



0.2

Supplementary file 2. SSU rDNA gene tree obtained by Maximum Likelihood analysis of 114 sequences and 830 aligned position. The tree is rooted with *Lamproderma echinosporum*. The newly obtained SSU sequences are in Bold. Supports are shown for ultrafast bootstrap replicates I and Bayesian posterior probabilities  $\geq 90/0.9$ ; dashes indicate a conflicting topology; dots – maximum support in both analyses. Details and discussion in the text.