

Article IV *Mycorrhizal communities of *Vanilla planifolia* in an introduction area (La Réunion) under varying cultural practices*

Supplementary Material

Fig. S1 Rarefaction curves

Fig. S2 Composition of total fungal community

Fig. S3 Phylogenetic tree of Tulasnellaceae

Fig. S4 Phylogenetic tree of Ceratobasidiaceae

Fig. S5 Phylogenetic tree of pathogens

Fig. S6 Fungal composition of *Vanilla* roots across cultivation practices

Fig. S7 Fungal composition of *Vanilla* roots in shade house

Fig. S8 OTU's preferences for cultivation practices

Fig. S9 Venn diagrams

Figure S1 Rarefaction curves of (A-B) total fungal and (C-D) putative OMF OTUs. Curves are shown for (A, C) all samples in each cultivation practices or (B, D) with terrestrial (T) and epiphytic (E) roots separated. No OMF OTUs was detected in the epiphytic roots of vanilla plant growing in shade house. Dotted lines give the maximum and minimum richness values at each sampling depth for each curve.

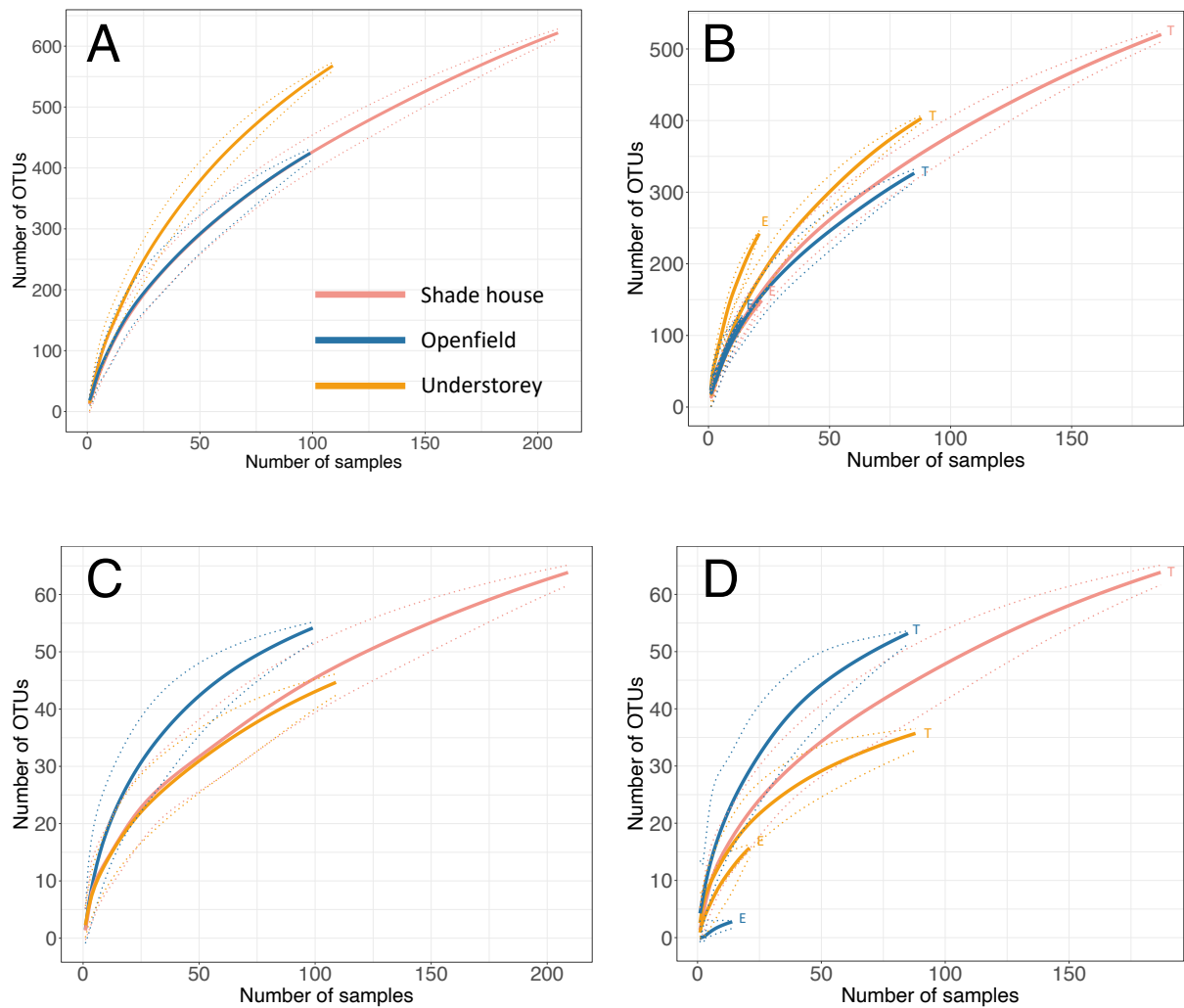
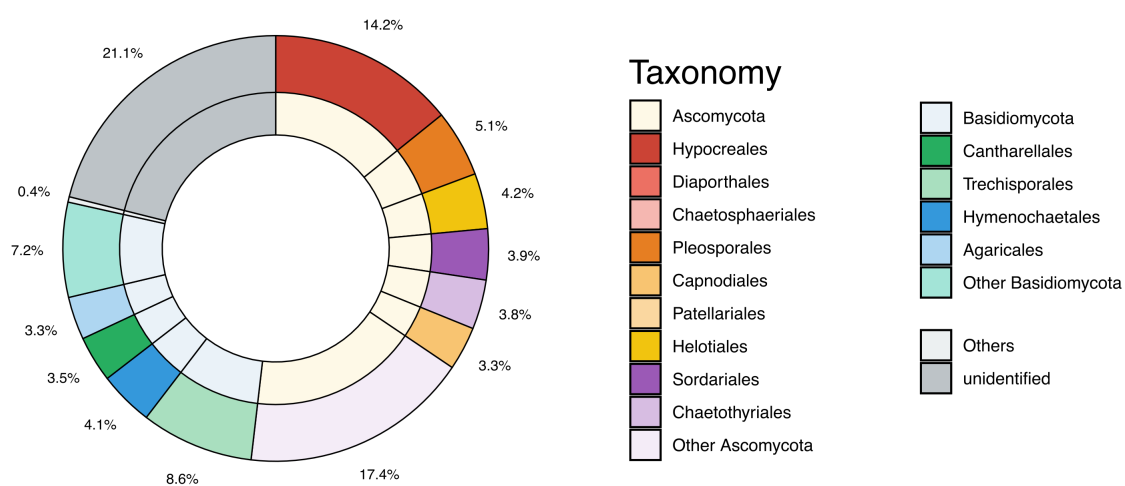


Figure S2 Composition of total fungal communities amplified with the primers (A) ITS86-F/ITS4 and (B) 5.8S-OF/ITS4-Tul. Cumulative relative abundances (RA) of the main fungal orders are shown as percentages. All the OTUs retrieved with the primers 5.8S-OF/ITS4-Tul belonged to the Tulasnellaceae family (see Fig. 1).

A ITS86-F/ITS4



B 5.8S-OF/ITS4-Tul

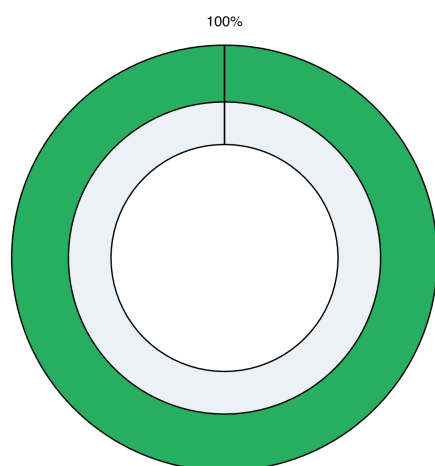


Figure S3 Phylogenetic tree of the Tulasnellaceae. OTUs identified in this study are coloured in red, sequences from Martos *et al.*, 2012 are coloured in blue, sequences from Porras-Alfaro *et al.*, 2007 are coloured in green; other sequences were retrieved from GenBank. Only the 20 most abundant OTUs of Tulasnellaceae are showed. Circles at nodes indicate sh-aLRT and bootstrap values both > 90% (grey) or >95% (black).

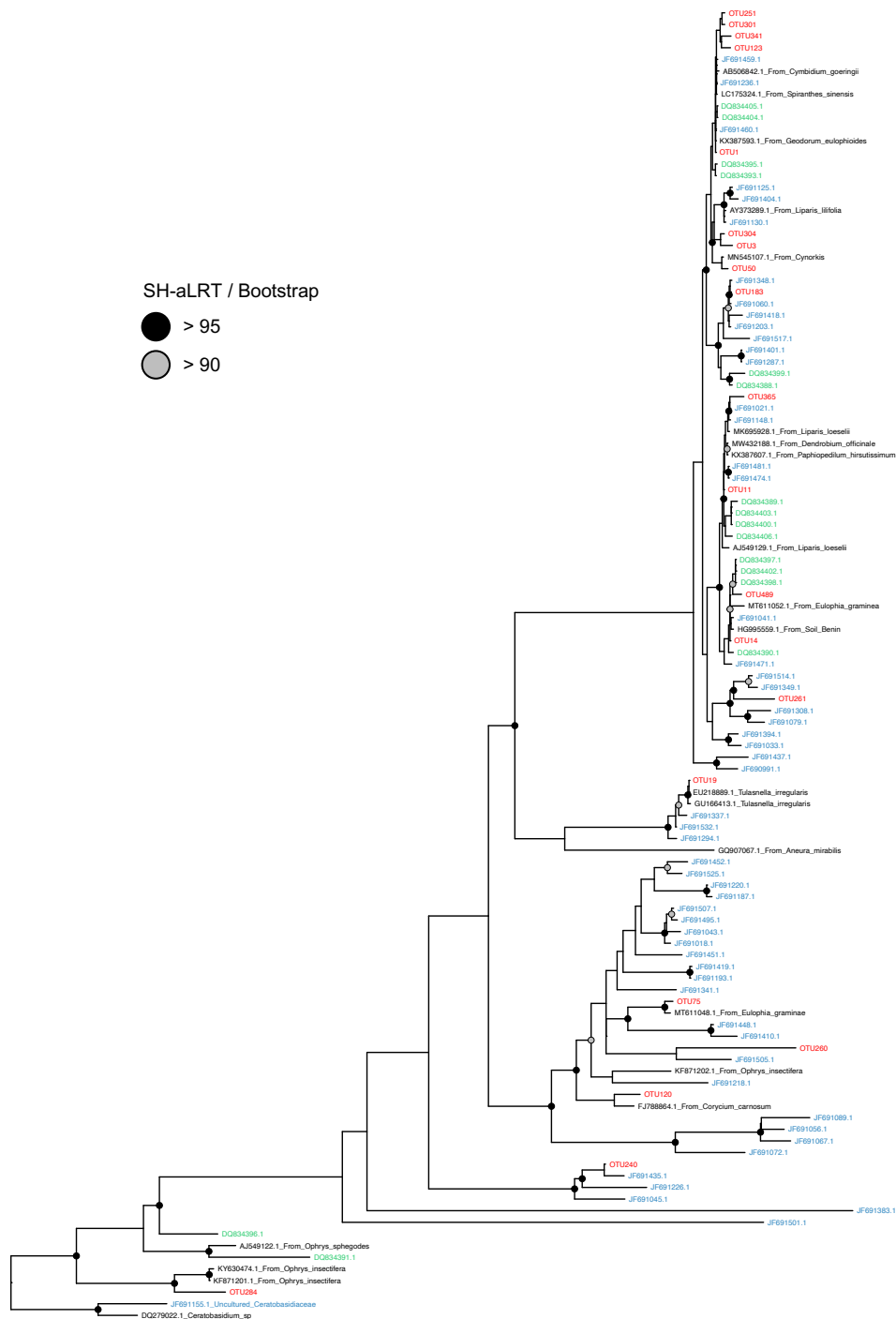


Figure S6 Fungal composition of *Vanilla* spp. roots considering (A) Tulasnellaceae, (B) other putative OMF families and (C) known pathogens. The height of each bar represents the cumulative relative abundances (RA) of each OTUs in samples. Note that the vertical scales are different between (A) and (B-C) due to the use of different PCR primers. Detailed results between substrates in the shade house are given Fig. S7. SH, shade house; OF, openfield; US, understorey; E, epiphytic; T, terrestrial.

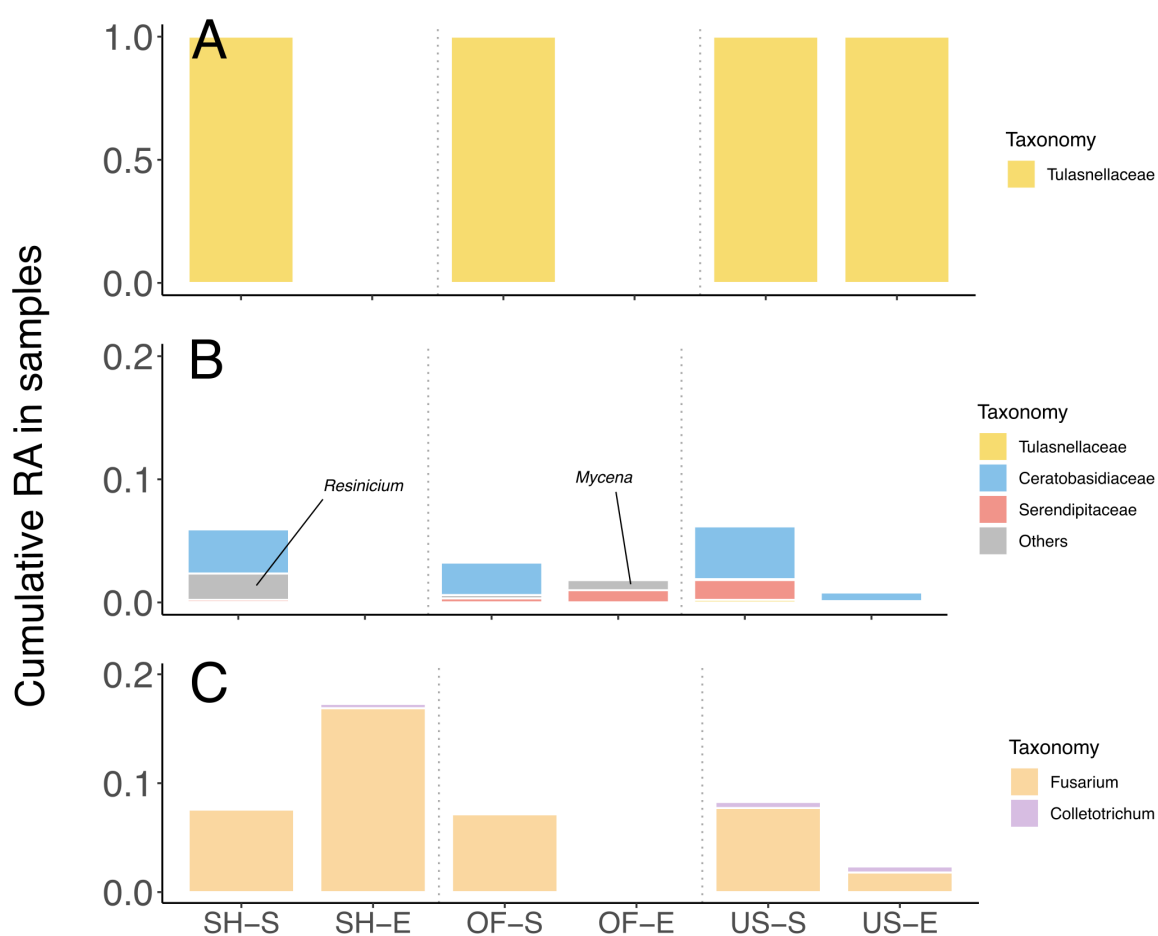


Figure S7 Fungal composition of *Vanilla* spp. roots in the shade house. (A) Cumulative frequencies considering (i) OMF families and (ii) vanilla pathogens. (B) Cumulative RA considering (i) Tulasnellaceae, (ii) other OMF families and (iii) vanilla pathogens.

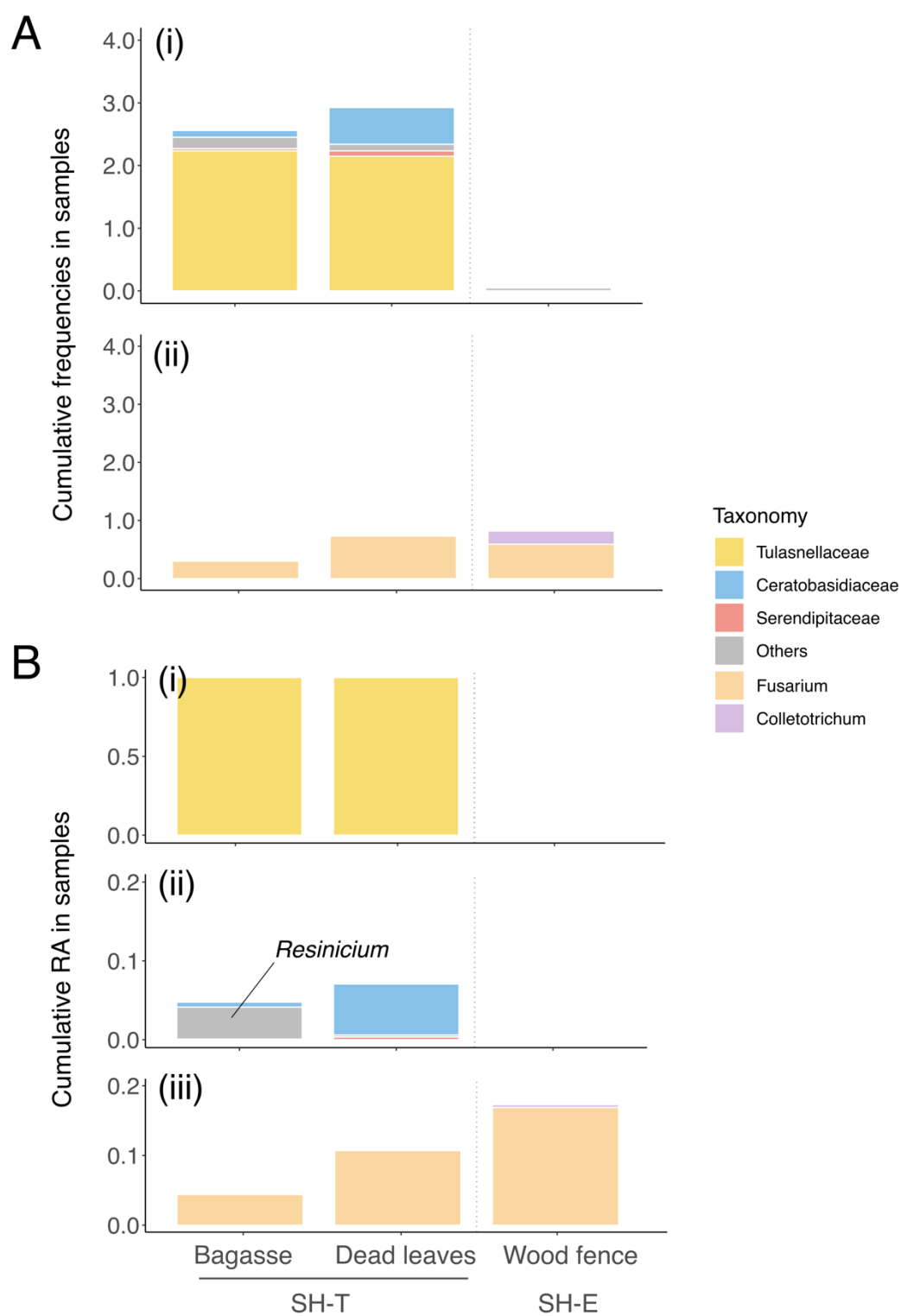


Figure S8 Fungal OTUs preferences for culture conditions and root types. Only putative-OMF OTUs with significant ($p < 0.05$) preferences for sample types (in grey in panel A) are displayed. The strength of the correlation is shown on the x-axis (ϕ , panel B) and OTUs are coloured according to their taxonomy. The only non-rhizoctonia OMF OTU (OTU25) belonged to the genus *Resinicium*. OF, openfield; SH, shade house; US, understorey; E, epiphytic; T, terrestrial.

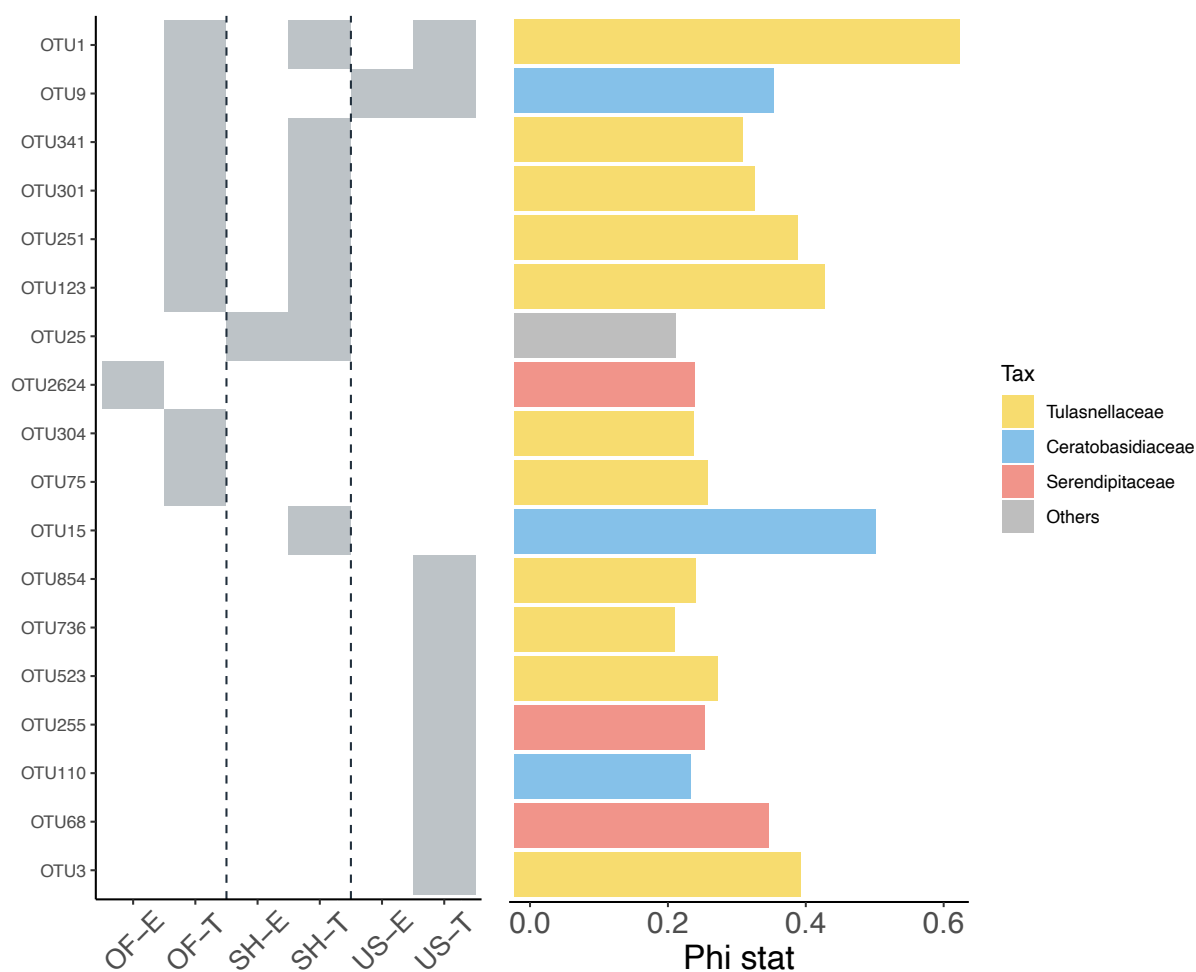
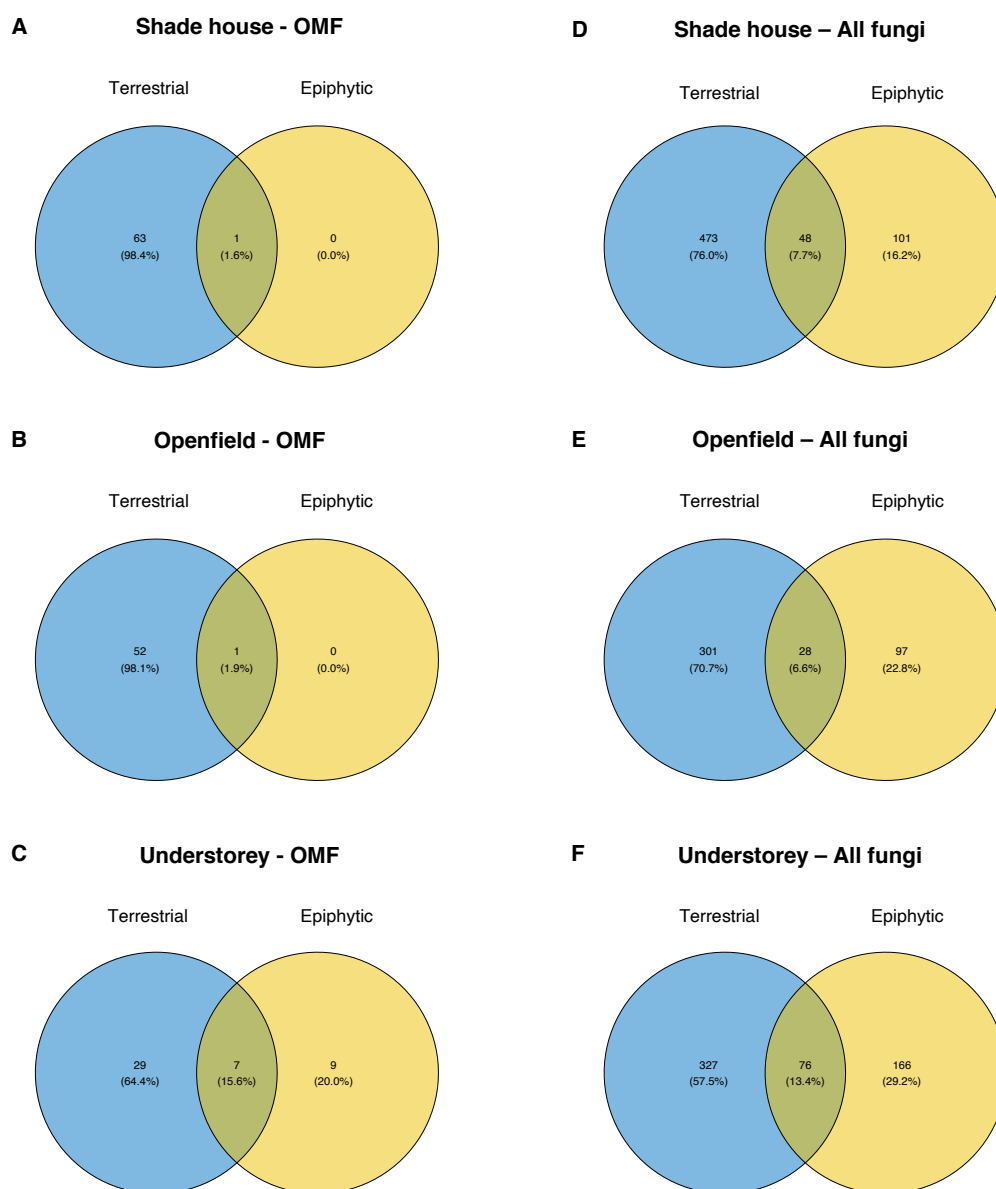


Figure S9 Venn diagrams showing the numbers of fungal OTUs exclusive or shared between terrestrial and epiphytic roots of *Vanilla* sp. in each culture condition, considering (A-C) putative OMF families and (D-F) all fungi.



References

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