

Supplementary data

Fig S1: Rarefaction curves of bacterial 16S rRNA gene sequences recovered from the ectomycorrhizospheres of oak. The expected number of phylotypes (OTUs) was calculated from the number of sequences, with inclusion in the same species based on 97% sequence similarity. The five samples considered are presented as follow: *Xerocomus pruinatus* samples (C1B, grey line; C3A, black line) and *Scleroderma citrinum* samples (C3B, green line; C4A, blue line and C4B, red line).

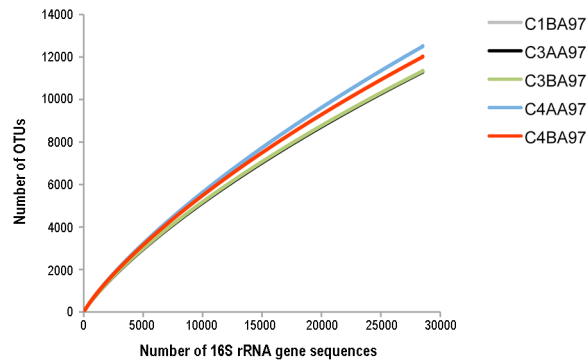
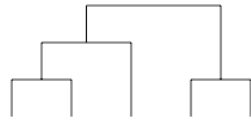
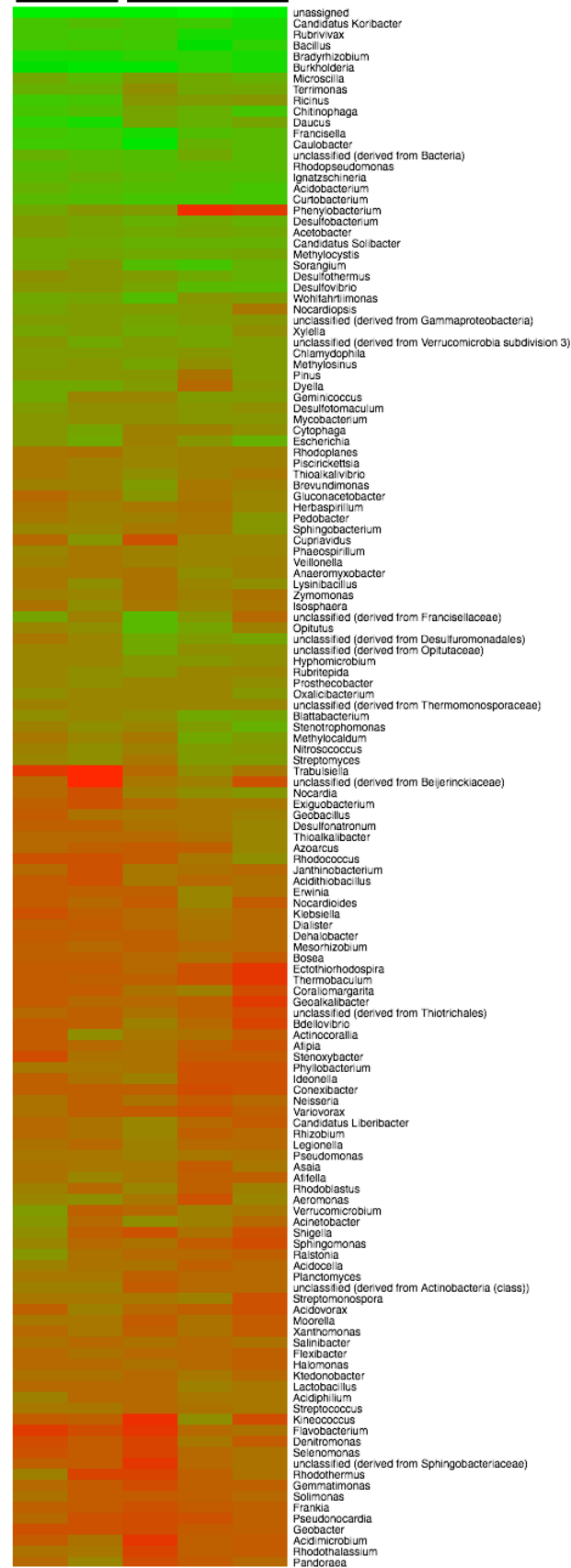


Fig S2: Distribution of the bacterial genera detected in the *X. pruinatus* and *S. citrinum* ectomycorrhizospheres. The heatmap analysis was performed using MG-RAST with an identity cutoff of 80%. The most present genera are presented in green and the less present in red. For legibility reason only the genera supported by a minimum of 100 reads are presented.



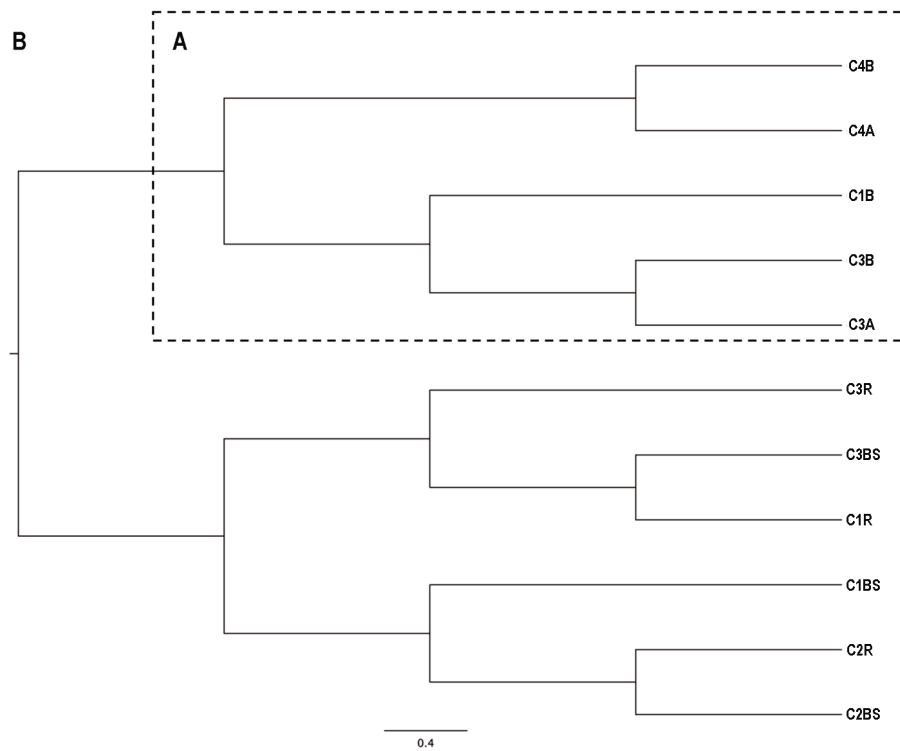
Xerococcus pruinatus

Sclerotinia citrinum



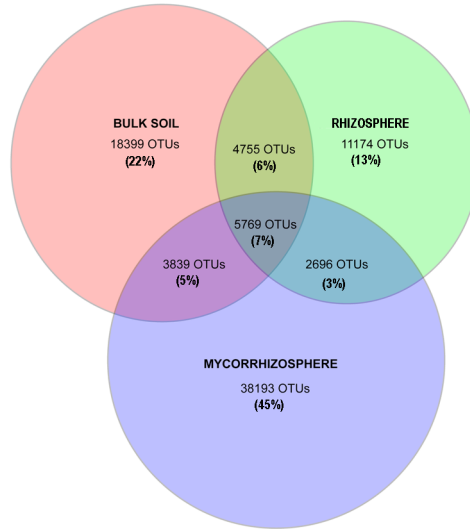
1 **Fig S3:** Bacterial community membership similarities between ectomycorrhizosphere, the global rhizosphere and
2 the surrounding bulk soil samples. The cluster analysis was performed using Mothur. **(A)** Bacterial community
3 membership similarities between ectomycorrhizosphere samples. C1B and C3A correspond to *X. pruinatus*
4 ectomycorrhizospheres; and C3B, C4A and C4B correspond to *S. citrinum* ectomycorrhizospheres. **(B)**
5 Comparison of all the samples (rhizosphere samples: C1R-C3R and bulk soil samples: C1BS-C3BS). Values are
6 based on 0.03 distances.

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1 **Fig S4:** Venn diagram comparing the OTUs (97%) from the ectomycorrhizosphere, the total rhizosphere and the
2 surrounding bulk soil. This figure presents the number of OTUs shared or only present in one the three
3 environments considered, as well as the relative percentage they represent in brackets.
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2 **Table S1:** Number of OTUs and Richness estimators based on Mothur analyses detected in the different ectomycorrhizosphere samples

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| | Label | Number of reads | OTU (97%) | OTU 97% normalized* with C1B | shannon | Chao1 (lower and upper 95% confidence intervals) | ACE (lower and upper 95% confidence intervals) |
|---------------------|-------|-----------------|--------------|------------------------------------|---------|--|--|
| <i>X. pruinatus</i> | C1B | 28,516 | 11,277 | 11,277 | 8.30 | 31,019 (29,742/32,383) | 57,599 (56,748/ 58,466) |
| | C3A | 34,913 | 13,060 | 11,333 | 8.31 | 35,474 (34,121/36,914) | 66,362 (65,477/ 67,262) |
| <i>S. citrinum</i> | C3B | 31,428 | 12,145 | 11,361 | 8.32 | 32,671 (31,391/34,035) | 59,776 (58,940/ 60,627) |
| | C4A | 37,358 | 14,516 | 12,523 | 8.63 | 39,268 (37,856/40,766) | 73,792 (72,856/ 74,743) |
| | C4B | 28,686 | 12,058 | 12,032 | 8.49 | 33,062 (31,746/34,465) | 62,043 (61,183/ 62,917) |

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5 * the number of OTUs 97% was calculated using the same number of reads for each sample, which corresponds to the minimal number of reads of the sample C1B of the *X.*6 *pruinatus* ectomycorrhizosphere.

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2 **Table S2: Bacterial genera associated with known functions (number of reads detected)**

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| Sample name | <i>X. pruinatus</i> | | <i>S. citrinum</i> | | |
|--|---------------------|------|--------------------|------|------|
| | C1B | C3A | C3B | C4A | C4B |
| <i>Nitrifying bacteria</i> | | | | | |
| <i>Nitrospira</i> | 4 | 6 | 1 | 20 | 7 |
| <i>Nitrosospira</i> | 0 | 0 | 0 | 0 | 0 |
| <i>Nitrosomonas</i> | 1 | 6 | 14 | 7 | 0 |
| <i>Nitrobacter</i> | 1 | 1 | 0 | 0 | 0 |
| | | | | | |
| <i>Nitrogen-fixing bacteria</i> | | | | | |
| <i>Bradyrhizobium</i> | 1111 | 1735 | 1494 | 1131 | 1253 |
| <i>Rhizobium</i> | 61 | 63 | 46 | 8 | 6 |
| <i>Sinorhizobium</i> | 0 | 1 | 1 | 0 | 0 |
| <i>Mesorhizobium</i> | 4 | 7 | 3 | 2 | 10 |
| | | | | | |
| <i>Methane-oxidizing bacteria</i> | | | | | |
| <i>Methylocystis</i> | 14 | 1 | 3 | 10 | 10 |
| | | | | | |

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|--|------|------|------|------|------|
| <i>Planctomycete anammox (anaerobic ammonium oxidation)</i> | 71 | 179 | 163 | 135 | 90 |
| | | | | | |
| <i>Other genera with functions of interest (mineral weathering, antibiotic production, chitin hydrolysis..)</i> | | | | | |
| <i>Burkholderia</i> | 2279 | 2907 | 2654 | 1161 | 1215 |
| <i>Rhodoplane</i> | 974 | 1796 | 1514 | 2011 | 1268 |
| <i>Alterococcus</i> | 769 | 331 | 270 | 470 | 211 |
| <i>Streptomyces</i> | 26 | 13 | 25 | 51 | 60 |
| <i>Pseudomonas</i> | 6 | 3 | 4 | 8 | 0 |
| <i>Collimonas</i> | 8 | 0 | 1 | 5 | 0 |

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