Figure S5. Phylogeny of lichen-forming algae *Trebouxia* species based on the Randomized Axelerated Maximum Likelihood (RAxML) analysis of a concatenated three-locus dataset including internal transcribed spacer region (ITS), the large nuclear subunit ribosomal RNA gene (nuSSU), and chloroplast ribulose-bisphosphate carboxylase-RuBisCO (rbcL) sequences. 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 0.01 substitution per site.