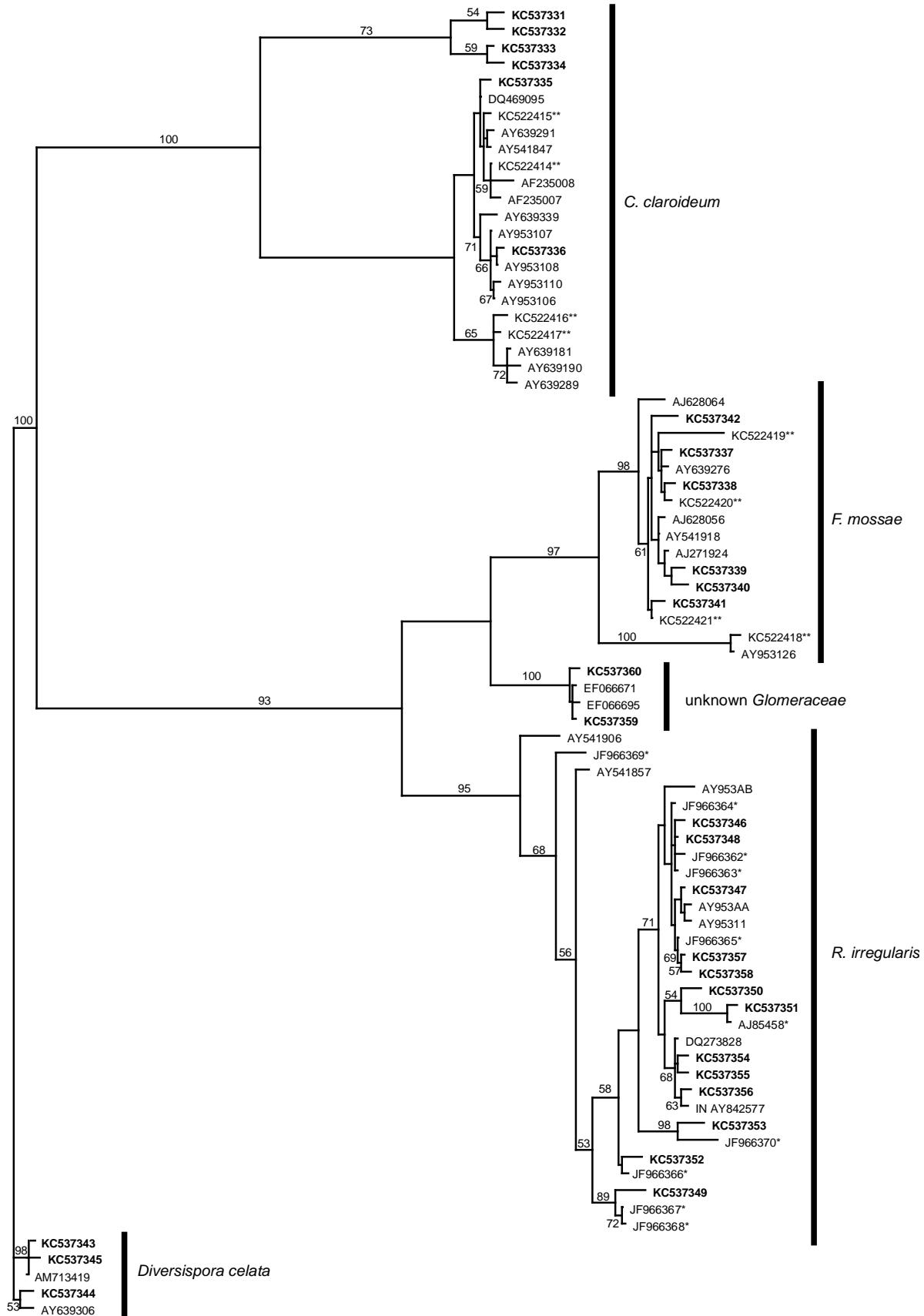


S1 Fig. Phylogenetic analysis of the native arbuscular mycorrhizal fungal community.

The analysis is based on sequences of partial large subunit of nuclear ribosomal DNA, the most parsimonious tree is presented. Bootstrap values higher than 50% are indicated by numbers above or below branches. The sequences obtained in the present study are given in bold.

* Sequences published by [1]; ** sequences published by [2].



References

1. Krak K, Janoušková M, Caklová P, Vosátka M, Štorchová H. Intraradical Dynamics of Two Coexisting Isolates of the Arbuscular Mycorrhizal Fungus *Glomus intraradices* Sensu Lato as Estimated by Real-Time PCR of Mitochondrial DNA. *Applied and Environmental Microbiology*. 2012;78(10):3630-7. doi: 10.1128/aem.00035-12.
2. Janoušková M, Krak K, Wagg C, Štorchová H, Caklová P, Vosátka M. Effects of Inoculum Additions in the Presence of a Preestablished Arbuscular Mycorrhizal Fungal Community. *Applied and Environmental Microbiology*. 2013;79(20):6507-15. doi: 10.1128/aem.02135-13.