# Habitat-driven variation in mycorrhizal communities in the terrestrial orchid genus *Dactylorhiza*

**Supporting Information**

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**Fig. S1** Highest likelihood tree obtained with the Maximum Likelihood analyses of the Tulasnellaceae dataset. Bootstrap support values of ≥50% are shown next to the nodes. Bar represents 0.5 substitutions per site.

**Fig. S2** Highest likelihood tree obtained with the Maximum Likelihood analyses of the Ceratobasidiaceae dataset. Bootstrap support values of ≥50% are shown next to the nodes. Bar represents 0.5 substitutions per site.

**Fig. S3** Highest likelihood tree obtained with the Maximum Likelihood analyses of the Sebacinales dataset. Bootstrap support values of ≥50% are shown next to the nodes. Bar represents 0.2 substitutions per site.

**Fig. S4** Highest likelihood tree obtained with the Maximum Likelihood analyses of the Thelephoraceae dataset. Bootstrap support values of ≥50% are shown next to the nodes. Bar represents 0.3 substitutions per site.

**Fig. S5** Number of operational taxonomic units (OTUs) of the four main orchid mycorrhizal families (Tulasnellaceae, Ceratobasidiaceae, Sebacinaceae and Thelephoraceae) obtained from the roots of 117 individuals of fourteen *Dactylorhiza* species collected in 35 populations across Europe.

**Fig. S6** Partitioning of mycorrhizal fungi across diploid, triploid and tetraploid *Dactylorhiza* species. Nonmetric multidimensional scaling (NMDS) plot of mycorrhizal fungi detected in fourteen different *Dactylorhiza* species sampled in 35 populations across Europe. Each point denotes a different *Dactylorhiza* species.

**Fig. S7** Map showing the locations of all sampled populations of fourteen different *Dactylorhiza* species in Europe. The map was created using ArcGis 9.0 (www.esri.com) and was subsequently edited in Adobe Photoshop (www.adobe.com).

**Table S1** List of operational taxonomic units (OTUs) corresponding to orchid-associating mycorrhizal families discovered in this study.

**Table S2** Overview of surveyed *Dactylorhiza* species and populations.

**Fig. S1**

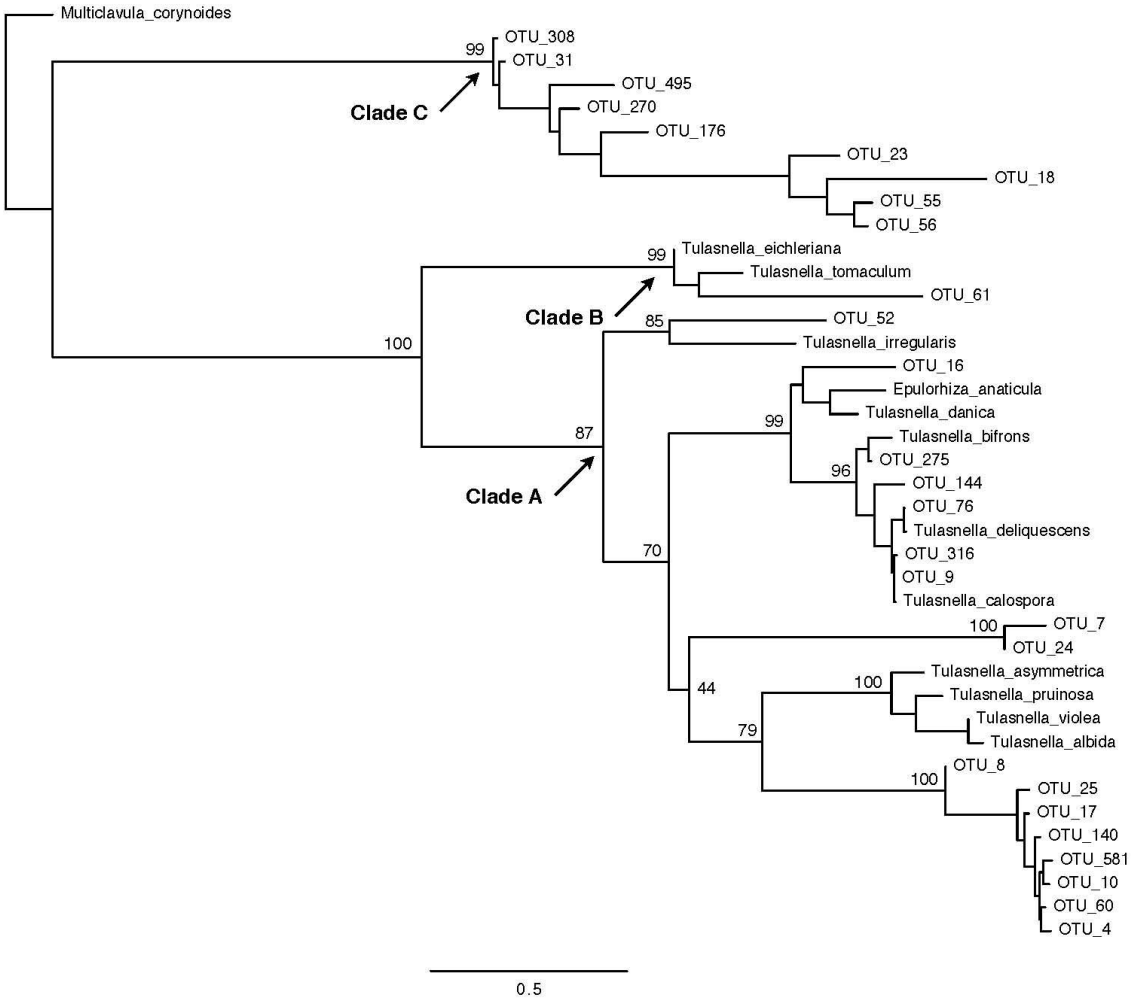

Multiclavula_corynoides
99
OTU_308
OTU_31
OTU_495
Clade C
OTU_270
OTU_176
OTU_23
OTU_18
OTU_55
OTU_56
99
Tulasnella_eichleriana
Tulasnella_tomaculum
OTU_61
Clade B
85
OTU_52
100
Tulasnella_irregularis
OTU_16
Epulorhiza_anaticula
Tulasnella_danica
99
87
Tulasnella_bifrons
OTU_275
96
Clade A
OTU_144
OTU_76
Tulasnella_deliquescens
70
OTU_316
OTU_9
Tulasnella_calospora
100
OTU_7
OTU_24
Tulasnella_asymmetrica
100
44
Tulasnella_pruinosa
Tulasnella_violea
79
Tulasnella_albida
OTU_8
100
OTU_25
OTU_17
OTU_140
OTU_581
OTU_10
OTU_60
OTU_4
0.5

**Fig. S2**

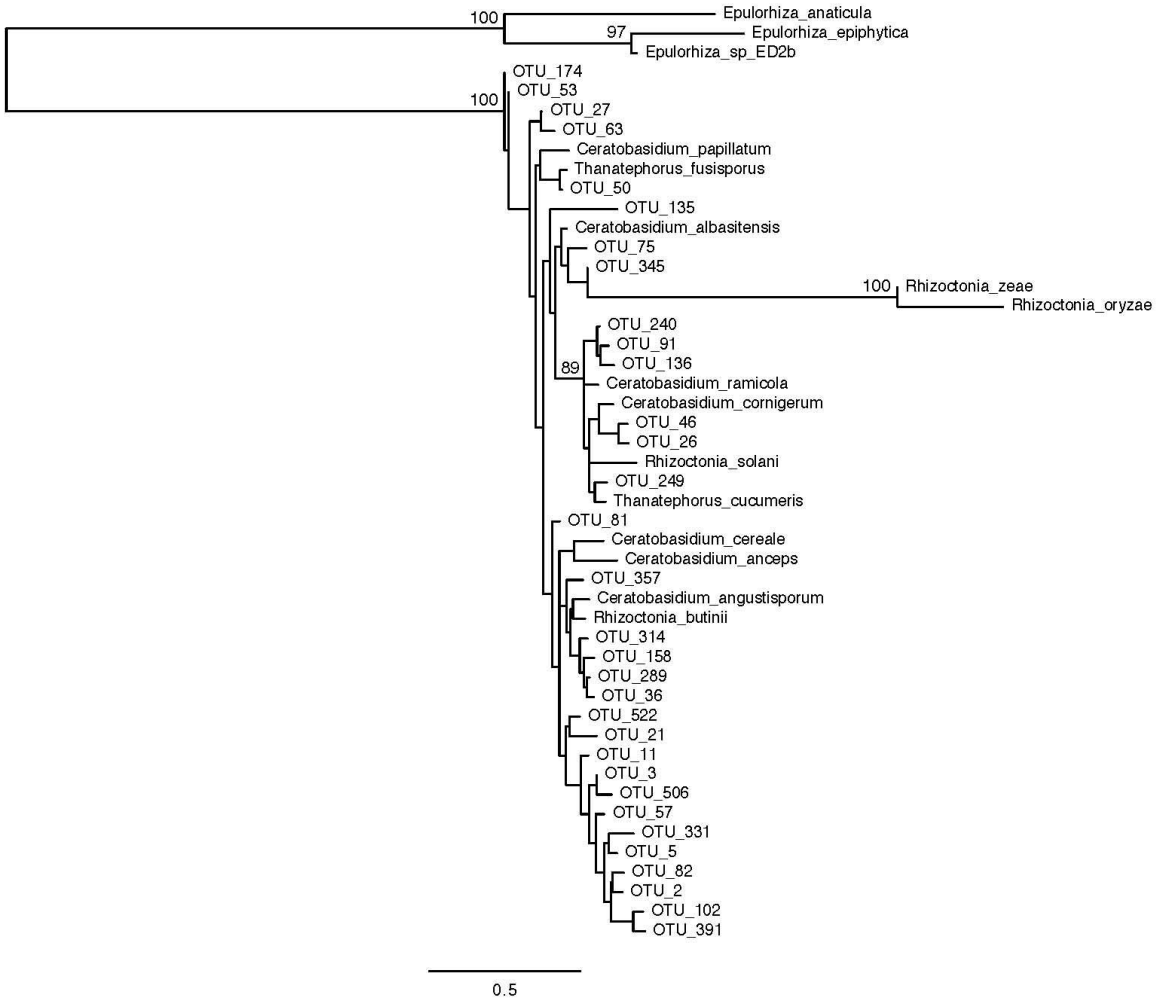
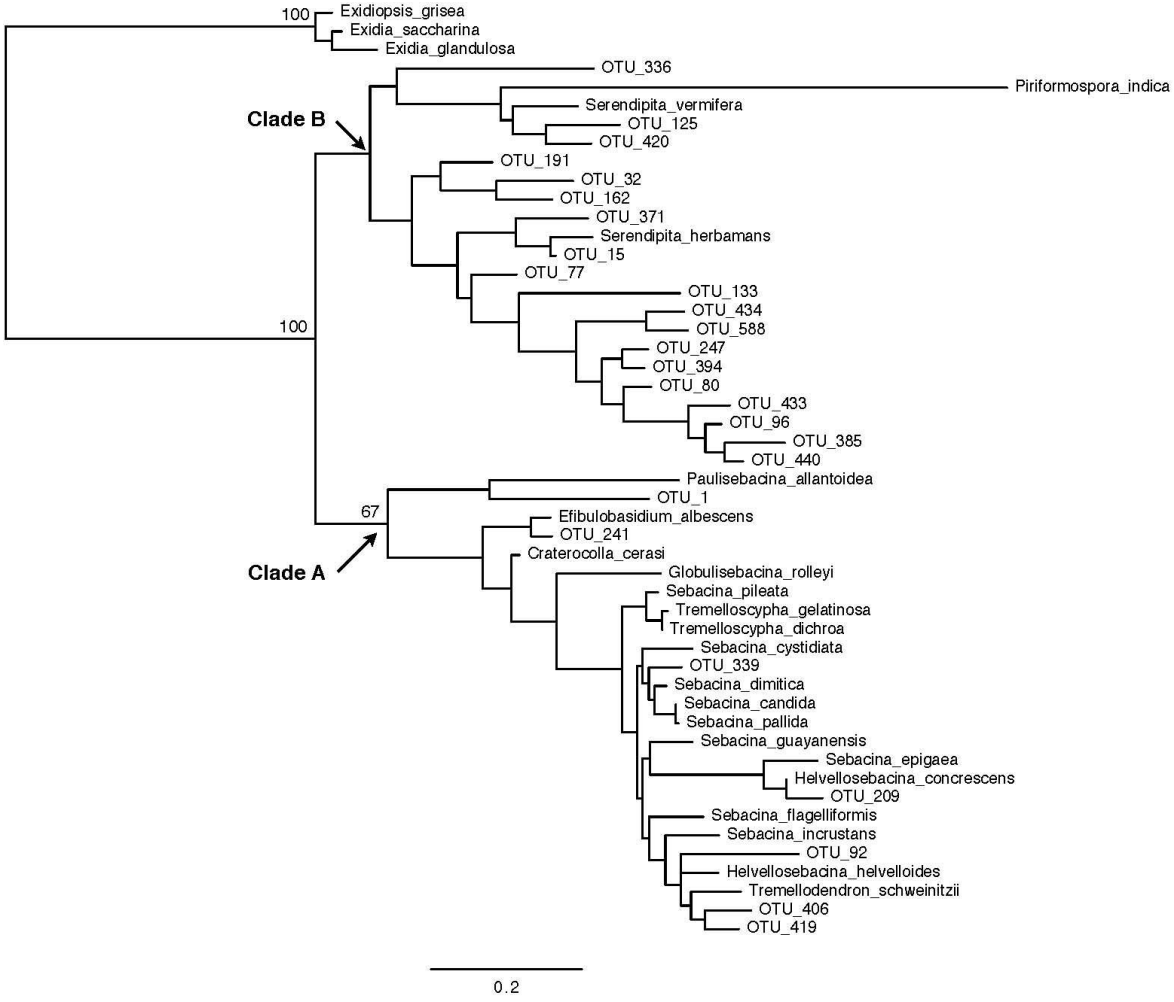

Epulorhiza_anaticula
Epulorhiza_epiphytica
Epulorhiza_sp_ED2b
OTU_174
OTU_53
OTU_27
OTU_63
Ceratobasidium_papillatum
Thanatephorus_fusisporus
OTU_50
OTU_135
Ceratobasidium_albasitensis
OTU_75
OTU_345
Rhizoctonia_zeae
Rhizoctonia_oryzae
OTU_240
OTU_91
OTU_136
Ceratobasidium_ramicola
Ceratobasidium_cornigerum
OTU_46
OTU_26
Rhizoctonia_solani
OTU_249
Thanatephorus_cucumeris
OTU_81
Ceratobasidium_cereale
Ceratobasidium_anceps
OTU_357
Ceratobasidium_angustisporum
Rhizoctonia_butinii
OTU_314
OTU_158
OTU_289
OTU_36
OTU_522
OTU_21
OTU_11
OTU_3
OTU_506
OTU_57
OTU_331
OTU_5
OTU_82
OTU_2
OTU_102
OTU_391
100
97
100
100
89
0.5

**Fig. S3**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Exidiopsis_grisea
Exidia_saccharina
Exidia_glandulosa
OTU_336
Piriformospora_indica
Clade B
Serendipita_vermifera
OTU_125
OTU_420
OTU_191
OTU_32
OTU_162
OTU_371
Serendipita_herbamans
OTU_15
OTU_77
OTU_133
OTU_434
OTU_588
100
OTU_247
OTU_394
OTU_80
OTU_433
OTU_96
OTU_385
OTU_440
Paulisebacina_allantoidea
OTU_1
67
Efibulobasidium_albescens
OTU_241
Clade A
Craterocolla_cerasi
Globulisebacina_rolleyi
Sebacina_pileata
Tremelloscypha_gelatinosa
Tremelloscypha_dichroa
Sebacina_cystidiata
OTU_339
Sebacina_dimitica
Sebacina_candida
Sebacina_pallida
Sebacina_guayanensis
Sebacina_epigaea
Helvellosebacina_concrescens
OTU_209
Sebacina_flagelliformis
Sebacina_incrustans
OTU_92
Helvellosebacina_helvelloides
Tremellodendron_schweinitzii
OTU_406
OTU_419
0.2

**Fig. S4**

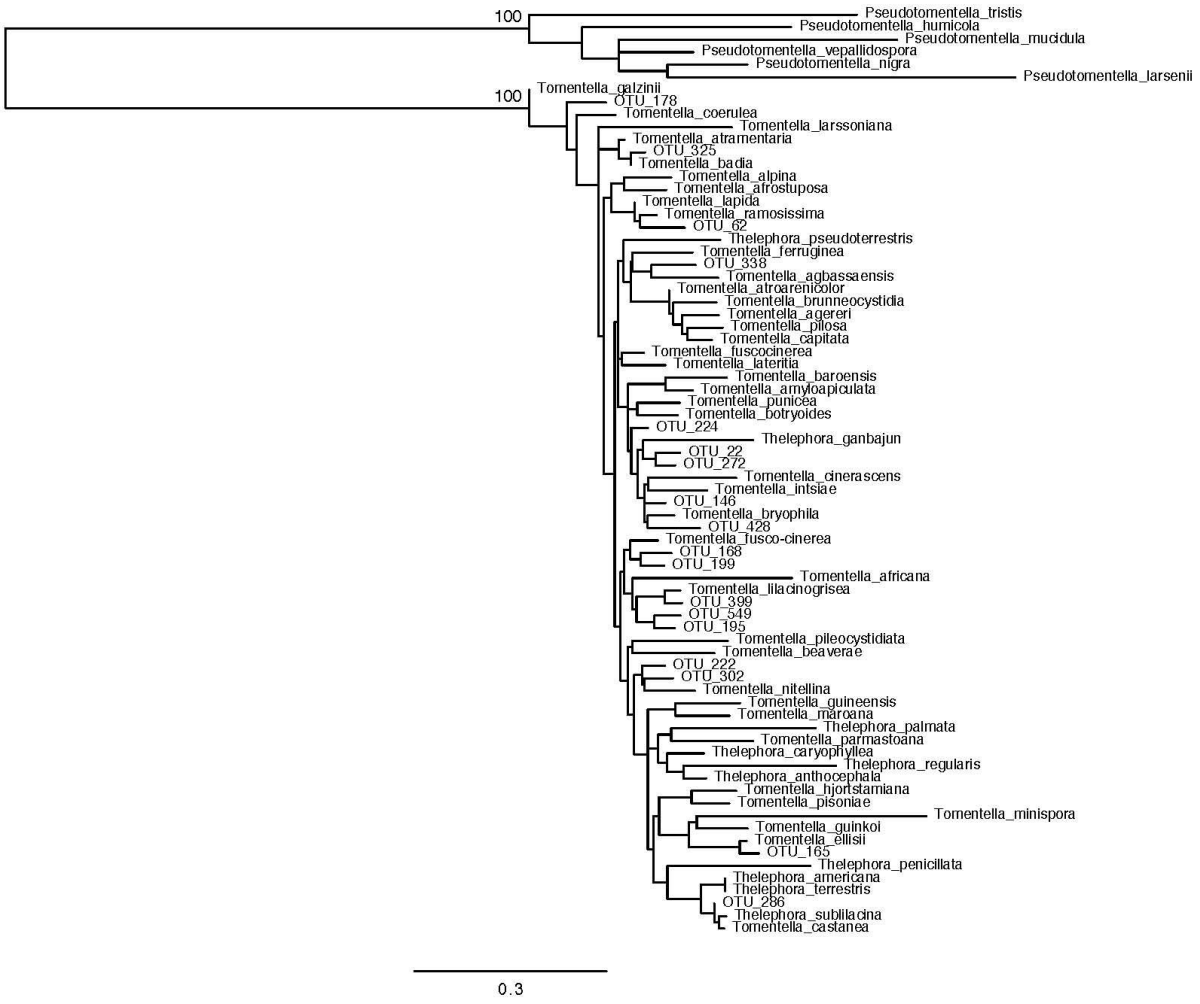
100
100
Pseudotomentella_tristis
Pseudotomentella_humicola
Pseudotomentella_mucidula
Pseudotomentella_vepallidospora
Pseudotomentella_nigra
Pseudotomentella_larsenii
Tomentella_galzinii
OTU_178
Tomentella_coerulea
Tomentella_larssoniana
Tomentella_atramentaria
OTU_325
Tomentella_badia
Tomentella_alpina
Tomentella_afrostuposa
Tomentella_lapida
Tomentella_ramosissima
OTU_62
Thelephora_pseudoterrestris
Tomentella_ferruginea
OTU_338
Tomentella_agbassaensis
Tomentella_atroarenicolor
Tomentella_brunneocystidia
Tomentella_agereri
Tomentella_pilosa
Tomentella_capitata
Tomentella_fuscocinerea
Tomentella_lateritia
Tomentella_baroensis
Tomentella_amyloapiculata
Tomentella_punicea
Tomentella_botryoides
OTU_224
Thelephora_ganbajun
OTU_22
OTU_272
Tomentella_cinerascens
Tomentella_intsiae
OTU_146
Tomentella_bryophila
OTU_428
Tomentella_fusco-cinerea
OTU_168
OTU_199
Tomentella_africana
Tomentella_lilacinogrisea
OTU_399
OTU_549
OTU_195
Tomentella_pileocystidiata
Tomentella_beaverae
OTU_222
OTU_302
Tomentella_nitellina
Tomentella_guineensis
Tomentella_maroana
Thelephora_palmata
Tomentella_parmastoana
Thelephora_caryophyllea
Thelephora_regularis
Thelephora_anthocephala
Tomentella_hjortstamiana
Tomentella_pisoniae
Tomentella_minispora
Tomentella_guinkoi
Tomentella_ellisii
OTU_165
Thelephora_penicillata
Thelephora_americana
Thelephora_terrestris
OTU_286
Thelephora_sublilacina
Tomentella_castanea
0.3

**Fig. S5**

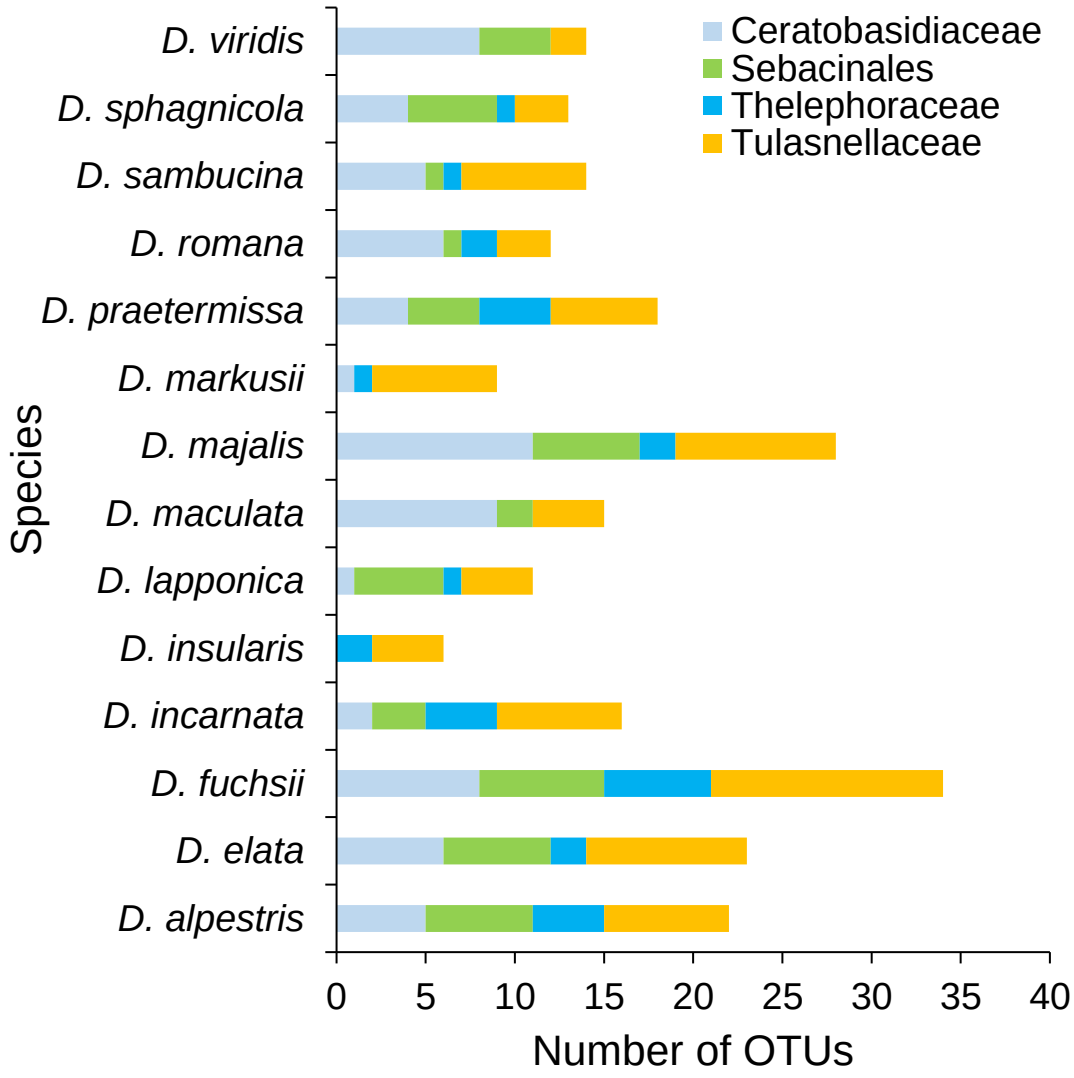
Ceratobasidiaceae
Sebacinales
Thelephoraceae
Tulasnellaceae
Species
D. viridis
D. sphagnicola
D. sambucina
D. romana
D. praetermissa
D. markusii
D. majalis
D. maculata
D. lapponica
D. insularis
D. incarnata
D. fuchsii
D. elata
D. alpestris
0
5
10
15
20
25
30
35
40
Number of OTUs

**Fig. S6**

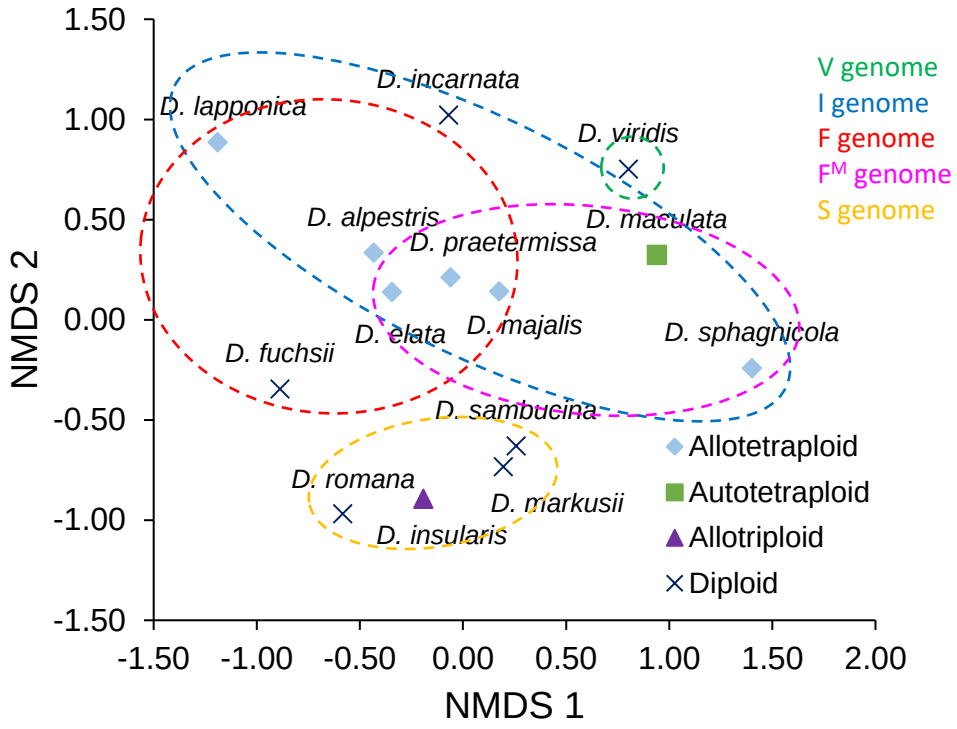
1.50
1.00
0.50
0.00
-0.50
-1.00
-1.50
NMDS 2
-1.50
-1.00
-0.50
0.00
0.50
1.00
1.50
2.00
NMDS 1
D. incarnata
D. lapponica
D. viridis
D. alpestris
D. praetermissa
D. maculata
D. elata
D. majalis
D. sphagnicola
D. fuchsii
D. sambucina
D. romana
D. markusii
D. insularis
V genome
I genome
F genome
FM genome
S genome
Allotetraploid
Autotetraploid
Allotriploid
Diploid

**Fig. S7**

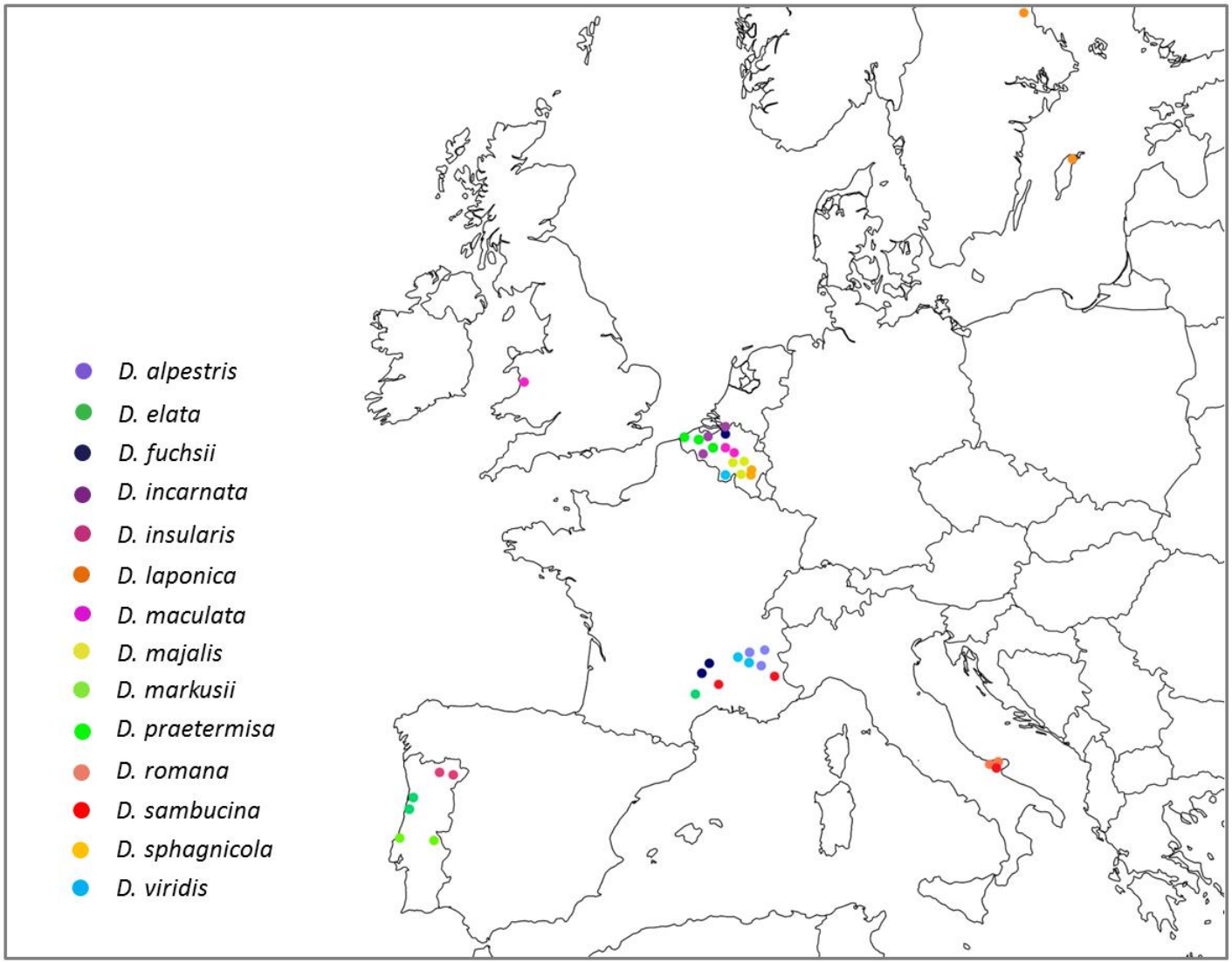
D. alpestris
D. elata
D. fuchsii
D. incarnata
D. insularis
D. laponica
D. maculata
D. majalis
D. markusii
D. praetermisa
D. romana
D. sambucina
D. sphagnicola
D. viridis

**Table S1**

| OTU Id | # sequences | Family | Species | Length | Score | E value | Sequence identity |
|---|---|---|---|---|---|---|---|
| **OTU 8** | 6149 | Tulasnellaceae | Uncultured Tulasnella clone | 300 | 532.9 | 3.9E-148 | 98.7% |
| **OTU 4** | 5929 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 311 | 442.5 | 6.8E-121 | 92.9% |
| **OTU 10** | 4620 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 301 | 505.3 | 8.6E-140 | 97.0% |
| **OTU 60** | 4285 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 312 | 475.7 | 6.7E-131 | 94.9% |
| **OTU 1** | 4245 | Sebacinaceae | Uncultured Sebacinales clone | 301 | 497.9 | 1.4E-137 | 95.7% |
| **OTU 5** | 3623 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae type OTU | 302 | 521.9 | 8.5E-145 | 98.0% |
| **OTU 18** | 3223 | Tulasnellaceae | Uncultured Tulasnella isolate GA6b | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 3** | 3193 | Ceratobasidiaceae | Ceratobasidium sp. UAMH 5443 18S ribosomal RNA gene | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 11** | 3084 | Ceratobasidiaceae | Uncultured Ceratobasidium clone | 301 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 2** | 3025 | Ceratobasidiaceae | Ceratobasidium sp. AG-C genes for ITS1 | 273 | 468.3 | 1.1E-128 | 97.8% |
| **OTU 9** | 2728 | Tulasnellaceae | Uncultured Tulasnella clone | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 7** | 2063 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 294 | 401.8 | 1.2E-108 | 91.5% |
| **OTU 16** | 1615 | Tulasnellaceae | Uncultured Tulasnella clone | 288 | 405.5 | 9.0E-110 | 92.4% |
| **OTU 17** | 1615 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 313 | 425.8 | 6.9E-116 | 92.0% |
| **OTU 21** | 1451 | Ceratobasidiaceae | Ceratobasidium sp. 2 MV-2011 | 301 | 455.4 | 8.7E-125 | 94.0% |
| **OTU 15** | 1310 | Sebacinaceae | Uncultured Sebacinales clone | 300 | 547.7 | 1.4E-152 | 99.7% |
| **OTU 24** | 1027 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 293 | 473.9 | 2.4E-130 | 95.9% |
| **OTU19** | 885 | Sebacinaceae | Uncultured Sebacina mycobiont | 301 | 499.7 | 4.0E-138 | 96.7% |
| **OTU 27** | 866 | Ceratobasidiaceae | Uncultured Ceratobasidium clone | 290 | 448.0 | 1.5E-122 | 94.8% |
| **OTU 52** | 768 | Tulasnellaceae | Uncultured Tulasnella clone | 277 | 483.1 | 4.0E-133 | 97.5% |
| **OTU 23** | 765 | Tulasnellaceae | Uncultured Tulasnellaceae isolate | 271 | 309.5 | 7.2E-81 | 88.2% |
| **OTU 25** | 730 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 302 | 442.5 | 6.8E-121 | 93.4% |
| **OTU 22** | 700 | Thelephoraceae | Uncultured Thelephoraceae clone | 286 | 514.5 | 1.4E-142 | 99.0% |
| **OTU 26** | 617 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae clone OpaBN01-aab93e01 | 296 | 451.7 | 1.1E-123 | 94.6% |
| **OTU 32** | 530 | Sebacinaceae | Uncultured Sebacina mycobiont | 270 | 475.7 | 6.7E-131 | 98.1% |
| **OTU 31** | 360 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 291 | 516.3 | 3.9E-143 | 98.6% |
| **OTU 43** | 348 | Inocybaceae | Uncultured fungus isolate | 272 | 462.8 | 5.2E-127 | 97.4% |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **OTU 308** | 337 | Tulasnellaceae | Uncultured Tulasnella clone | 281 | 473.9 | 2.4E-130 | 96.8% |
| **OTU 49** | 336 | Tulasnellaceae | Uncultured Tulasnellaceae isolate | 271 | 438.8 | 8.8E-120 | 95.9% |
| **OTU 57** | 312 | Ceratobasidiaceae | Uncultured Rhizoctonia isolate | 291 | 527.4 | 1.8E-146 | 99.3% |
| **OTU 35** | 306 | Clavulinaceae | Uncultured Agaricales isolate | 283 | 436.9 | 3.2E-119 | 95.1% |
| **OTU 76** | 305 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 296 | 532.9 | 3.9E-148 | 98.7% |
| **OTU 48** | 299 | Ceratobasidiaceae | Ceratobasidium sp. | 304 | 518.2 | 1.1E-143 | 97.7% |
| **OTU 36** | 291 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 301 | 464.6 | 1.5E-127 | 94.7% |
| **OTU 61** | 257 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 311 | 322.4 | 9.3E-85 | 86.2% |
| **OTU 55** | 252 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 289 | 492.3 | 6.7E-136 | 96.3% |
| **OTU 140** | 246 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 311 | 470.2 | 3.1E-129 | 94.5% |
| **OTU 50** | 221 | Ceratobasidiaceae | Uncultured ectomycorrhiza (Ceratobasidiaceae) | 273 | 490.5 | 2.4E-135 | 98.6% |
| **OTU 581** | 204 | Tulasnellaceae | Uncultured mycorrhiza (Tulasnellaceae) | 303 | 540.3 | 2.4E-150 | 99.0% |
| **OTU 46** | 202 | Ceratobasidiaceae | Ceratobasidium sp. | 291 | 532.9 | 3.9E-148 | 99.7% |
| **OTU 289** | 194 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 303 | 466.5 | 4.1E-128 | 94.7% |
| **OTU 62** | 189 | Thelephoraceae | Uncultured ectomycorrhiza (Thelephoraceae) | 300 | 532.9 | 3.9E-148 | 98.7% |
| **OTU 72** | 188 | Tulasnellaceae | Uncultured Tulasnellaceae isolate | 278 | 514.5 | 1.4E-142 | 100.0% |
| **OTU 56** | 176 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 295 | 440.6 | 2.5E-120 | 93.9% |
| **OTU 79** | 176 | Armillaria | Uncultured fungus clone | 304 | 411.1 | 1.9E-111 | 91.8% |
| **OTU 67** | 163 | Sebacinaceae | Uncultured Sebacina clone | 300 | 544.0 | 1.8E-151 | 99.3% |
| **OTU 53** | 150 | Ceratobasidiaceae | Ceratobasidium sp. | 262 | 348.3 | 1.5E-92 | 91.6% |
| **OTU 82** | 130 | Ceratobasidiaceae | Ceratobasidium sp. | 291 | 538.5 | 8.5E-150 | 100.0% |
| **OTU 96** | 130 | Sebacinaceae | Uncultured Sebacina isolate | 301 | 470.2 | 3.1E-129 | 95.0% |
| **OTU 63** | 129 | Ceratobasidiaceae | Uncultured Basidiomycota clone | 300 | 549.5 | 3.9E-153 | 99.7% |
| **OTU 174** | 116 | Ceratobasidiaceae | Ceratobasidium sp. AG-Ba isolate | 309 | 350.1 | 4.3E-93 | 88.7% |
| **OTU 81** | 107 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae clone | 302 | 473.9 | 2.4E-130 | 95.0% |
| **OTU 80** | 106 | Sebacinaceae | Uncultured Sebacina | 297 | 459.1 | 6.8E-126 | 94.9% |
| **OTU 77** | 90 | Sebacinaceae | Sebacina vermifera partial 18S rRNA | 301 | 499.7 | 4.0E-138 | 96.7% |
| **OTU 75** | 89 | Ceratobasidiaceae | Uncultured Rhizoctonia | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 91** | 79 | Ceratobasidiaceae | Ceratobasidium sp. | 301 | 460.9 | 1.9E-126 | 94.4% |
| **OTU 106** | 76 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 291 | 538.5 | 8.5E-150 | 100.0% |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **OTU 92** | 68 | Sebacinaceae | Uncultured Sebacinales clone | 279 | 505.3 | 8.6E-140 | 99.3% |
| **OTU 102** | 66 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 304 | 472.0 | 8.7E-130 | 95.1% |
| **OTU 123** | 65 | Clavulinaceae | Uncultured Agaricomycetes clone | 274 | 435.1 | 1.1E-118 | 95.6% |
| **OTU 112** | 62 | Cortinariaceae | Uncultured Cortinarius clone | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 133** | 61 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 125** | 60 | Sebacinaceae | Sebacina vermifera strain | 308 | 381.5 | 1.5E-102 | 89.6% |
| **OTU 144** | 56 | Tulasnellaceae | Uncultured Tulasnella voucher | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 176** | 48 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 292 | 529.3 | 5.1E-147 | 99.3% |
| **OTU 104** | 42 | Inocybaceae | Inocybe petiginosa | 300 | 555.1 | 8.7E-130 | 100.0% |
| **OTU 138** | 38 | Agaricaceae | Coprinopsis argentea strain | 260 | 468.3 | 1.1E-128 | 99.2% |
| **OTU 161** | 37 | Clavulinaceae | Uncultured Agaricales isolate | 279 | 516.3 | 3.9E-143 | 100.0% |
| **OTU 156** | 35 | Marasmius | Uncultured ascomycete clone | 300 | 544.0 | 1.8E-151 | 99.3% |
| **OTU 162** | 35 | Sebacinaceae | Sebacina vermifera isolate | 303 | 512.6 | 5.1E-142 | 97.4% |
| **OTU 165** | 34 | Thelephoraceae | Uncultured Thelephoraceae | 272 | 507.1 | 2.4E-140 | 97.9% |
| **OTU 135** | 31 | Ceratobasidiaceae | Uncultured Ceratobasidium clone | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 169** | 28 | Sebacinaceae | Uncultured Sebacinales clone | 276 | 505.3 | 8.6E-140 | 99.6% |
| **OTU 136** | 25 | Ceratobasidiaceae | Ceratobasidium sp. | 280 | 466.5 | 4.1E-128 | 96.8% |
| **OTU 171** | 24 | Inocybaceae | Uncultured ectomycorrhizal fungus clone | 300 | 542.2 | 6.6E-151 | 99.3% |
| **OTU 146** | 23 | Thelephoraceae | Uncultured Tomentella genomic DNA | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 240** | 22 | Ceratobasidiaceae | Thanatephorus cucumeris | 300 | 453.5 | 3.2E-124 | 94.3% |
| **OTU 158** | 21 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae clone | 301 | 521.9 | 8.5E-145 | 98.0% |
| **OTU 222** | 19 | Thelephoraceae | Uncultured ectomycorrhizal fungus clone | 300 | 533.0 | 3.9E-148 | 98.7% |
| **OTU 224** | 19 | Thelephoraceae | Thelephoraceae sp. | 301 | 527.4 | 1.8E-146 | 98.3% |
| **OTU 270** | 19 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 288 | 516.3 | 4.0E-143 | 99.0% |
| **OTU 191** | 18 | Sebacinaceae | Uncultured Sebacina mycobiont | 300 | 532.9 | 3.9E-148 | 98.0% |
| **OTU 195** | 18 | Thelephoraceae | Uncultured ectomycorrhiza (Thelephoraceae) | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 272** | 17 | Thelephoraceae | Uncultured Tomentella genomic DNA | 300 | 544.0 | 1.8E-151 | 99.3% |
| **OTU 345** | 17 | Ceratobasidiaceae | Ceratobasidium sp. AG-A isolate | 291 | 533.0 | 3.9E-148 | 99.7% |
| **OTU 159** | 16 | Psathyrellaceae | Psathyrella sp. | 302 | 424.0 | 2.5E-115 | 92.4% |
| **OTU 249** | 15 | Ceratobasidiaceae | Ceratobasidium sp. | 301 | 499.7 | 4.0E-138 | 96.7% |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **OTU 302** | 15 | Thelephoraceae | Uncultured Thelephoraceae clone | 301 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 181** | 14 | Tricholomataceae | Uncultured Mycena clone | 302 | 499.7 | 4.0E-138 | 96.7% |
| **OTU 275** | 14 | Tulasnellaceae | Uncultured Tulasnella mycobiont | 300 | 532.9 | 3.9E-148 | 98.7% |
| **OTU 178** | 13 | Thelephoraceae | Uncultured ectomycorrhiza (Tomentella) | 280 | 518.2 | 1.1E-143 | 100.0% |
| **OTU 223** | 13 | Inocybaceae | Uncultured Inocybe genomic DNA | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 168** | 12 | Thelephoraceae | Uncultured ectomycorrhiza (Thelephoraceae) | 300 | 532.9 | 3.9E-148 | 98.7% |
| **OTU 209** | 12 | Sebacinaceae | Uncultured Sebacinales clone | 273 | 457.2 | 2.4E-125 | 97.1% |
| **OTU 210** | 12 | Inocybaceae | Inocybe malenconii | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 241** | 12 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 314** | 12 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 300 | 525.6 | 6.6E-140 | 98.3% |
| **OTU 399** | 12 | Thelephoraceae | Tomentella sp. ECM 21 | 300 | 510.8 | 1.8E-148 | 97.3% |
| **OTU 199** | 11 | Thelephoraceae | Uncultured ectomycorrhiza (Thelephoraceae) | 301 | 509.0 | 6.6E-141 | 97.3% |
| **OTU 247** | 11 | Sebacinaceae | Uncultured Sebacina clone | 301 | 527.4 | 1.8E-146 | 98.3% |
| **OTU 269** | 11 | Tricholomataceae | Mycena maurella voucher | 300 | 544.0 | 1.8E-151 | 99.3% |
| **OTU 297** | 10 | Clavulinaceae | Uncultured Agaricomycetes clone | 275 | 466.5 | 4.1E-128 | 97.5% |
| **OTU 250** | 9 | Sebacinaceae | Uncultured Sebacina isolate | 279 | 494.2 | 1.9E-136 | 98.6% |
| **OTU 439** | 9 | Atractiella | Uncultured endophytic fungus clone | 188 | 348.3 | 1.5E-92 | 100.0% |
| **OTU 232** | 8 | Sebacinaceae | Uncultured Sebacina mycobiont | 305 | 464.6 | 1.5E-127 | 94.4% |
| **OTU 366** | 8 | Agaricaceae | Uncultured soil basidiomycete isolate | 301 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 395** | 8 | Inocybaceae | Uncultured Inocybe genomic DNA | 300 | 531.1 | 1.4E-147 | 98.7% |
| **OTU 519** | 8 | Psathyrellaceae | Psathyrella typhae | 300 | 529.3 | 5.1E-147 | 98.7% |
| **OTU 287** | 7 | Sebacinaceae | Uncultured Sebacinaceae clone | 273 | 418.5 | 1.2E-113 | 94.5% |
| **OTU 414** | 7 | Clavulinaceae | Uncultured fungus clone | 303 | 457.2 | 2.4E-125 | 94.4% |
| **OTU 316** | 6 | Tulasnellaceae | Uncultured Tulasnellaceae clone | 160 | 296.6 | 5.6E-77 | 100.0% |
| **OTU 357** | 6 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 302 | 436.9 | 3.2E-119 | 93.0% |
| **OTU 370** | 6 | Cortinariaceae | Uncultured ectomycorrhiza (Cortinarius) clone | 302 | 510.8 | 1.8E-141 | 97.4% |
| **OTU 273** | 5 | Thelephoraceae | Uncultured ectomycorrhiza (Tomentella) clone | 291 | 514.5 | 1.4E-142 | 98.6% |
| **OTU 274** | 5 | Tricholomataceae | Uncultured Cortinarius genomic DNA | 300 | 529.3 | 5.1E-147 | 98.7% |
| **OTU 280** | 5 | Clavulinaceae | Uncultured ectomycorrhiza (Clavulinaceae) clone | 302 | 529.3 | 5.1E-147 | 98.3% |
| **OTU 286** | 5 | Thelephoraceae | Uncultured Tomentella genomic DNA | 300 | 555.1 | 8.4E-155 | 100.0% |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **OTU 336** | 5 | Sebacinaceae | Uncultured Sebacinaceae clone | 250 | 226.4 | 7.5E-56 | 80.4% |
| **OTU 339** | 5 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 521.9 | 8.5E-145 | 98.0% |
| **OTU 391** | 5 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 294 | 483.1 | 4.0E-133 | 96.6% |
| **OTU 419** | 5 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 544.0 | 1.8E-151 | 99.3% |
| **OTU 420** | 5 | Sebacinaceae | Sebacina vermifera strain | 312 | 374.1 | 2.5E-100 | 89.1% |
| **OTU 433** | 5 | Sebacinaceae | Uncultured Sebacinales clone | 298 | 470.2 | 3.1E-129 | 95.3% |
| **OTU 495** | 5 | Tulasnellaceae | Uncultured Tulasnellaceae clone OmiA | 291 | 532.9 | 3.9E-148 | 99.7% |
| **OTU 325** | 4 | Thelephoraceae | Uncultured ectomycorrhiza (Tomentella) isolate | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 331** | 4 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae type OTU | 301 | 516.3 | 4.0E-143 | 97.7% |
| **OTU 338** | 4 | Thelephoraceae | Thelephoraceae sp. | 300 | 533.0 | 3.9E-148 | 98.7% |
| **OTU 385** | 4 | Sebacinaceae | Uncultured Sebacinales | 300 | 481.2 | 1.4E-132 | 95.7% |
| **OTU 580** | 4 | Inocybaceae | Inocybe praetervisa isolate | 301 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 371** | 3 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 540.3 | 2.4E-150 | 99.0% |
| **OTU 394** | 3 | Sebacinaceae | Uncultured Sebacina mycobiont | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 406** | 3 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 428** | 3 | Thelephoraceae | Uncultured ectomycorrhiza (Thelephoraceae) | 301 | 427.7 | 1.9E-116 | 92.7% |
| **OTU 434** | 3 | Sebacinaceae | Uncultured Sebacina isolate | 307 | 357.5 | 2.5E-95 | 88.3% |
| **OTU 440** | 3 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 442** | 3 | Tricholomataceae | Uncultured basidiomycete clone | 293 | 414.7 | 1.5E-112 | 92.5% |
| **OTU 459** | 3 | Tricholomataceae | Uncultured cf. Mycena sp. clone | 300 | 555.1 | 8.4E-155 | 100.0% |
| **OTU 506** | 3 | Ceratobasidiaceae | Ceratobasidium sp. UAMH | 301 | 492.3 | 6.7E-136 | 96.3% |
| **OTU 522** | 3 | Ceratobasidiaceae | Uncultured Ceratobasidiaceae isolate | 302 | 425.8 | 6.9E-116 | 92.4% |
| **OTU 536** | 3 | Tricholomataceae | Mycena vitilis | 300 | 549.6 | 3.9E-153 | 99.7% |
| **OTU 549** | 3 | Thelephoraceae | Uncultured Tomentella clone | 300 | 499.7 | 8.4E-138 | 98.7% |
| **OTU 588** | 3 | Sebacinaceae | Uncultured Sebacina isolate | 300 | 549.6 | 3.9E-153 | 99.7% |

**Table S2**

| Species | Country | Sampling site | No. Plants sampled |
|---|---|---|---|
| ***D. alpestris*** | France | Col Bayard | 3 |
| | France | Col du Lautaret 1 | 3 |
| | France | Col du Lautaret 2 | 3 |
| ***D. elata*** | France | Avène | 3 |
| | Portugal | Senhora de Vagos | 3 |
| | Portugal | Santo André | 3 |
| ***D. fuchsii*** | France | Meyrueis 1 | 3 |
| | France | Meyrueis 2 | 3 |
| | Belgium | Hobokense Polder | 3 |
| ***D. incarnata*** | Belgium | Westhoek | 3 |
| | Belgium | Ekers Moeras | 3 |
| | Belgium | Vaarttaluds (Moen) | 3 |
| ***D. insularis*** | Portugal | Mogadouro | 3 |
| | Portugal | Macedo de Cavaleiros | 3 |
| ***D. lapponica*** | Sweden | Hälsningland, Loos parish, locality Långtjärnen | 3 |
| | Sweden | Gotland, Rute parish, Kauparve | 3 |
| ***D. maculata*** | Belgium | Papendel 1 | 3 |
| | Belgium | Vorsdonkbos | 3 |
| | UK (Wales) | Edem | 3 |
| ***D. majalis*** | Belgium | Aardgat (Tienen) | 3 |
| | Belgium | Malendriesbeekvallei (Kerkom) | 3 |
| | Belgium | Revogne | 3 |
| ***D. markusii*** | Portugal | Carvalhal | 3 |
| | Portugal | Castelo de Vide | 3 |
| ***D. praetermissa*** | Belgium | Leiemeeersen | 3 |
| | Belgium | Gavers Harelbeke | 3 |
| | Belgium | Warandeduinen (Middelkerke) | 3 |

| | | | |
|---|---|---|---|
| ***D. romana*** | Italy | Gargano3 | 3 |
| | Italy | Cagnano Varano | 3 |
| ***D. sambucina*** | France | L'Esperou | 3 |
| | France | Merlette-Orcieres | 3 |
| | Italy | Monte Calvo | 3 |
| ***D. sphagnicola*** | Belgium | St. Hubert 1 | 3 |
| | Belgium | St. Hubert 2 | 3 |
| | Belgium | Warinsart | 3 |
| ***D. viridis*** | France | Col de Menée | 3 |
| | France | Romeyer | 3 |
| | Belgium | Bonnerieu | 3 |
| | | | |
| | | Total | 114 |