

OIK-06363

Xing, X., Jacquemyn, H., Gai, X., Gao, Y., Liu, Q., Zhao, Z. and Guo, S. 2019. The impact of life form on the architecture of orchid mycorrhizal networks in tropical forest. – Oikos doi: 10.1111/oik.06363

Appendix 1

Table A1. Different life forms of orchid species collected from Xishuangbanna, Yunnan province, China and their fungal associates.

Trib	Subtrib	Genus	Orchid species	Life forms	Species No.	Fungal associates (OTU No.)
Epidendreae	Bulbophyllinae	<i>Bulbophyllum</i>	<i>Bulbophyllum ambrosia</i>	Epiphytic	Epi 1	1, 4, 5, 6, 7, 38
				Lithophytic	Litho 1	1, 4, 5, 75
			<i>Bulbophyllum andersonii</i>	Epiphytic	Epi 2	7
			<i>Bulbophyllum forrestii</i>	Epiphytic	Epi 3	1, 4, 5, 6, 7
				Lithophytic	Litho 2	1, 5, 7
			<i>Bulbophyllum helenae</i>	Epiphytic	Epi 4	7, 11, 58
			<i>Bulbophyllum menlunense</i>	Epiphytic	Epi 5	9
			<i>Bulbophyllum odoratissimum</i>	Epiphytic	Epi 6	5, 10, 40, 41, 66, 69
				Lithophytic	Litho 3	5, 10, 85
			<i>Bulbophyllum delitescens</i>	Lithophytic	Litho 4	5, 7, 9
	<i>Bulbophyllum protractum</i>	Epiphytic	Epi 7	10		
	<i>Bulbophyllum shweliense</i>	Epiphytic	Epi 8	10, 40, 58, 62, 63		
	<i>Sunipia</i>	<i>Sunipia andersonii</i>	Epiphytic	Epi 9	10, 11	
	Dendrobiinae	<i>Epigeneium</i>	<i>Epigeneium amplum</i>	Lithophytic	Litho 5	10
		<i>Flickingeria</i>	<i>Flickingeria albopurpurea</i>	Lithophytic	Litho 6	7, 84
	Coelogyneae	<i>Panisea</i>	<i>Panisea uniflora</i>	Epiphytic	Epi 11	7
		<i>Pholidota</i>	<i>Pholidota articulata</i>	Epiphytic	Epi 12	10, 44, 67
				Lithophytic	Litho 7	80, 81
		<i>Coelogyne</i>	<i>Coelogyne ovalis</i>	Lithophytic	Litho 8	7, 79, 87
			<i>Coelogyne viscosa</i>	Epiphytic	Epi 13	2, 7, 10, 52
Lithophytic	Litho 9	5, 7, 78, 79, 83				
Nervillinae	<i>Nervilia</i>	<i>Nervilia aragoana</i>	Terrestrial	Ter 2	23, 27, 35	

			<i>Nervilia infundibulifolia</i>	Terrestrial	Ter 3	11, 12
			<i>Nervilia crociformis</i>	Terrestrial	Ter 4	25, 35
			<i>Nervilia sp.</i>	Terrestrial	Ter 5	22,24,27,28,33
			<i>Nervilia plicata</i>	Terrestrial	Ter 12	21
	Liparidinae	<i>Liparis</i>	<i>Liparis viridiflora</i>	Epiphytic	Epi 14	1, 2, 3, 39
				Lithophytic	Litho 10	1, 2, 3, 12, 76, 77
		<i>Malaxis</i>	<i>Malaxis matsuda</i>	Terrestrial	Ter 6	12, 16, 20, 29, 32
		<i>Oberonia</i>	<i>Oberonia variabilis</i>	Epiphytic	Epi 15	60
	Eriaceae	<i>Eria</i>	<i>Eria bambusifolia</i>	Lithophytic	Litho 11	6, 7, 82, 86
			<i>Eria obvia</i>	Epiphytic	Epi 16	5, 44, 45, 46, 58, 68, 71
			<i>Eria pannea</i>	Epiphytic	Epi 17	61
Thelasiinae	<i>Thelasis</i>	<i>Thelasis pygmaea</i>	Epiphytic	Epi 18	5	
Eulophiinae	<i>Euophia</i>	<i>Euophia graminea</i>	Terrestrial	Ter 1	14	
Vandeae	Aeridinae	<i>Aerides</i>	<i>Aerides rosea</i>	Epiphytic	Epi 19	8, 37
				Lithophytic	Litho 12	8
		<i>Cleisostoma</i>	<i>Cleisostoma fuerstenbergianum</i>	Epiphytic	Epi 20	42, 43, 48, 50, 55, 57, 59, 72, 74
		<i>Gastrochilus</i>	<i>Gastrochilus obliquus</i>	Lithophytic	Litho 13	2, 5
		<i>Luisia</i>	<i>Luisia morsei</i>	Epiphytic	Epi 21	8, 48, 49, 53, 54, 70, 73
		<i>Ornithochilus</i>	<i>Ornithochilus difformis</i>	Epiphytic	Epi 22	8, 10, 13, 47, 58, 64, 65
		<i>Pelatantheria</i>	<i>Pelatantheria rivesii</i>	Epiphytic	Epi 23	43
		<i>Rhynchostylis</i>	<i>Rhynchostylis retusa</i>	Epiphytic	Epi 24	2, 41, 51, 56
		<i>Sarcoglyphis</i>	<i>Sarcoglyphis smithianus</i>	Lithophytic	Litho 14	5
				Epiphytic	Epi 25	5
		<i>Acampe</i>	<i>Acampe rigida</i>	Epiphytic	Epi 10	10
Neottieae	Goodyerinae	<i>Cheirostylis</i>	<i>Cheirostylis yunnanensis</i>	Terrestrial	Ter 11	15, 19, 31

		<i>Goodyera</i>	<i>Goodyera procera</i>	Terrestrial	Ter 8	22, 27
		<i>Hetaeria</i>	<i>Hetaeria rubens</i>	Terrestrial	Ter 7	30, 36
		<i>Zeuxine</i>	<i>Zeuxine nervosa</i>	Terrestrial	Ter 9	14, 18, 26, 35
		<i>Rhomboda</i>	<i>Rhomboda abbreviata</i>	Terrestrial	Ter 10	12, 17, 27
Orchideae	Orchidinae	<i>Habenaria</i>	<i>Habenaria furcifera</i>	Terrestrial	Ter 13	12, 34

Table A2. List of fungal operational taxonomic units (OTU)^a identified using cloning techniques.

OTU	Representative Sequences	Phylogenetic relationship		Sequence identity (%)	Host life forms		
		Taxonomic affiliation	Closest match in GenBank (accession number)		Terrestrial	Epiphytic	Lithophytic
OTU1	MH005840	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-1-7(KP053821)	98			
OTU2	MH005841	Tulasnellaceae	Uncultured Tulasnellaceae clone DFi-XL19 (JX545221)	99			
OTU3	MH005842	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-2-20 (KP053822)	97			
OTU4	MH005843	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-2-23 (KP053820)	96			
OTU5	MH005844	Tulasnellaceae	Uncultured Tulasnellaceae clone 4G2 (JX024731)	96			
OTU6	MH005845	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-2-20 (KP053822)	93			
OTU7	MH005846	Tulasnellaceae	Uncultured Tulasnellaceae clone DFi-YC2 (JX545218)	99			
OTU8	MH005847	Tulasnellaceae	Uncultured Tulasnellaceae clone PM1(GQ241802)	99			
OTU9	MH005848	Tulasnellaceae	Uncultured Tulasnellaceae clone FM372.1(JF691399)	99			
OTU10	MH005849	Tulasnellaceae	Uncultured Tulasnellaceae clone FM356.1(JF691392)	99			
OTU11	MH005850	Atractiellales	Uncultured Atractiellales clone 4EB2-2(GU079604)	84			
OTU12	MH005851	Tulasnellaceae	<i>Tulasnella calospora</i> isolate Pv-PC-2-2(GU166406)	99			
OTU13	MH005852	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. CBS 569.83(DQ278942)	92			
OTU14	MH005853	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. AG-U isolate (HQ269812)	99			
OTU15	MH005854	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. D495aShBmS2(HQ914112)	97			
OTU16	MH005855	Russulaceae	Uncultured <i>Russula</i> clone ECM196(JQ991821)	97			
OTU17	MH005856	Ceratobasidiaceae	Uncultured Ceratobasidiaceae isolate 767(HM141030)	97			
OTU18	MH005857	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. AG-F isolate Str52(DQ102436)	93			
OTU19	MH005858	Thelephoraceae	Uncultured Thelephoraceae clone 363.2(GQ240903)	97			
OTU20	MH005859	Thelephoraceae	Uncultured Thelephoraceae clone YN15-5(KP053817)	99			
OTU21	MH005860	Tulasnellaceae	Uncultured Tulasnellaceae clone PM90(GQ241852)	96			
OTU22	MH005861	Corticaceae	Uncultured <i>Laetisaria</i> clone 1.46E(KP235581)	95			
OTU23	MH005862	Polyporales	<i>Oxyporus</i> sp. MEL 2382667(KP013030)	99			
OTU24	MH005863	Sebacinales	Uncultured Sebacinales (FN663666)	82			

OTU25	MH005864	Sebacinales	<i>Sebacina</i> sp. Seb2I(AB831788)	98	
OTU26	MH005865	Marasmiaceae	<i>Tetrapyrgos</i> sp. AHH-2007parv(EF175551)	97	
OTU27	MH005866	Tulasnellaceae	Uncultured Tulasnellaceae clone Z51h-2A(KC243934)	98	
OTU28	MH005867	Basidiomycota	Uncultured Basidiomycete(AJ810902)	88	
OTU29	MH005868	Basidiomycota	Uncultured Basidiomycota clone OTUB11(KJ194419)	94	
OTU30	MH005869	Tremellales	<i>Trichosporon</i> sp. IFM 56913(AB456738)	100	
OTU31	MH005870	Ceratobasidiaceae	Ceratobasidiaceae sp. 2 MB-2012(JX138539)	96	
OTU32	MH005871	Ceratobasidiaceae	Uncultured Ceratobasidiaceae clone 207(HQ667799)	96	
OTU33	MH005872	Agaricomycetes	Uncultured Agaricomycetes clone: M293(AB712269)	93	
OTU34	MH005873	Tulasnellaceae	<i>Tulasnella calospora</i> isolate Pch-QS-0-1(GU166407)	96	
OTU35	MH005874	Schizophyllaceae	<i>Porothelium fimbriatum</i> voucher CFMR (KJ140596)	86	
OTU36	MH005875	Tulasnellaceae	Uncultured <i>Tulasnella</i> clone OF4(JF926476)	95	
OTU37	MH005876	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-2-23(KP053820)	97	
OTU38	MH005877	Tulasnellaceae	Uncultured Tulasnellaceae clone FM390.1(JF691411)	95	
OTU39	MH005878	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-1-25(KP053815)	100	
OTU40	MH005879	Tulasnellaceae	<i>Tulasnella</i> sp. C1-DT-TC-1(GU166428)	93	
OTU41	MH005880	Erythrobasidiaceae	<i>Sporobolomyces phyllomatis</i> CBS 7198(NR_077097)	86	
OTU42	MH005881	Tulasnellaceae	<i>Tulasnella calospora</i> isolate DCr-QS-0-1(GU166419)	95	
OTU43	MH005882	Tulasnellaceae	<i>Epulorhiza</i> sp. Ss(AJ313438)	99	
OTU44	MH005883	Cantharellales	Uncultured Cantharellales clone 1EG2_6(HM451551)	88	
OTU45	MH005884	Tulasnellaceae	Uncultured Tulasnellaceae clone 3D3(JX024734)	95	
OTU46	MH005885	Cantharellales	Uncultured Cantharellales clone 1EG2_4(HM451549)	88	
OTU47	MH005886	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. FO 38200(DQ520098)	88	
OTU48	MH005887	Septobasidiaceae	<i>Septobasidium</i> sp. JBO-2010f(HQ267956)	90	
OTU49	MH005888	Basidiomycota	Basidiomycete sp. LC5(AY605709)	99	
OTU50	MH005889	Sebacinales	Uncultured <i>Sebacina</i> clone HCB1.26(JX317109)	93	
OTU51	MH005890	Ceratobasidiaceae	<i>Ceratobasidium</i> sp. AG-G isolate Str14 (DQ102402)	99	
OTU52	MH005891	Basidiomycota	Uncultured Basidiomycota R087R4_C1(JX998757)	94	

OTU53	MH005892	Coniophorineae	<i>Coniophora</i> sp. Braz-6(GU187517)	87
OTU54	MH005893	Hymenogastraceae	Uncultured <i>Hymenogaster</i> clone d210a_4_8(JQ346831)	84
OTU55	MH005894	Tricholomataceae	Tricholomataceae sp. Z39(JN198389)	99
OTU56	MH005895	Ceratobasidiaceae	Uncultured Ceratobasidiaceae DOF-YC11(JX545227)	97
OTU57	MH005896	Septobasidiaceae	<i>Septobasidium ramorum</i> DAH(045a) (DQ241450)	95
OTU58	MH005897	Tulasnellaceae	Uncultured Tulasnellaceae clone FM032.1(JF691072)	90
OTU59	MH005898	Tulasnellaceae	Uncultured <i>Tulasnella</i> clone RW09(HM802322)	86
OTU60	MH005899	Tulasnellaceae	<i>Tulasnella</i> sp. C2-DT-TC-1(GU166427)	86
OTU61	MH005900	Tulasnellaceae	<i>Tulasnella</i> sp. C1-DT-TC-1(GU166428)	85
OTU62	MH005901	Tulasnellaceae	Uncultured Tulasnellaceae clone FM032.1(JF691072)	90
OTU63	MH005902	Tulasnellaceae	Uncultured Tulasnellaceae clone FM356.1(JF691392)	98
OTU64	MH005903	Basidiomycota	Uncultured Basidiomycota clone C27O2(KF718208)	91
OTU65	MH005904	Ceratobasidiaceae	Uncultured Ceratobasidiaceae FM186.1(JF691318)	99
OTU66	MH005905	Corticaceae	<i>Phlebia livida</i> subsp. tuberculata MG127(HQ153424)	88
OTU67	MH005906	Cantharellales	Uncultured Cantharellales clone 1EG2_7(HM451552)	87
OTU68	MH005907	Cantharellales	Uncultured Cantharellales clone 1EA3_7(HM451505)	93
OTU69	MH005908	Atractiellales	Uncultured Atractiellales clone 3EE2-1(GU079590)	85
OTU70	MH005909	Septobasidiaceae	<i>Septobasidium</i> sp. JBO-2010f(HQ267956)	96
OTU71	MH005910	Atractiellales	Uncultured Atractiellales clone 4EB2-2 (GU079604)	85
OTU72	MH005911	Septobasidiaceae	<i>Septobasidium velutinum</i> voucher DAH (DQ241467)	95
OTU73	MH005912	Basidiomycota	Uncultured Basidiomycota clone R045_R3(JX998759)	95
OTU74	MH005913	Tulasnellaceae	Uncultured Tulasnellaceae clone (JX998858)	93
OTU75	MH005914	Tulasnellaceae	<i>Epulorhiza</i> sp. UAMH 9844(DQ068772)	94
OTU76	MH005915	Tulasnellaceae	Uncultured <i>Tulasnella</i> clone 56-2-12(KP053816)	100
OTU77	MH005916	Tulasnellaceae	Uncultured Tulasnellaceae clone 56-2-23(KP053820)	99
OTU78	MH005917	Tulasnellaceae	<i>Epulorhiza</i> sp. HK-03(JN253529)	94
OTU79	MH005918	Tulasnellaceae	Uncultured Tulasnellaceae clone (JX998901)	80
OTU80	MH005919	Tulasnellaceae	Uncultured Tulasnellaceae clone DFi-YC5(JX545217)	97

OTU81	MH005920	Tulasnellaceae	Uncultured Tulasnellaceae isolate P213(DQ925494)	91
OTU82	MH005921	Tricholomataceae	Uncultured <i>Mycena</i> (FR750620)	93
OTU83	MH005922	Tulasnellaceae	Uncultured Tulasnellaceae clone (JX998909)	80
OTU84	MH005923	Tulasnellaceae	Uncultured Tulasnellaceae clone (JX998908)	81
OTU85	MH005924	Tulasnellaceae	Uncultured Tulasnellaceae clone FM043.1(JF691112)	97
OTU86	MH005925	Tricholomataceae	<i>Mycena alnetorum</i> voucher 393(JF908426)	98
OTU87	MH005926	Tricholomataceae	Tricholomataceae sp. BJ38(KJ702588)	95

^a Fungi were grouped into OTUs defined by 97% internal transcribed spacer (ITS) sequence similarity

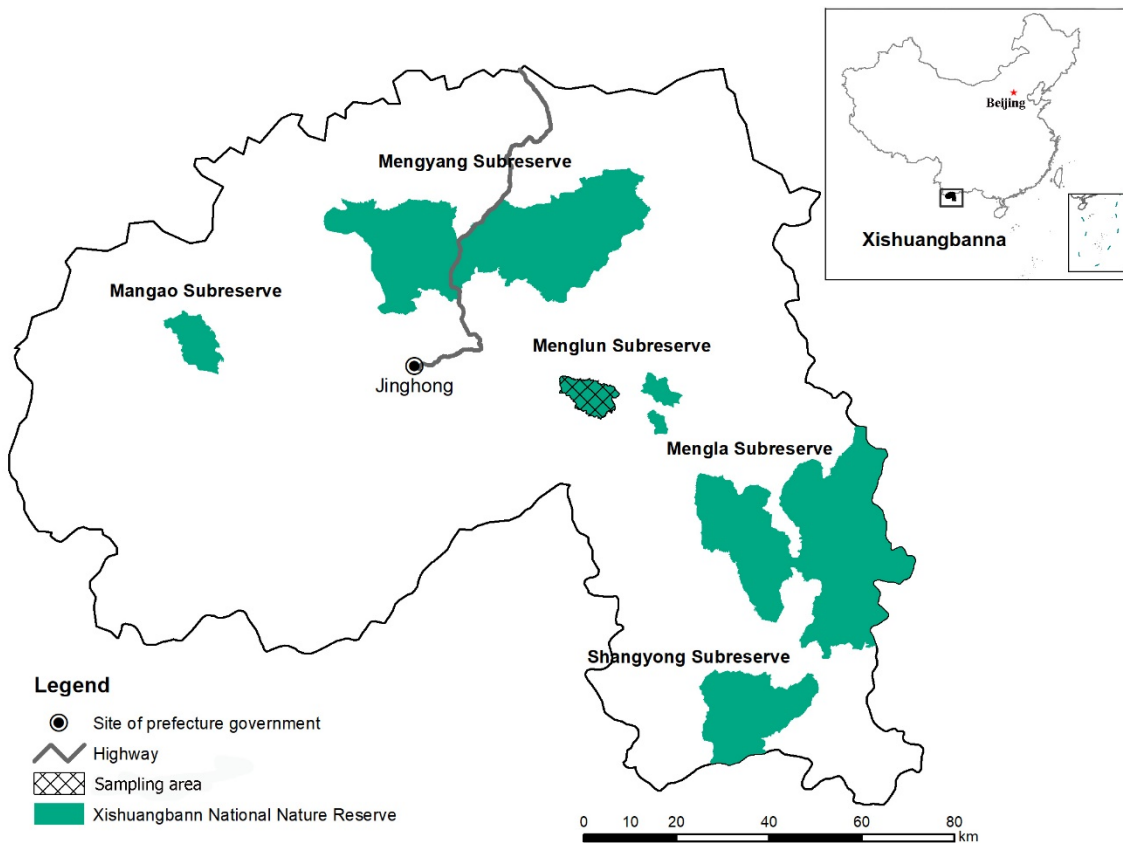


Figure A1. Map of Xishuangbanna showing the National Natural Reserve and Menglun subreserve where 44 orchid species (including 8 epi-/lithophytic species) were sampled.

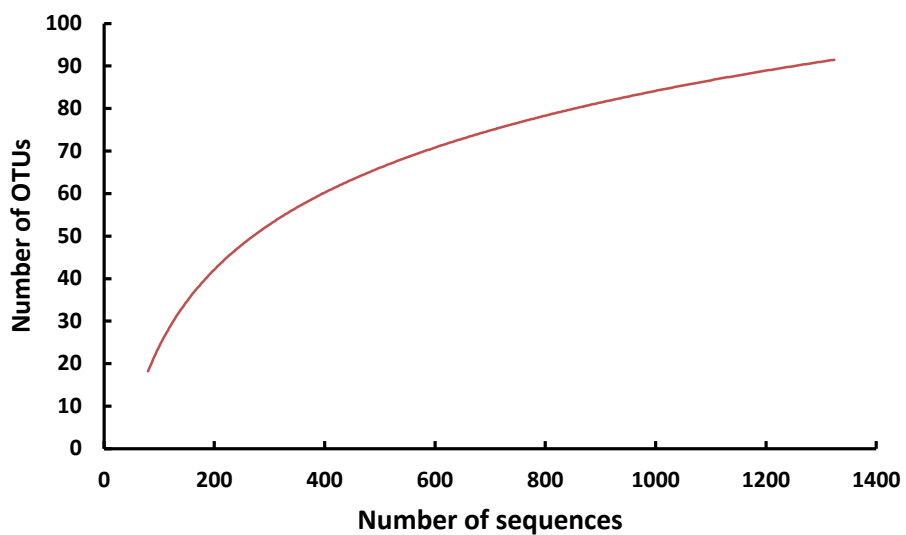


Figure A2. Rarefaction analysis performed on the internal transcribed spacer sequence data obtained from the clone libraries for all orchid species (1324 sequences), using a 97 % sequence similarity threshold value.

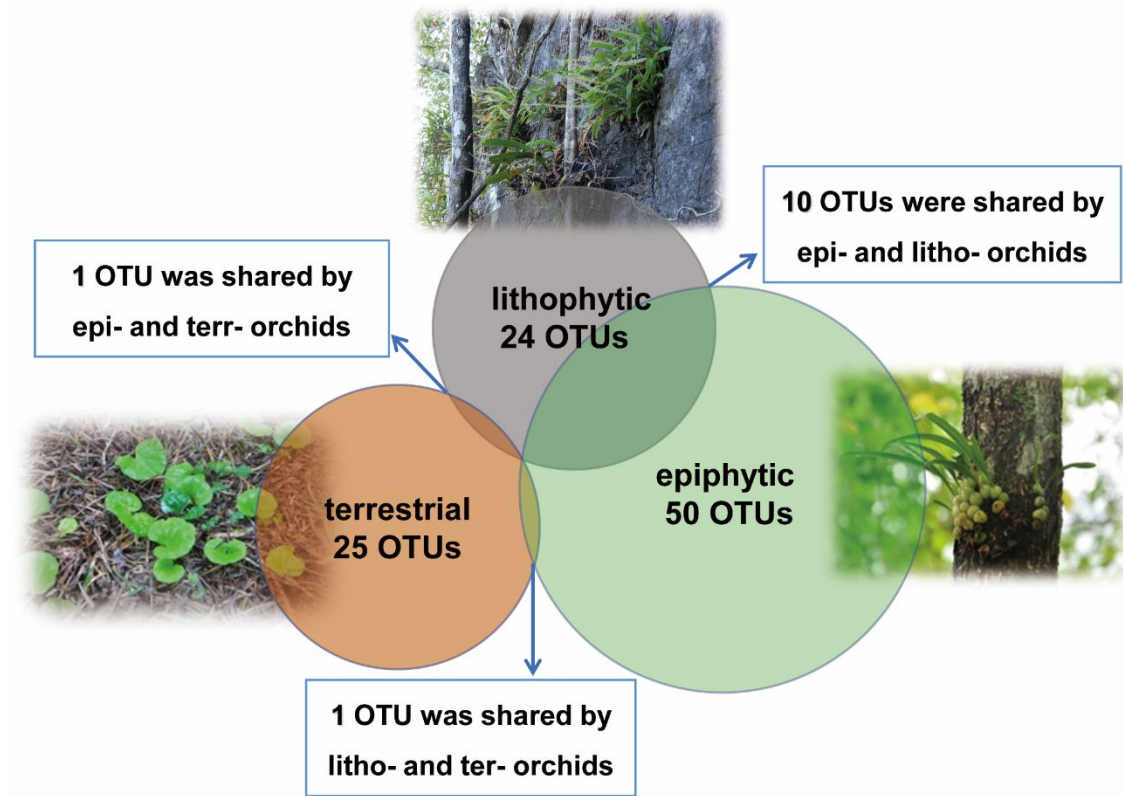


Figure A3. Sharing of orchid mycorrhizal OTUs between terrestrial, lithophytic and epiphytic orchids.

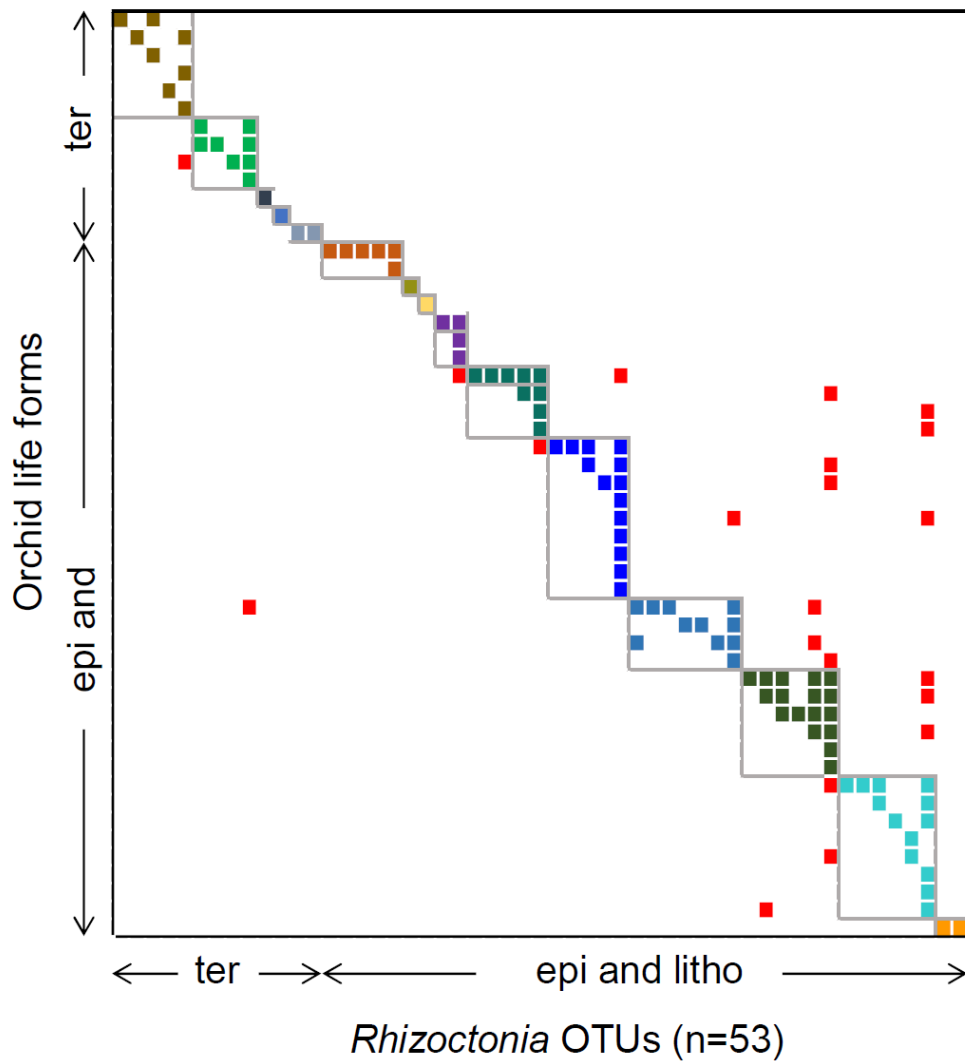


Figure A4. Matrix representation of the interactions between 44 orchid species (including 8 epi-/lithophytic species) (columns) and 53 *Rhizoctonia* OTUs (rows). The overall network was significantly modular. The clusters displaying the largest modularity include terrestrial, epiphytic and lithophytic orchid–fungus interactions. The 15 identified modules are shown in different colors. Red cells are species links to other modules, and non-red cells are links within modules.