Bio-Scales Pilot Project: Defining gene function and its connection to ecosystem processes

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Project Goals: The Bio-Scales Pilot Project focuses on understanding how genes influence traits and ecosystem-level processes. Initial efforts examine specific combinations of host and microbial traits that influence nitrogen transformation patterns and fluxes across the coupled plant-soil-microbial system and consists of two objectives. In our first objective, we will sample a subset of *Populus* genotypes with differential phenotypes related to N transformation and biomass production, sequence their associated microbiomes (in collaboration with the Joint Genome Institute), and collect environmental metadata. Our second objective is to prepare data and metadata for integration and analysis using the National Microbiome Data Collaborative and other tools and approaches (e.g., GWAS, network analysis) to predict how plant traits influence soil microbiome functions and how together the plant and the microbiome modify ecosystem processes.

The new Bio-Scales pilot project aims to rapidly determine gene functions and traits and how they scale to influence ecosystem-level processes. Our current work hypothesizes that specific combinations of host and microbial traits influence rhizosphere elemental cycling patterns and fluxes across the coupled plant-soil-microbial system, and that these transformations will have important ramifications for nutrient cycling and availability with the rhizosphere. Key plant chemical traits that influence the plant microbiome, rhizosphere biogeochemical processes, and subsequent rhizophere nitrogen cycling are being examined. Using *Populus* as a model host system, we are assessing key plant genotypic traits known to influence nitrifying and denitrifying microbial activity across a genome-wide association mapping study population. The three plant chemotypic traits initially targeted involve production of alpha-linolenic acid, para-coumeric acid and ferulic acid, that are hypothesized to influence rhizospheric microbial communities and activities leading to altered N cycle transformations. Target plant genotypes with high and low expression levels for these secondary metabolites, as well as rhizosphere and bulk soils, were collected in Oregon in the fall of 2020. Metagenomic analyses of soil and root microbiomes, plant transcriptomics, and metabolomics datasets are being generated in collaboration with the Joint Genome Institute (JGI) to be integrated together with soil environmental metadata and used to identify the effects of these host-microbiome-environment relationships. The resulting data and metadata in our study will be produced in collaboration with the National Microbiome Data Collaborative (NMDC) to generate a highly integrated microbiome data set with rich and validated metadata. This high-dimensional dataset will formalize how to collect and curate field microbiome data related to nutrient cycling; provide a data set from which to build predictive models of gene function within a plant microbiome; and illustrate the Bio-Scales concept of determining how gene functions scales across biological systems and influences broader ecosystem properties and processes.