





S1 Fig. Maximum likelihood phylogenetic trees inferred from the datasets of ITS (A), *tef1- α* (B), β -tubulin (C), *cal* (D) and *his3* (E) sequences of isolate 1A and BLAST best hits. *Diaporthella corylina* was used as outgroup. ML analysis was based on the Tamura-Nei model and the tree was obtained from an initial bio-neighbour-joining tree automatically generated by the software, followed by a heuristic search using the nearest-neighbor interchange algorithm. A discrete gamma distribution was used to model evolutionary rate differences among sites. The percentage of trees in which the associated taxa clustered together is shown next to the branches.