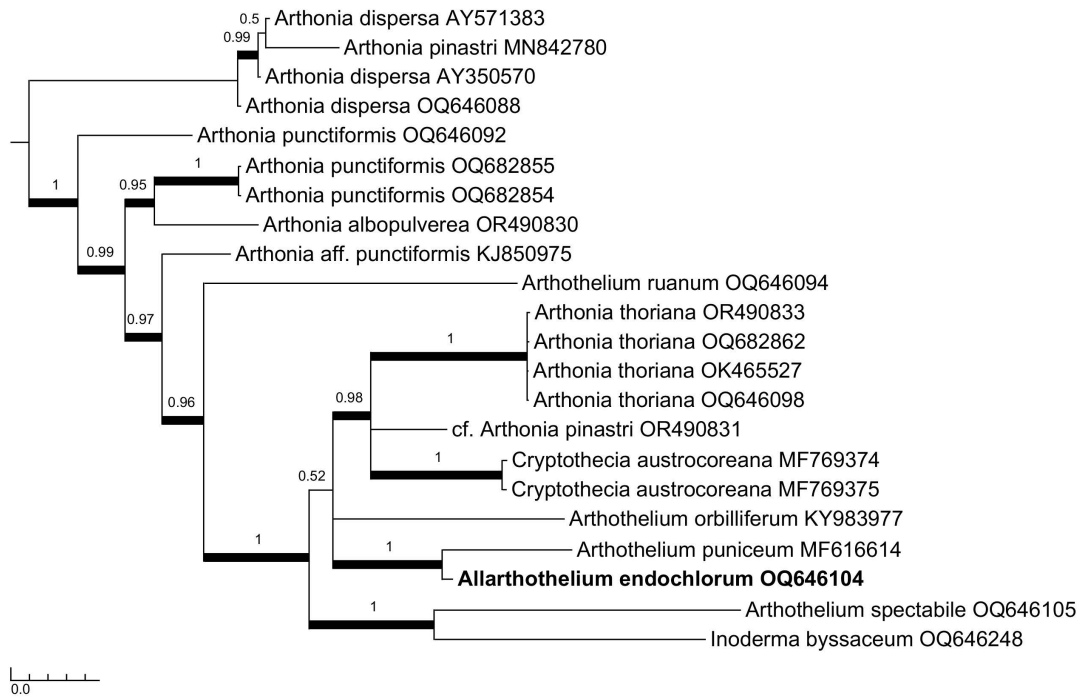
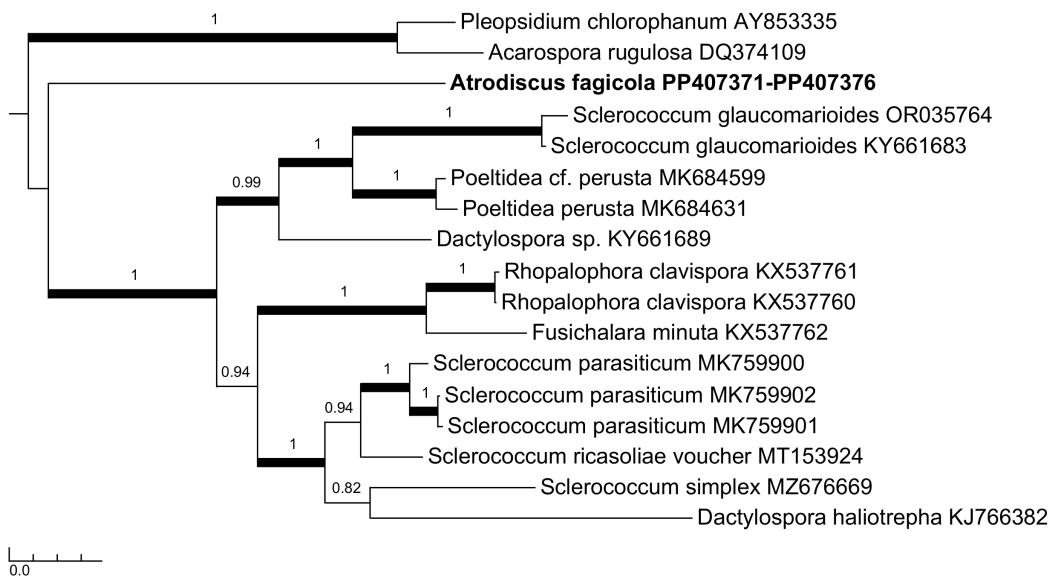


**Vondrák J., Svoboda S., Malíček J., Šoun J., Košnar J., Svensson M., Timdal E., Machač J. & Palice Z. (2024) Combining environmental DNA data and taxonomic surveys provides an unprecedented understanding of lichen diversity and accelerates the discovery of new species. – *Preslia* 96: 351–417.**

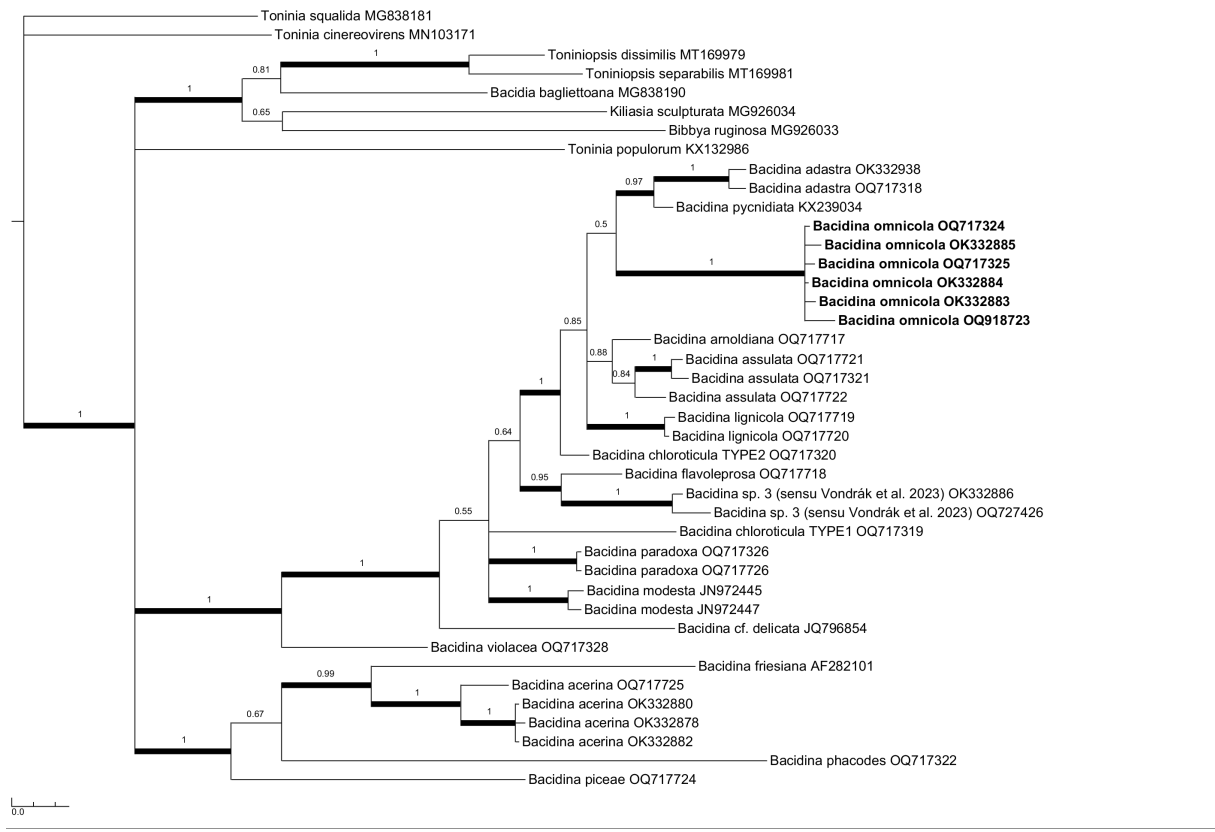
**Supplementary Figs S1–S12.** Phylogenetic trees with the new species.



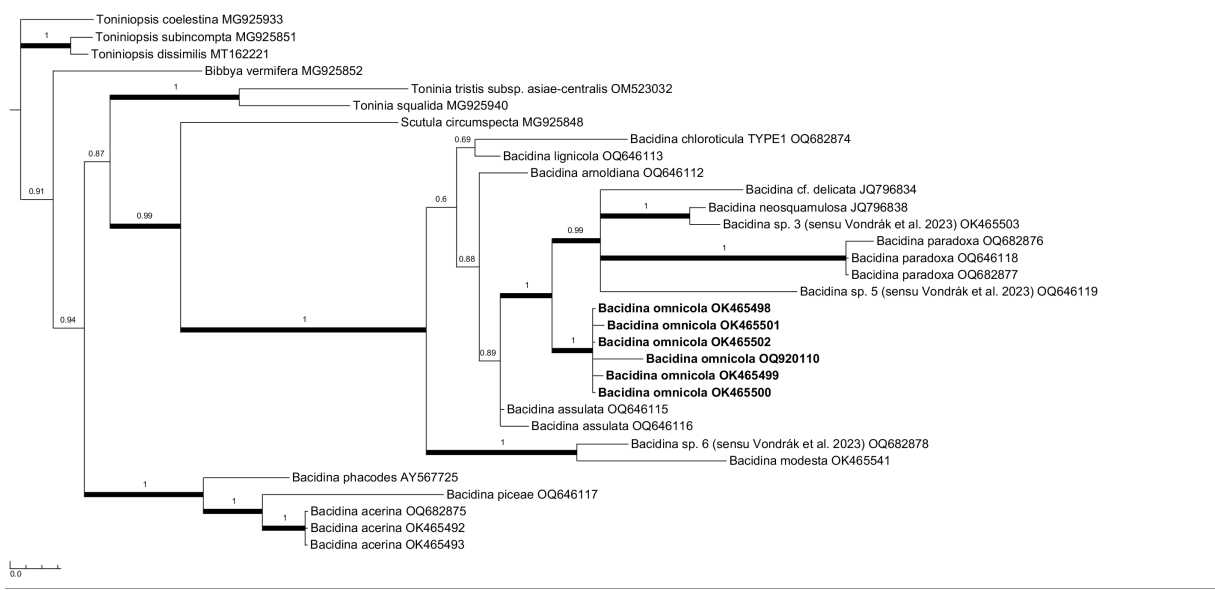
**Supplementary Figure 1.** MtSSU tree with *Allarthothelium endochlorum* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 89,000 generations.



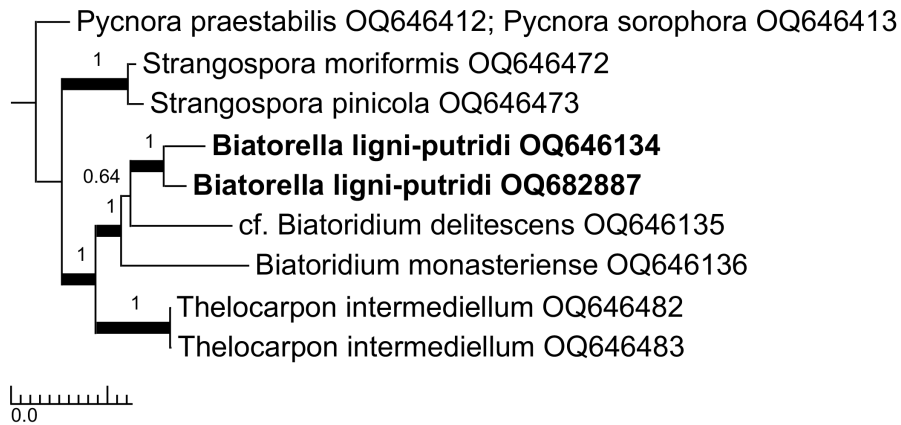
**Supplementary Figure 2.** MtSSU tree with *Atrodiscus fagicola* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 8,000 generations.



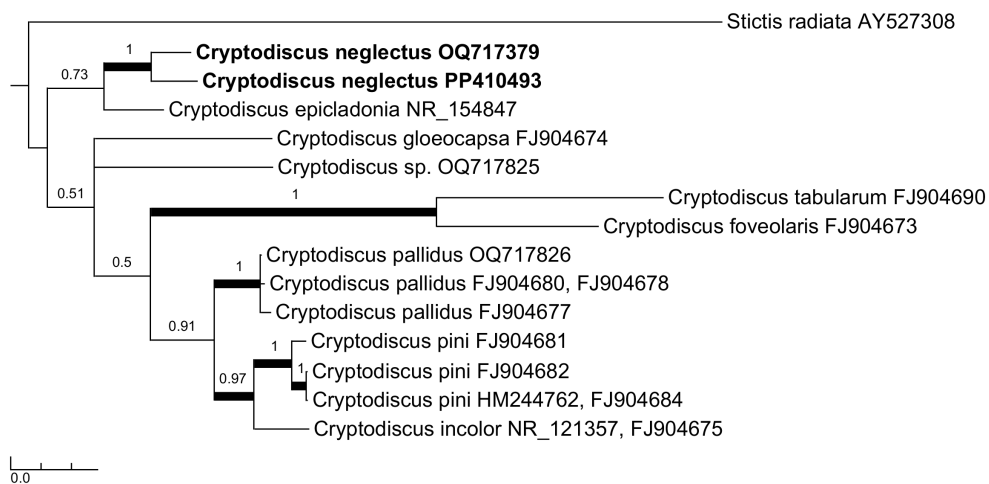
**Supplementary Figure 3.** ITS tree with *Bacidina omnicola* and related species. F80+I model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 8,000 generations.



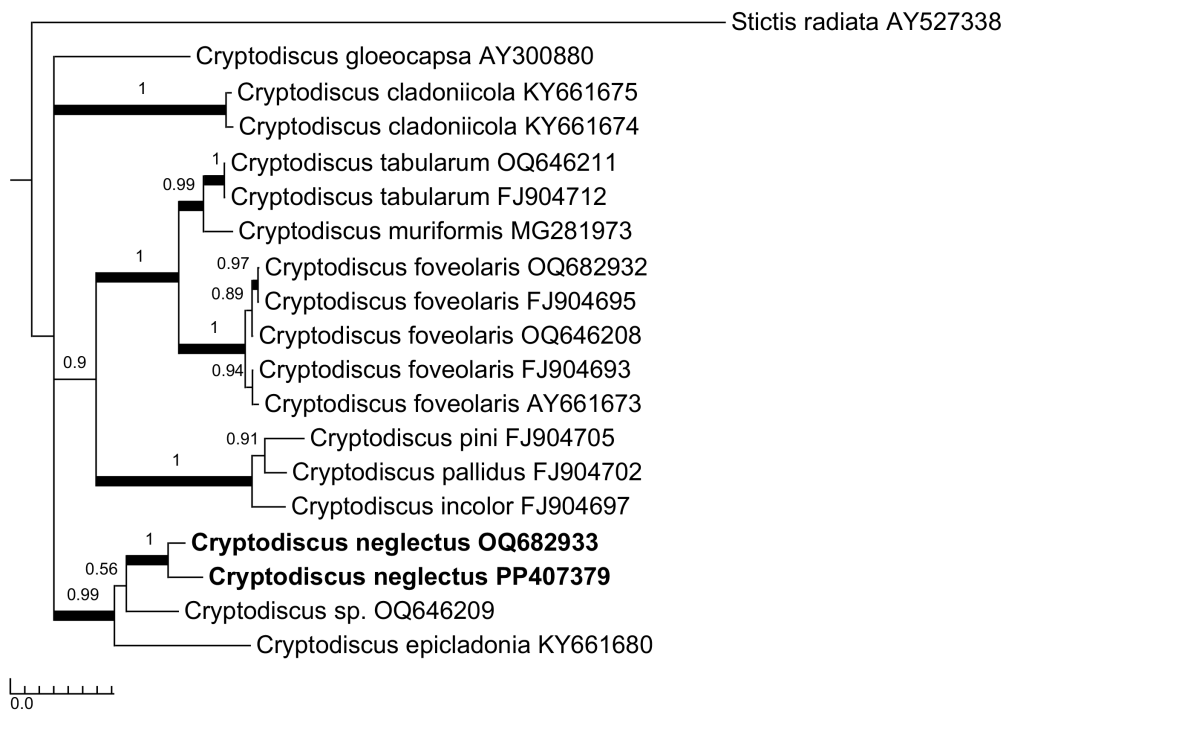
**Supplementary Figure 4.** MtSSU tree with *Bacidina omnicola* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 181,000 generations.



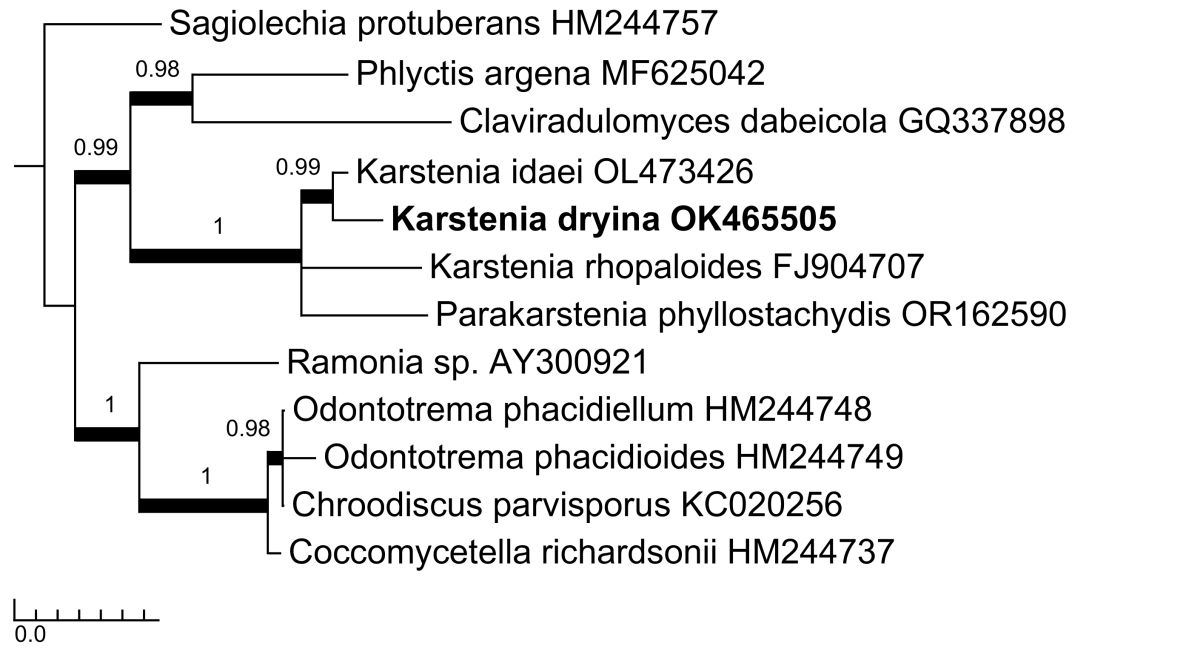
**Supplementary Figure 5.** MtSSU tree with *Biatorella ligni-putridi* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 10,000 generations.



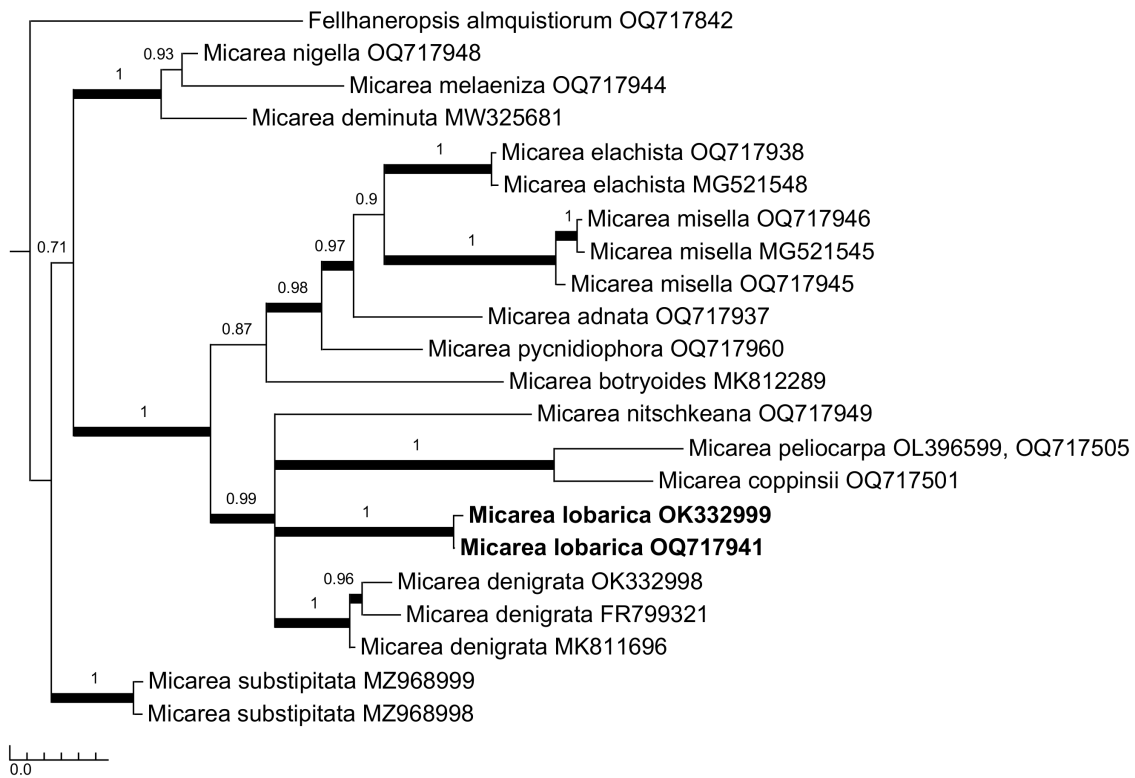
**Supplementary Figure 6.** ITS tree with *Cryptodiscus neglectus* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 146,000 generations.



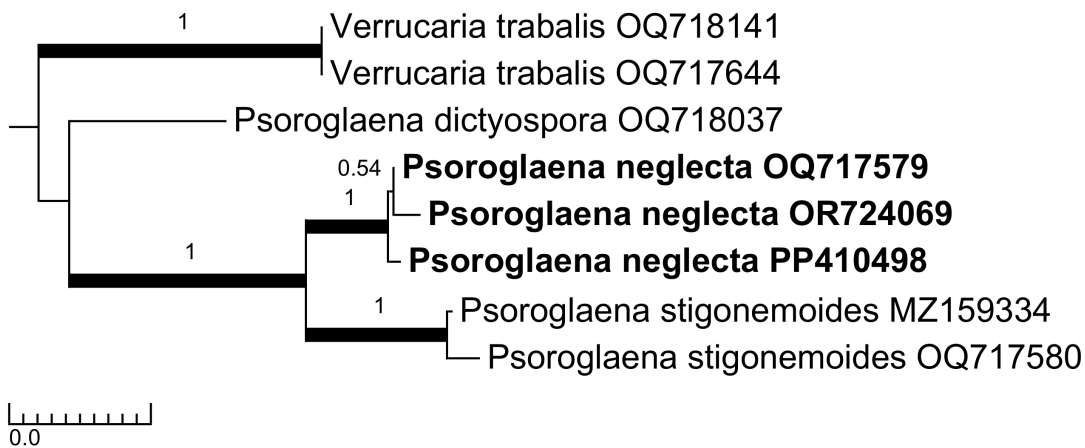
**Supplementary Figure 7.** MtSSU tree with *Cryptodiscus neglectus* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 104,000 generations.



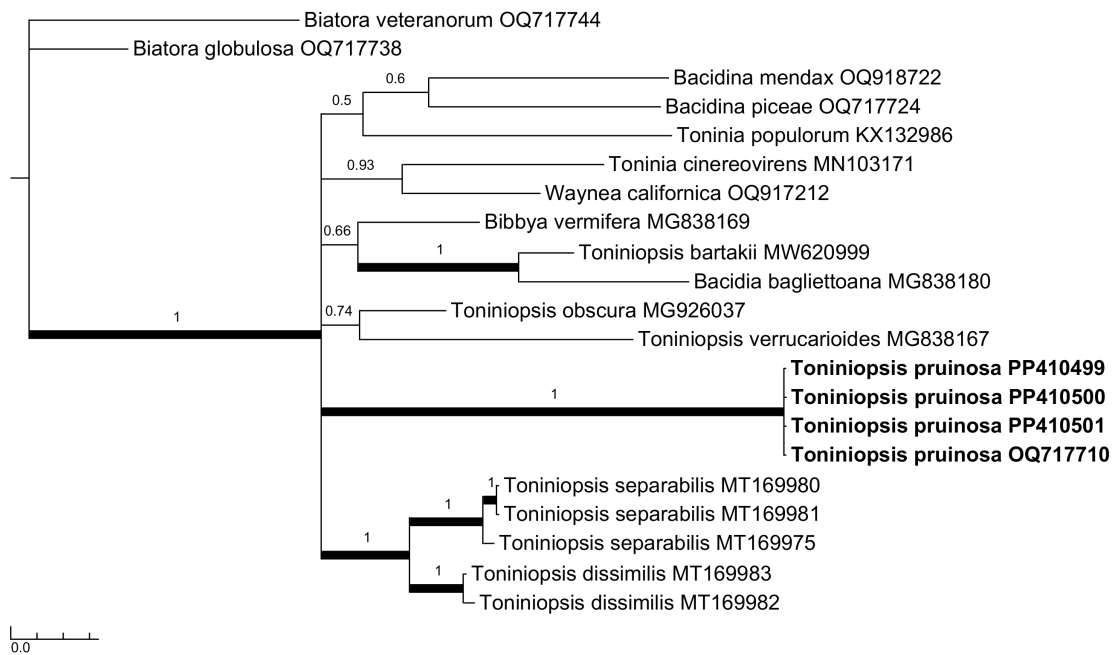
**Supplementary Figure 8.** MtSSU tree with *Karstenia dryina* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 18,000 generations.



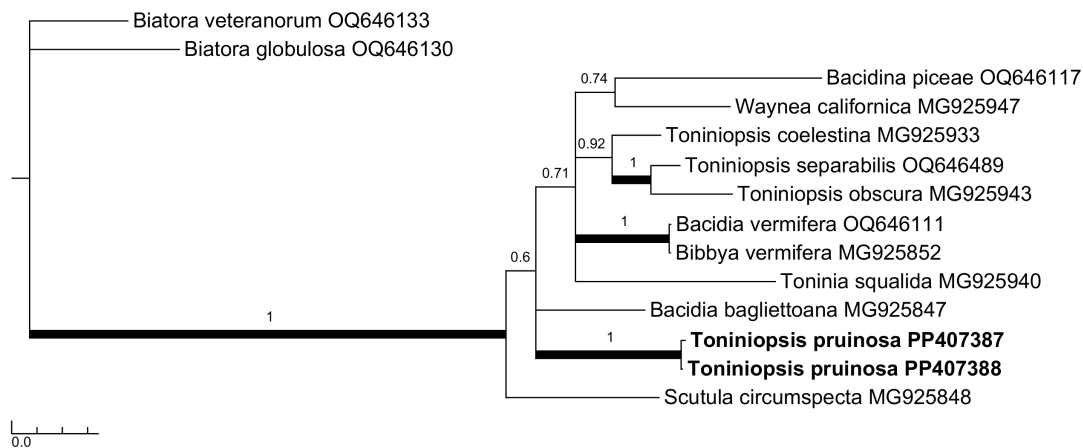
**Supplementary Figure 9.** ITS tree with *Micarea lobarica* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 78,000 generations.



**Supplementary Figure 10.** ITS tree with *Psoroglaena neglecta* and related species. HKY model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 1,000 generations.



**Supplementary Figure 11.** ITS tree with *Toniniopsis pruinosa* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 302,000 generations.



**Supplementary Figure 12.** MtSSU tree with *Toniniopsis pruinosa* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 159,000 generations.