



Figure S1. Phylogenetic tree based on internal transcribed spacer (ITS) sequences alignment. The evolutionary history was inferred using the Neighbor-Joining method [31]. The optimal tree is shown. The evolutionary distances were computed using the Maximum Composite Likelihood method [32] and are in the units of the number of base substitutions per site. This analysis involved 6 nucleotide sequences. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There was a total of 596 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [33].