Functional Genomics of Moss-Cyanobacteria Interactions in Boreal Forest Ecosystems

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Abstract: Boreal forests are important ecosystems involved in global carbon cycling. The nitrogen cycling in these ecosystems is largely determined by feather moss-associated cyanobacteria that fix the majority of nitrogen flowing into boreal ecosystems. Because carbon cycling is dependent upon availability of fixed nitrogen, the interaction between the cyanobacteria and the mosses greatly affect the productivity of this ecosystem. The proposed work seeks greater understanding of the genetic diversity of the cyanobacteria associated with the mosses and the biochemical signals exchanged between the host and the cyanobacteria during establishment of nitrogen-fixing associations. Coupled genomics, transcriptomics, and proteomics will be used to characterize this feather moss-cyanobacteria association. We will use an experimental setup that allows for communication between the moss and cyanobacterial partners without colonization. This novel setup allows the initial signaling phase to be differentiated from the subsequent establishment phase of the interaction. Cyanobacterial strains that are able to form associations will be compared to strains that are not able to form nitrogen-fixing associations. The resulting comparisons will identify many genes that are up- or down-regulated during the signaling and establishment phases of the association. To add the power of genetics to the 'omics approach, we propose to utilize JGI's DNA synthesis capacity to assemble gene knockout cassettes that will enable genetic analysis of candidate cyanobacterial genes that may affect the outcome of a successful moss-cyanobacteria association. The result of this project will be a functional genomic model of both the moss and cyanobacteria with detailed information on the genetic control of this critical ecosystem function.