Bog ecosystems: Playgrounds for plant–microbe coevolution

Wisnu Adi Wicaksono

Tomislav Cernava

Christian Berg

Gabriele Berg

Video Byte

Keywords: bog ecosystems, bryophytes, vascular plants, Microbiome, coevolution, evolution, microbes, microbiota, bog, ecology, shotgun metagenomics, metagenome-assembled genome (MAG), Betaproteobacteria, Actinobacteria, bacteria, plant–microbe interaction, carbon fixation, bacterial richness, bacterial diversity, functional specification

Posted Date: October 13th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-967278/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

Bogs are unique ecosystems, which have important ecological functions in carbon storage, climate stability, water quality, and biodiversity. The bog microbiome, composed mostly of bacteria that live in association with bog plants, plays key roles in these functions. However, the differences in associated bacteria between vascular plants and the non-vascular bryophytes that predominate in bogs remain unclear. Researchers recently used shotgun metagenomics to investigate the microbes associated with 12 representative bog species. Vascular plants tended to be colonized by specific bacteria, while bryophytes exhibited greater bacterial species richness and diversity. The two plant groups also had different marker species. The gene profiles of vascular plant- and bryophyte-associated microbes revealed functional differences, including differences in nitrogen cycling. More detailed analyses of metagenome-assembled genomes (MAGs) highlighted the major bacterial phylogenetic groups and their functions and revealed the presence of novel Betaproteobacteria and Actinobacteria capable of RuBisCo-mediated carbon fixation, as well as potentially pathogenic bacteria that harbored virulence genes. Although further research is needed to determine the mechanisms behind these findings, the results reveal that evolutionarily distinct bog plants are home to distinct communities of bacteria and emphasize the roles of bog ecosystems as playgrounds for plant-microbe coevolution.