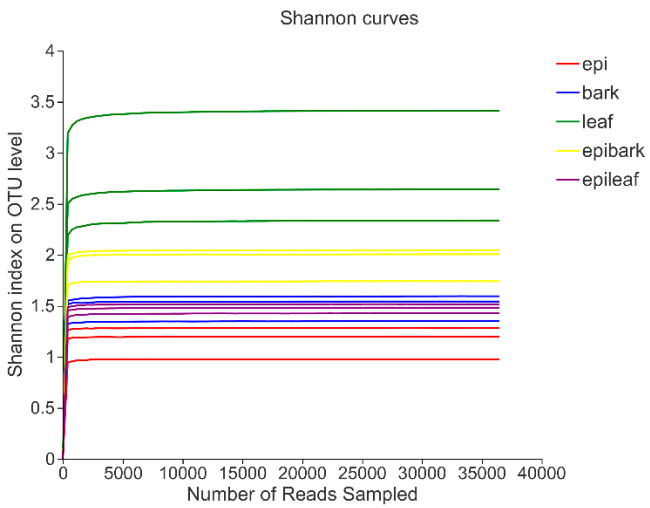


Figure S1. Shannon rarefaction curves of the ITS reads based on OTUs at 97% sequence similarity

```
OTU762          ------------------------------------------------------GAGAGCC
Epi128          GAATTCTGCAATTCACATTACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAGCC
                                                                       *******

OTU762          AAGAGATCCGTTGTTGAAACTTAGTTTAATGATGCGTTACATCAAGTACATTCAGTTCAA
Epi128          AAGAGATCCGTTGTTGAAACTTAGTTTAATGATGCGTTACATCAAGTACATTCAGTTCAA
                ************************************************************

OTU762          TTAAATGAGTTTGTATATGAATTTAGCAGACTGAAAGCTTTTTACGGCCTCCAGTCTCAC
Epi128          TTAAATGAGTTTGTATATGAATTTAGCAGACTGAAAGCTTTTTACGGCCTCCAGTCTCAC
                ************************************************************

OTU762          AGGTGCACAGGGGTGTGTGGATGAAAGGAGAAGGCGTGCACATGCTGCCAAAGACAGCCA
Epi128          AGGTGCACAGGGGTGTGTGGATGAAAGGAGAAGGCGTGCACATGCTGCCAAAGACAGCCA
                ************************************************************

OTU762          GCGACAACCAACCCCAAGTTCATTCAATAATGATCCTTCCGCAGGTTCACCTACGGAAAC
Epi128          GCGACAACCAACCCCAAGTTCATTCAATAATGATCCTTCCGCAGGTTCACCTACGGA---
                ************************************************************

OTU762          CTTGTTACGACTT
Epi128          -------------
```

Figure S2. Sequence alignment between OTU762 and Epi128. Asterisk represents that the nucleotide base in the two sequences at this site is identical.

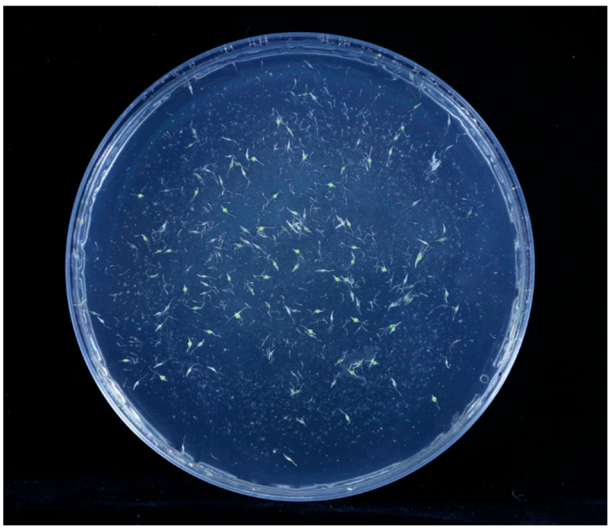


Figure S3. Germination of *E. radicans* on OMA medium in 90 mm Petri dish

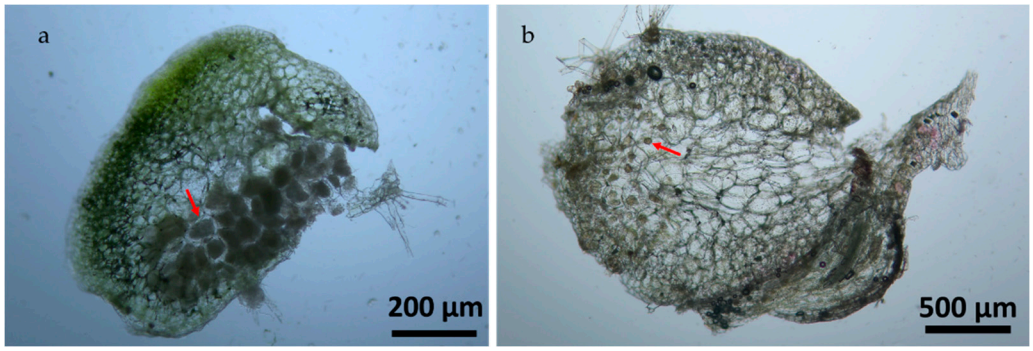


Figure S4. Fungal hyphae colonized in the inner cells at the basal part (the suspensor end) of protocorms and formed the intracellular hyphae coils after *in vitro* symbiotic germination with Epi128 (a) and Epi221 (b). The red arrow indicates the intracellular fungal peloton.

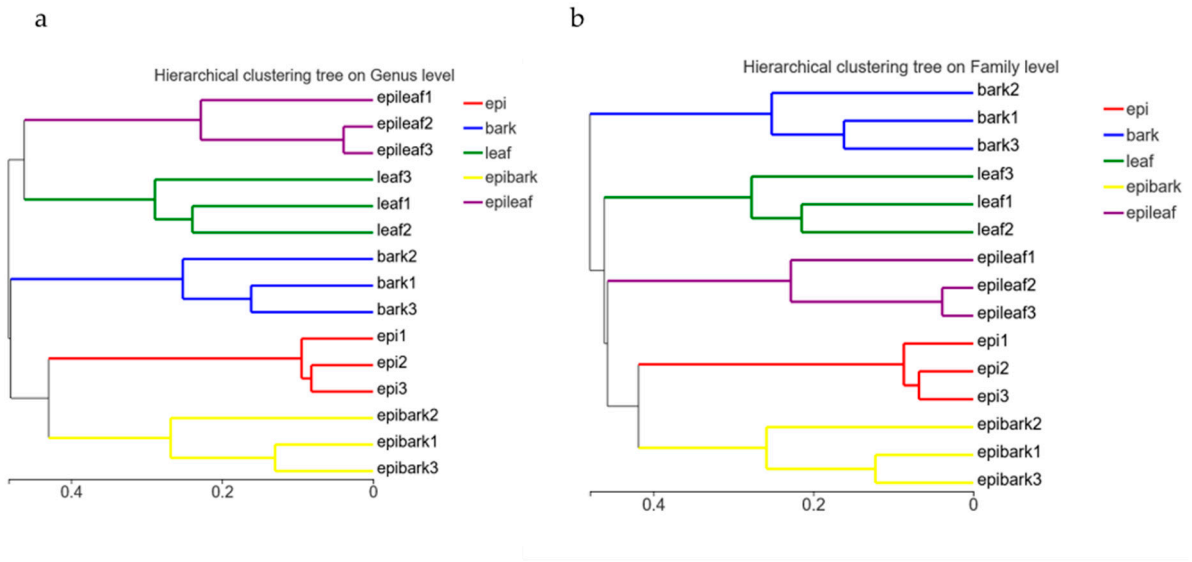


Figure S5. Hierarchical clustering tree of the samples on genus level (a) and family level (b)