



Figure S4. Comparison of different *Trebouxia* species delimitations resulting from three species delimitation approaches, i.e., Automatic Barcoding Gap Discovery (ABGD), a Bayesian implementation of the PTP (bPTP) (Zhang et al., 2013), and the coalescent-based General Mixed Yule Coalescent (GMYC), along with the species scenarios proposed by Muggia et al. (2020) and. The phylogeny was constructed by Randomized Axelerated Maximum Likelihood (RAXML) analysis based on the combined internal transcribed spacer region (ITS) and chloroplast ribulose-bisphosphate carboxylase-RuBisCO gene (rbcl) gene sequences. Scale in 0.02 substitution per site. The numbers in the seven columns represent the species numbers defined by different methods.