0	5.0	32.0	398.0	762.0	36.0	1697.0	104.0	2.0	9.0	89.0	52.0	0.0	482.0	2177.0	366.0	175.0	4.0
M	990.0	21.0	7.0	58.0	4.0	0.0	105	17.0	3.0	109	33.0	1.0	140	2.0	0.0	128	957	196.0	236	11.0

[illegible]

Group	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB	SB0	SB	SB	SBOT	SB	SBOT
	OT	OTU	OT	OTU	OTU	OTU	OTU	OTU_35	OTU	OTU	OTU_41	OTU	OTU	OTU_1	TU_	OTU_	OTU	U_16	OT	U_1	
	U_30	_69	U_70	_64	_27	_12	_28		_11	_3		_24	_25	0	4	18	_6		U_5		
	g_R	f_Sol	g_S	g_Aci	f_Sol	o_Rho	p_Aci	f_Xanthomon	p_Aci	p_Aci	f_Xanthomon	f_Caulob	o_Rhod	f_Rhizobi	p_Aci	f_Acido	g_Bra	f_Acido	g_V	f_Acido	
	osiba	iba	or	dot	iba	dos	dob	adales	dob	dob	adales	lob	dos	ales_	dob	bact	dyr	bact	ar	bact	
	ei	cte	an	her	cte	pir	act	_Incer	act	act	_Incer	act	pir	Incer	act	eria	hiz	eria	ii	eria	
	ar	rac	gi	mus	rac	ill	eri	tae_Se	eri	eri	tae_Se	era	ill	tae_S	eri	ceae	obi	ceae	ba	ceae	
cus	eae	um ¹		eae	ale	a	dis	a	a	dis	cea	ale	edis	a	_	um		cter	_		
SBK12	516.0	165.0	25.0	315.0	304.0	239.0	157.0	487.0	158.0	231.0	186.0	450.0	547.0	428.0	391.0	496.0	117.0	769.0	1073.0	567.0	
SBK2	175.0	226.0	79.0	181.0	399.0	90.0	275.0	278.0	123.0	642.0	397.0	278.0	273.0	448.0	441.0	618.0	272.0	1358.0	662.0	1375.0	
SBK3	182.0	57.0	50.0	380.0	141.0	640.0	51.0	302.0	58.0	333.0	27.0	124.0	647.0	137.0	96.0	283.0	668.0	430.0	1052.0	230.0	
SB	14	75.	16	277	200	364	187	207.0	617	161	477.0	219	371	212.0	138	172.	996	304.	14	551.	

B E 1	9. 0 1	0	3. 0	.0	.0	.0	.0		.0	.0		.0	.0		.0	0	.0	0	54 .0	0
S B E 2	16 3. 0 2	357 .0	20 1. 0	144 .0	303 .0	58. 0	180 .0	204.0	168 .0	377 .0	283.0	520 .0	52. 0	537.0	807 .0	1202 .0	274 .0	794. 0	46 5. 0	2770 .0
S B E 3	14 8. 0 3	49. 0	66 .0	119 .0	127 .0	229 .0	729 .0	136.0	427 .0	363 .0	288.0	135 .0	572 .0	114.0	360 .0	313. 0	662 .0	630. 0	97 1. 0	739. 0
S B E 4	26 2. 0 4	121 .0	16 1. 0	263 .0	127 .0	341 .0	274 .0	152.0	674 .0	310 .0	206.0	198 .0	321 .0	183.0	439 .0	381. 0	815 .0	917. 0	10 75 .0	907. 0
S B S 1	12 9. 0 1	723 .0	18 2. 0	163 .0	249 .0	26. 0	72. 0	321.0	61. 0	110 .0	572.0	423 .0	35. 0	473.0	501 .0	1341 .0	185 .0	468. 0	54 4. 0	2126 .0
S B S 2	26 4. 0 2	222 .0	16 4. 0	204 .0	204 .0	147 .0	217 .0	279.0	146 .0	98. 0	384.0	562 .0	170 .0	464.0	620 .0	842. 0	629 .0	790. 0	74 0. 0	1124 .0

A

B

C

D

E

F

A Ectomycorrhizal *Russula*

B Extramatrix mycelium of *Russula*

C

Russula and extramatrix mycelium of *Russula*