



Figure S3. Phylogeny of lichen-forming algae *Trebouxia* species based on the Randomized Axelerated Maximum Likelihood (RAxML) analysis of a concatenated two-locus dataset including internal transcribed spacer region (ITS) and chloroplast ribulose-bisphosphate carboxylase-RuBisCO (*rbcL*) gene sequences with reference sequences from the study of Muggia et al. (2020) marked in black. 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 0.09 substitution per site.