



Figure S1. Phylogeny of 41 species of lichen-forming fungi based on Randomized Axelerated Maximum Likelihood (RAxML) analysis using the internal transcribed spacer region (ITS) sequences. The species names and accession numbers of type strains were marked in red. The number in each node represents bootstrap support (BS) and posterior probability (PP). BS values of 70 and PP values of 0.95 were plotted on the branches. Scale in 0.02 substitution per site.