



Suppl. Fig. 1. The initial alignment of ITS sequences was made using MAFFT v7.140b with the L-INSI option (Katoh & Standley 2013). Using the aligned sequences, a Neighbor-Joining (Saitou & Nei 1987) tree was generated in MEGA v6 (Tamura et al. 2013) with the Kimura 2-parameter method (Kimura 1980). The rate of variation among sites was modeled with a gamma distribution (shape parameter = 1.54). The tree file served as a guide tree in the second alignment using RAxML v10.10.1 (Stamatakis & Goloboff 2005) and the -f option. A phylogenetic reconstruction was conducted using Maximum Likelihood analysis in raxmlGUI v1.3 under the GTR+I model (Silvestro & Michalak 2011). The ITS region was partitioned into ITS1, ITS2 and 5.8S rDNA. The analysis was run with 500 bootstrap replicates.

Saitou N, Nei M (1987). The neighbour-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4: 406-425.

Tamura K (1990). A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 18: 116-120.

Tamura K, et al. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2726-2729.

Likhtova E, Goloboff A (2005). An algorithm for progressive multiple alignment of sequences with insertions. *Proceedings of the National Academy of Sciences of the United States of America* 102: 10557-10562.

Katoh K, Standley DM (2013). MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30: 772-780.

Silvestro D, Michalak I (2011). RaxmlGUI: a graphical front-end for RAxML. *Organisms Diversity & Evolution* 12: 335-337.