Phylosymbiosis in the Microcystis microbiome

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Abstract

Cyanobacteria blooms in freshwater ecosystems are difficult to predict and can be harmful to humans and animals. Microcystis is a genus of cyanobacteria that can cause these toxic blooms. They form close associations with heterotrophic bacteria - their microbiome, but the details of these associations are not well understood. To examine this relationship, researchers characterized the genetic diversity of over 100 Microcystis colonies. They identified 18 distinct Microcystis genotypes. The genetic diversity was greater between colonies than within them, suggesting that Microcystis forms colonies via clonal expansion. Each Microcystis genotype had its own microbiome composition and related genotypes had similar microbiomes. Two of the nine most prevalent colony-associated bacteria genera, Roseomonas and Rhodobacter, showed strong signs of co-phylogeny with Microcystis. These closely associated bacteria may be expanding the metabolic capabilities of Microcystis. Other colony-associated bacteria had weaker signs of co-phylogeny, but stronger evidence of horizontal gene transfer with Microcystis. This study expands the known genetic diversity of Microcystis and suggests that there are strong interactions between Microcystis and its microbiome. However more research is needed to determine the details and nature of these interactions.