

Figure S1. Phylogram obtained from Maximum Likelihood (ML) analyses of the ITS1/2 data for the isolated fungal taxa. Sequences obtained during this study are presented in bold type. The Bootstrap values $\geq 75\%$ for ML and Bayesian Inference (BI) analyses are presented at branch as follows: ML/BI. * Bootstrap values $<75\%$. The tree is drawn to scale (see bar) with branch length measured in the number of substitutions per site. *Fellozyma inositophila* and *Fellozyma* sp. represent the outgroup.

