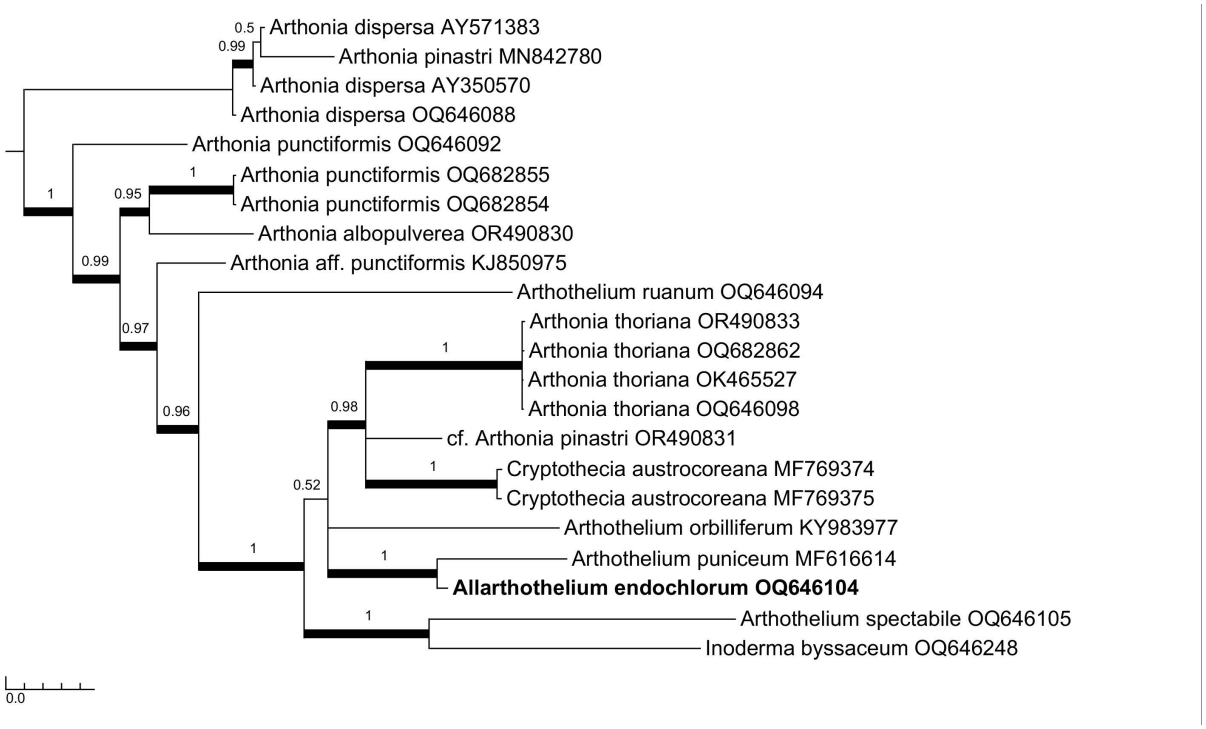
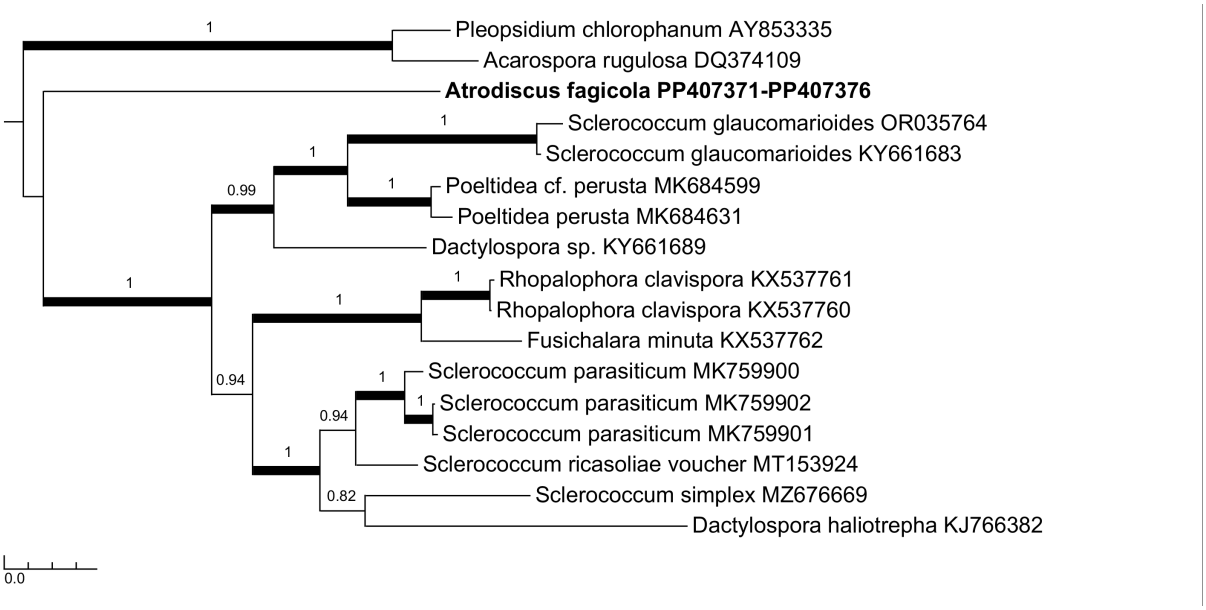
Vondrák J., Svoboda S., Malíček J., Šoun J., Košnar J., Svensson M., Timdal E., Machač J. & Palice Z. (2024) Combining environmental DNA data and taxonomic surveys provides an unprecedented understanding of lichen diversity and accelerates the discovery of new species. – Preslia 96: 351–417.

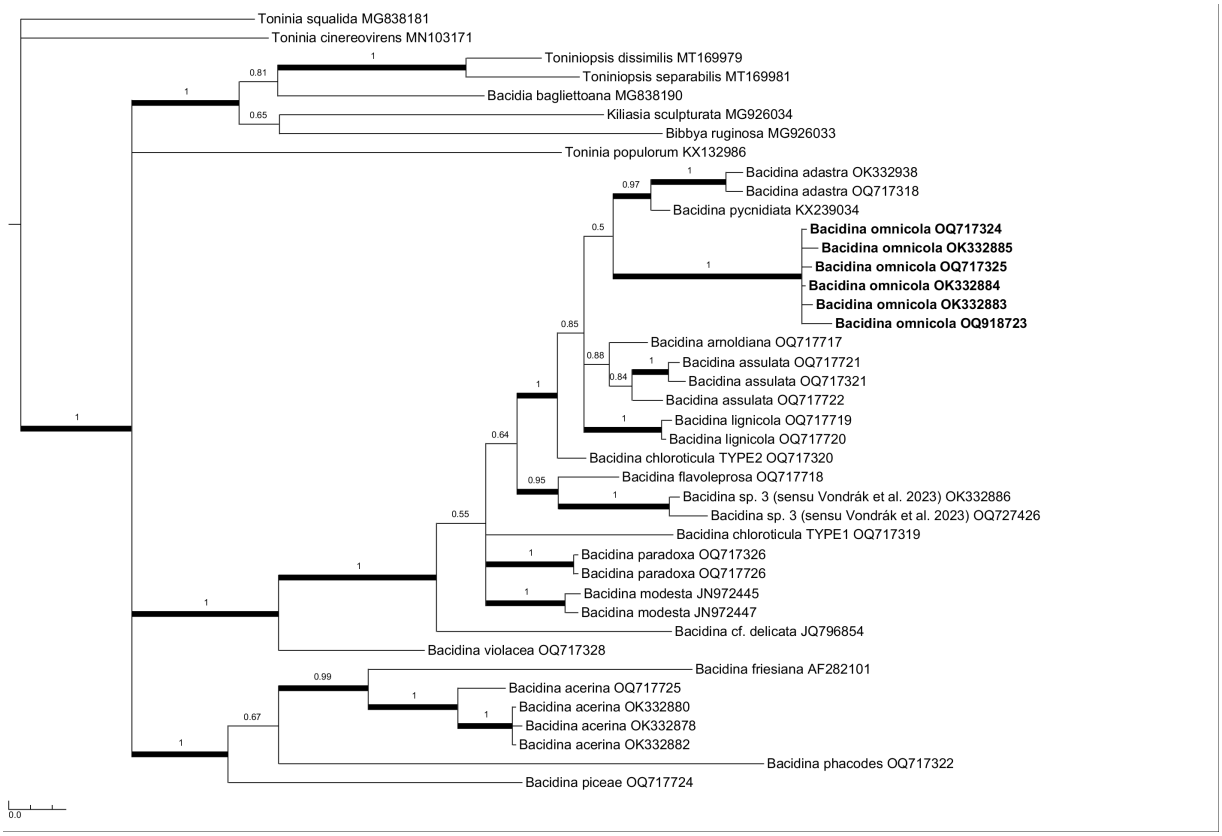
Supplementary Figs S1–S12. Phylogenetic trees with the new species.



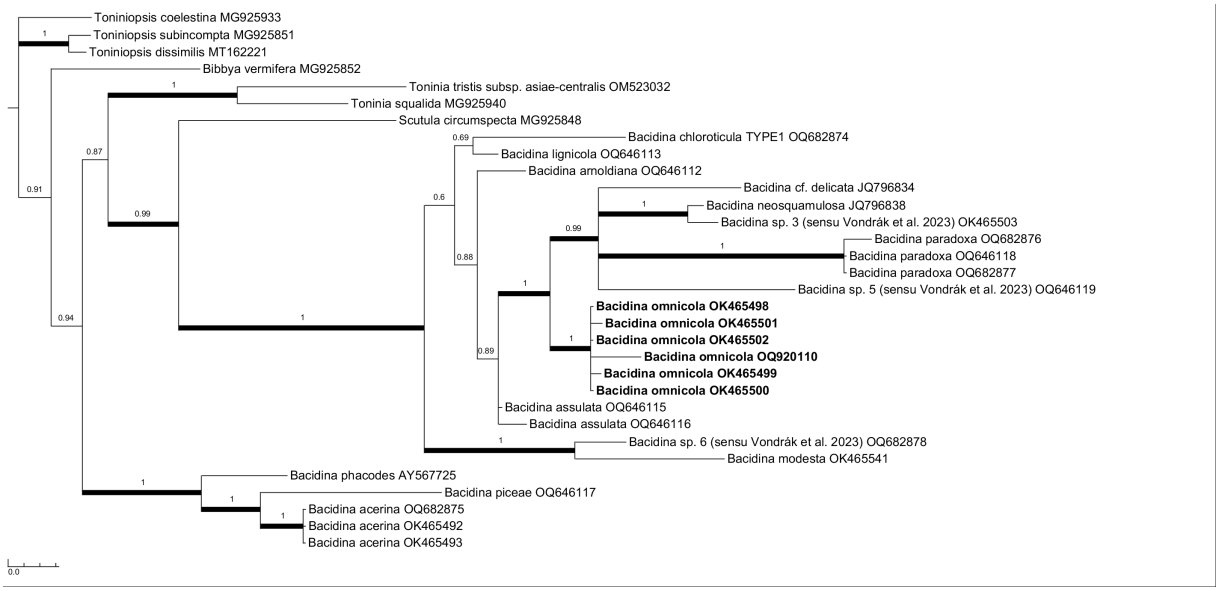
Supplementary Figure 1. MtSSU tree with *Allarthothelium endochlorum* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 89,000 generations.



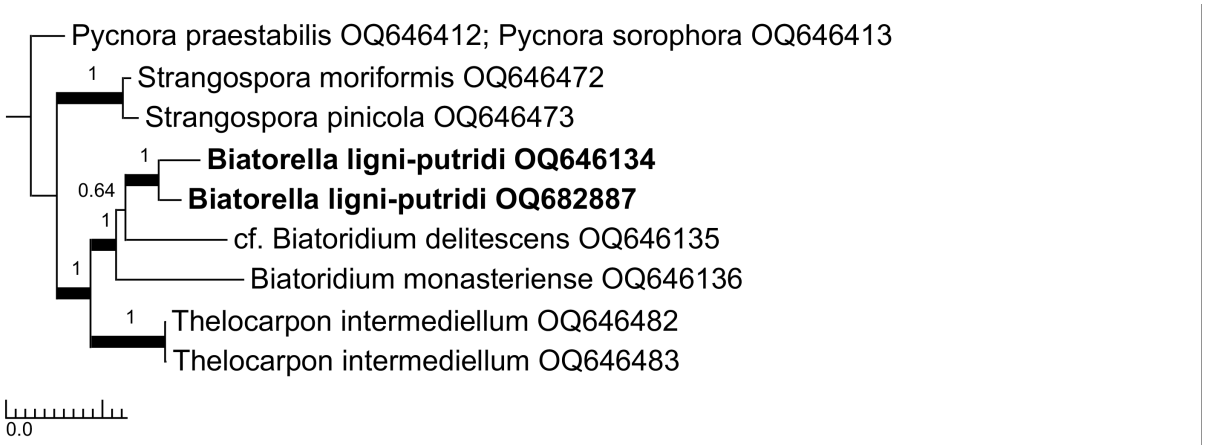
Supplementary Figure 2. MtSSU tree with *Atrodiscus fagicola* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 8,000 generations.



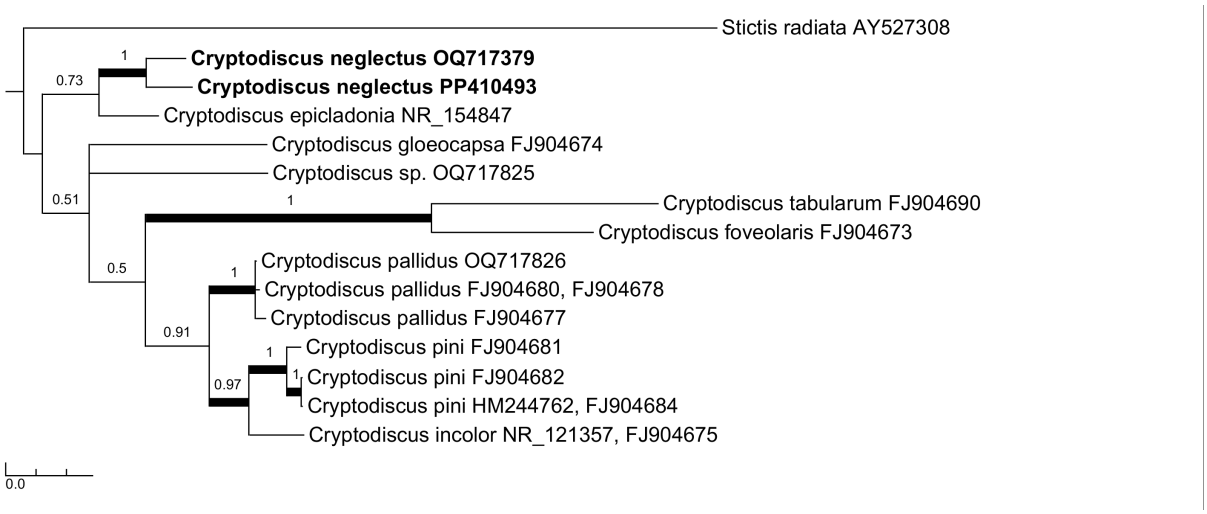
Supplementary Figure 3. ITS tree with *Bacidina omnicola* and related species. F80+I model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 8,000 generations.



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.



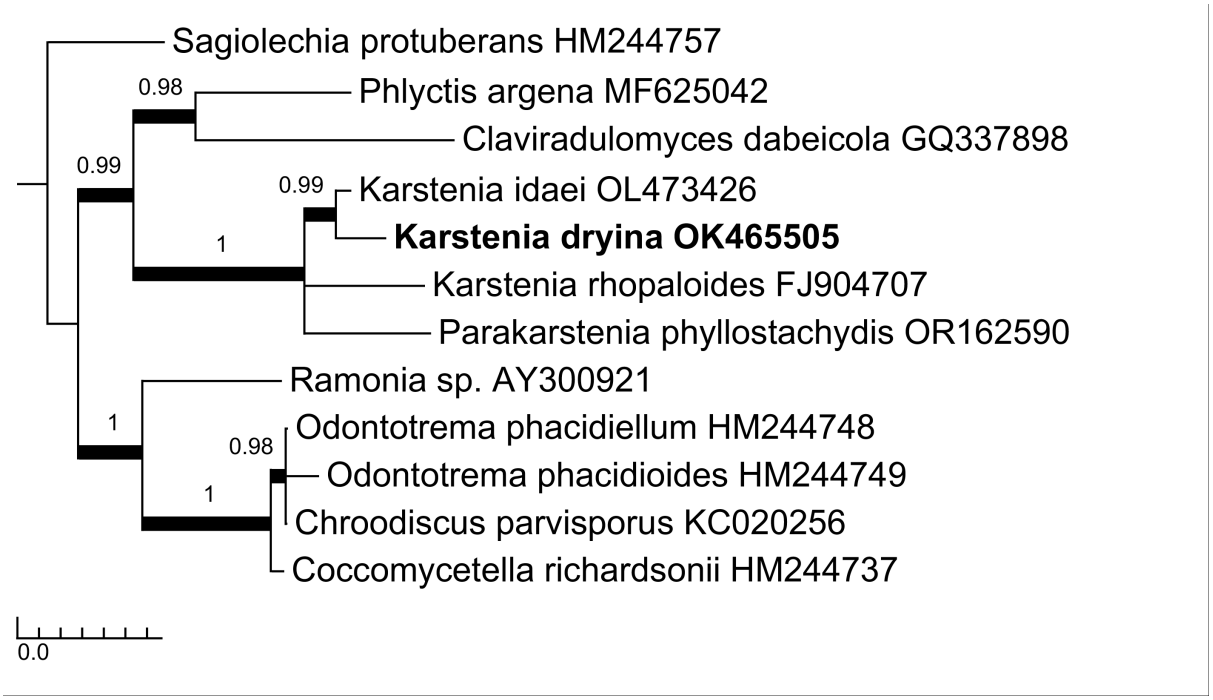
Supplementary Figure 5. MtSSU tree with *Biatorella ligni-putridi* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 10,000 generations.



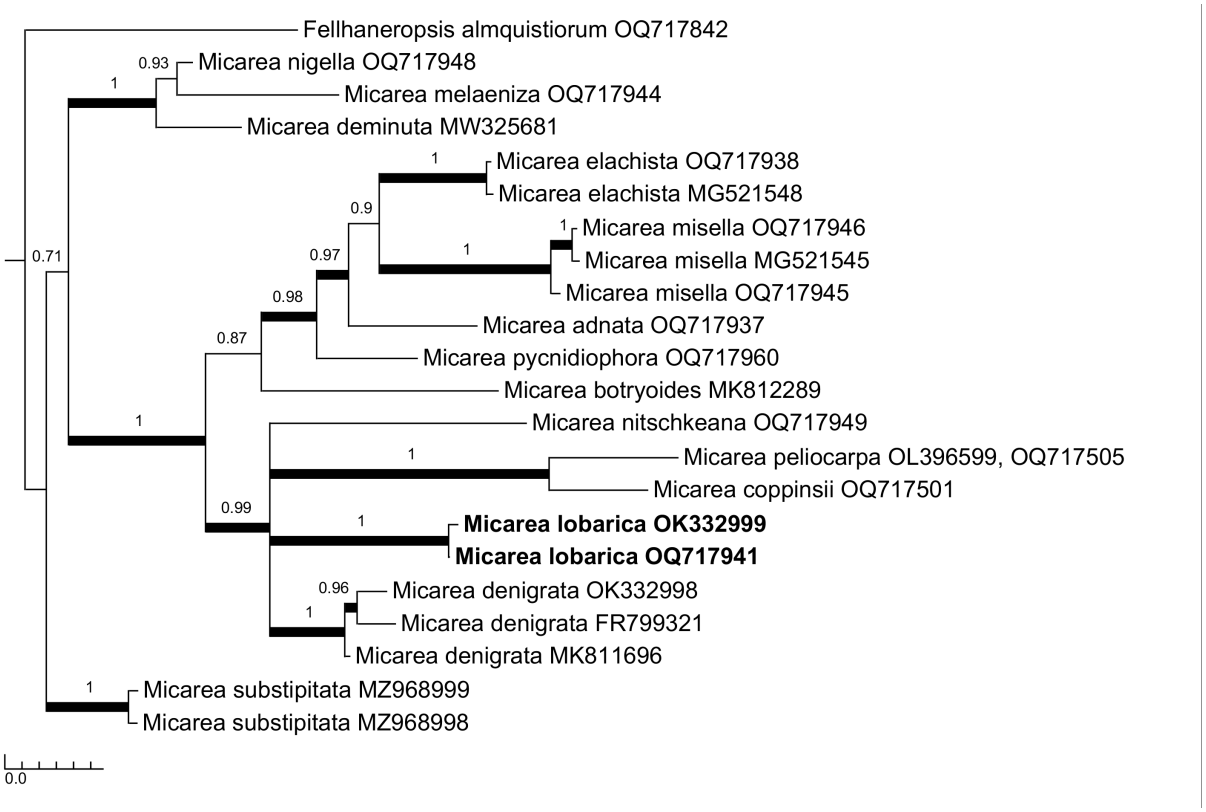
Supplementary Figure 6. ITS tree with *Cryptodiscus neglectus* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 146,000 generations.



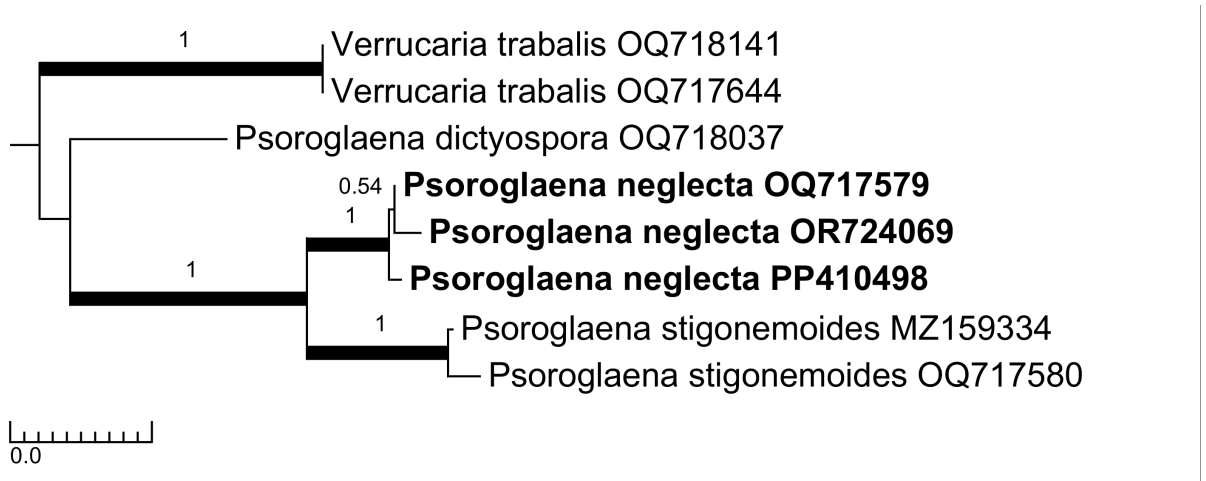
Supplementary Figure 7. MtSSU tree with *Cryptodiscus neglectus* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 104,000 generations.



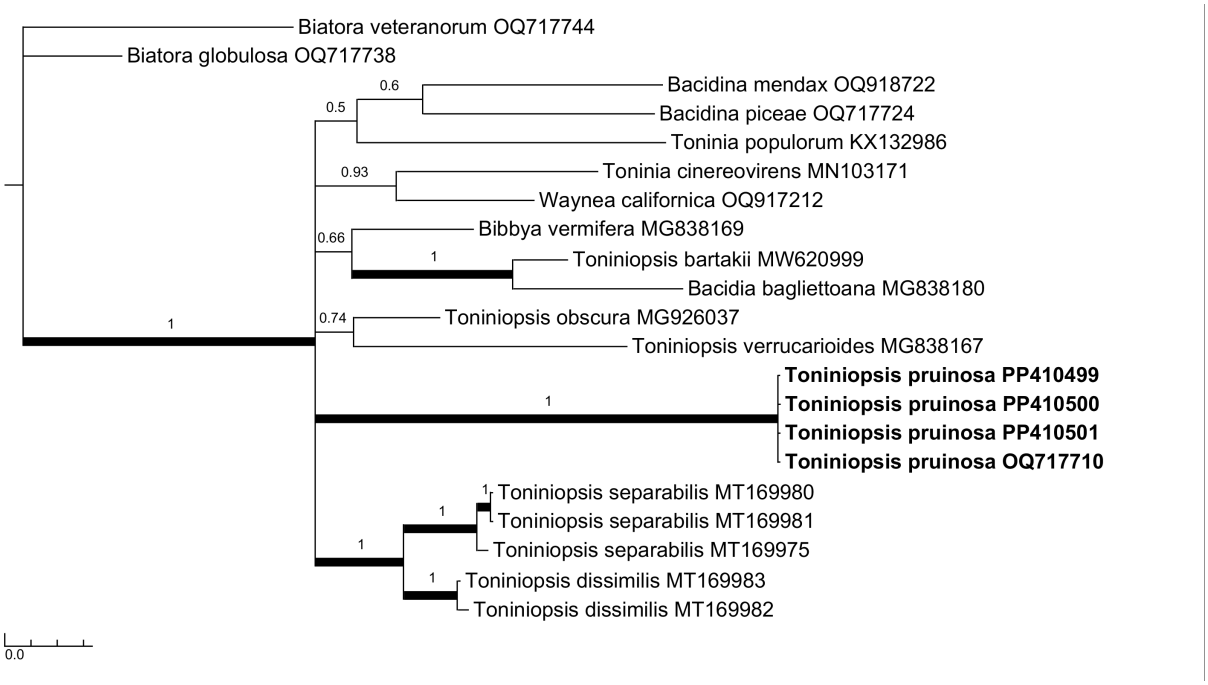
Supplementary Figure 8. MtSSU tree with *Karstenia dryina* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 18,000 generations.



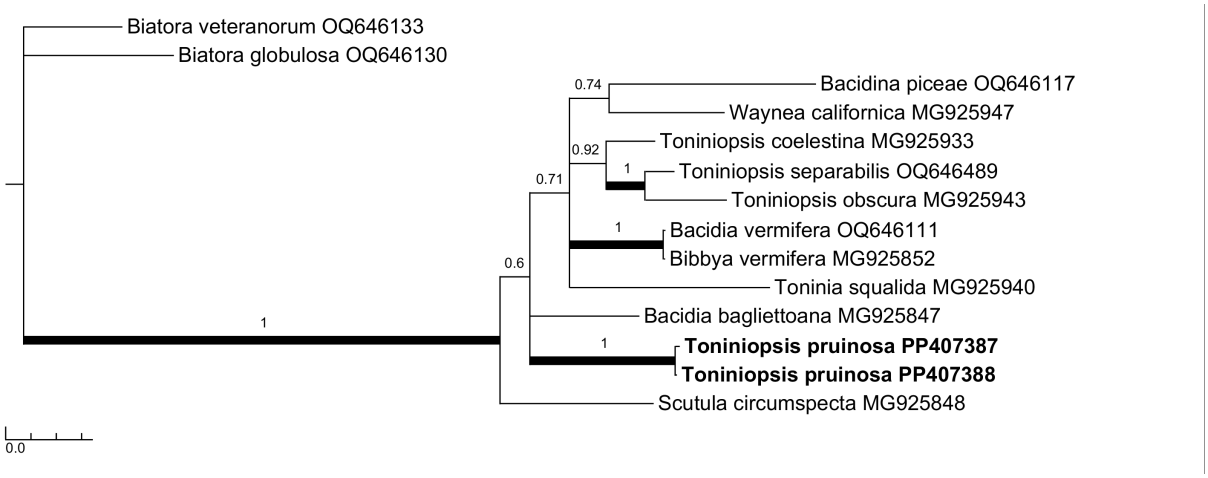
Supplementary Figure 9. ITS tree with *Micarea lobarica* and related species. GTR model with gamma distribution used as a model of sequence evolution. Tree constructed using Bayesian inference run for 78,000 generations.



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.