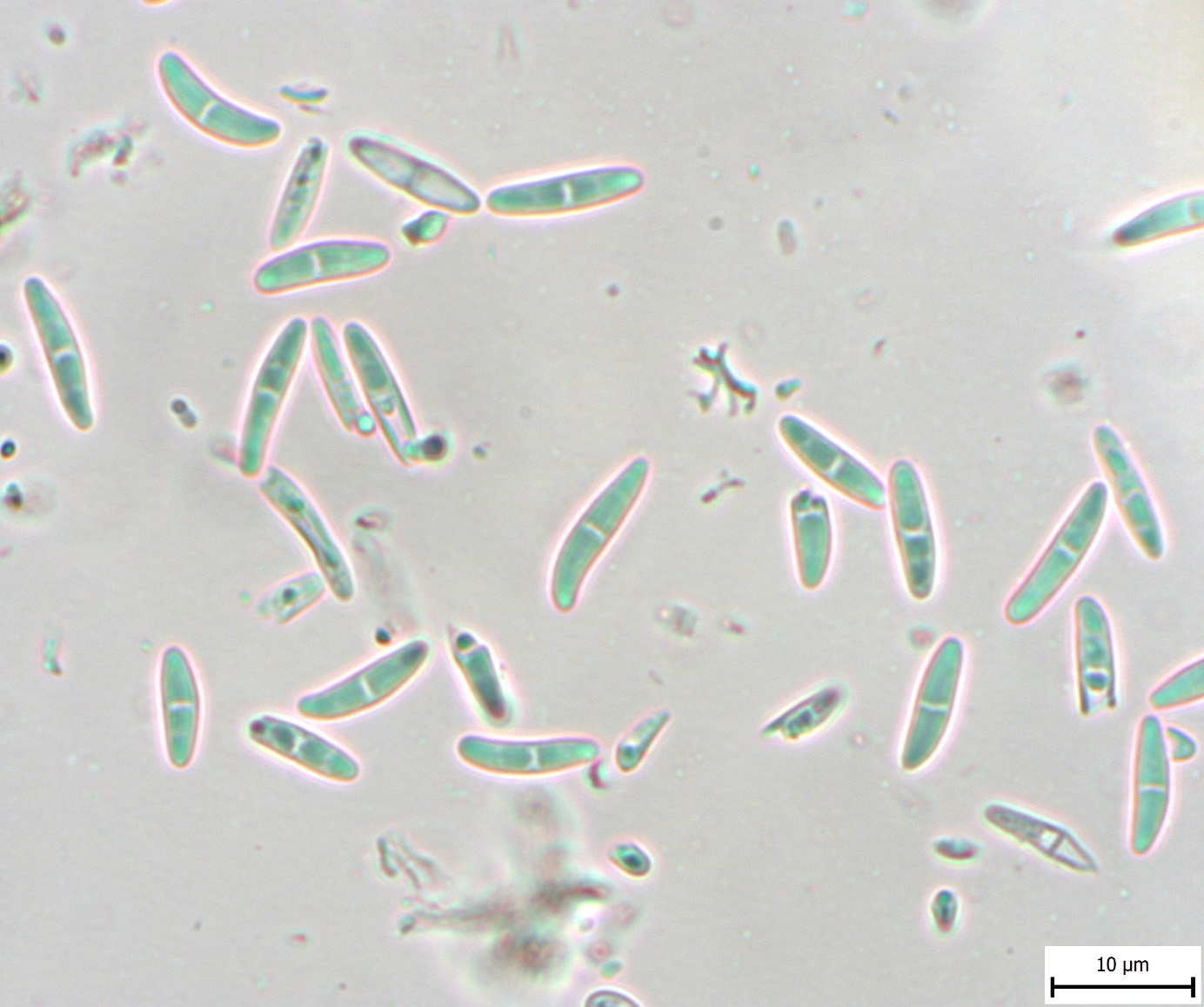
**SUPPLEMENTARY MATERIAL**



**Fig. S1.** Phylogenetic hypothesis of *Coenogonium* resulting from the Bayesian analysis of ITS rDNA sequences. Values at the nodes indicate the statistical supports of Bayesian posterior probability (left), maximum-likelihood bootstrap (middle) and maximum parsimony bootstrap (right). Fully supported branches (1.0/100/100) are marked with an asterisk. Scale bar shows the estimated number of substitutions per site.



**Fig. S2.** Phylogenetic hypothesis of *Coenogonium* resulting from the Bayesian analysis of mtSSU sequences. Values at the nodes indicate the statistical supports of Bayesian posterior probability (left), maximum-likelihood bootstrap (middle) and maximum parsimony bootstrap (right). Fully supported branches (1.0/100/100) are marked with an asterisk. Scale bar shows the estimated number of substitutions per site.



**Fig. S3.** *Coenogonium nimisii*, ascospores in water (Sanderson 436).

**Fig. S4.** Phylogenetic hypothesis (unrooted tree) of Trentepohliales resulting from the Bayesian analysis of rbcL sequences. Values at the nodes indicate the statistical supports of Bayesian posterior probability (left), maximum-likelihood bootstrap (middle) and maximum parsimony bootstrap (right). Fully supported branches (1.0/100/100) are marked with an asterisk. Scale bar shows the estimated number of substitutions per site. Newly obtained sequences are marked in bold, *Coenogonium* photobionts are marked in orange, *Porina* photobionts are marked in violet. Clade numbering corresponds to Nelsen et. al. (2011).

