

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

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Project Goals: The Bio-Scales project focuses on understanding how genes influence traits and ecosystem-level processes. Our initial use case examines 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 are sampling a subset of *Populus* genotypes with differential phenotypes related to N transformation and biomass production, characterizing their associated microbiomes using multi-omic approaches (in collaboration with the Joint Genome Institute), and collecting extensive environmental metadata. An important second objective is to prepare data and metadata for integration and analysis using the National Microbiome Data Collaborative, KBase and other tools and approaches (e.g., GWAS, network analysis).

The Bio-Scales project aims to rapidly determine gene functions and traits and how they scale to influence ecosystem-level processes. A current use case hypothesizes that specific combinations of plant 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 within the rhizosphere. Key plant chemical traits that influence the plant microbiome, rhizosphere biogeochemical processes, and subsequent rhizosphere 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 from two field study sites near Corvallis and Clatskanie Oregon. 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. Metagenomic and biogeochemical data on nitrification and denitrification capacity of the soils collected and analyzed to date show that the effects of tree genotypic and chemotypic *Populus* traits scale differently across the two study sites analyzed, and that these data are related to overall nitrogen pools, nitrification and denitrification potential, and overall site soil characteristics.

The data and metadata resulting from the use case above have been developed 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 dataset 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.

Our next step in Bio-Scales will integrate data from the Advanced Plant Phenotyping Laboratory (APPL) and continue our focus on rigorous data management. APPL is capable of growing up to 500 plants on a conveyor system that advances individual plants through a suite of imaging technologies. These images include a 3D point cloud along with 2D chlorophyll fluorescence imaging, hyperspectral imaging and more. The hyperspectral images are known to vary by plant chemotype, and our goal will be to observe chemotypic differences among plants based on their chemotype and nitrogen uptake ability. The APPL Public Interface (or APPL-PI) will be developed to host data for our Bio-Scales use case and other APPL experiments.

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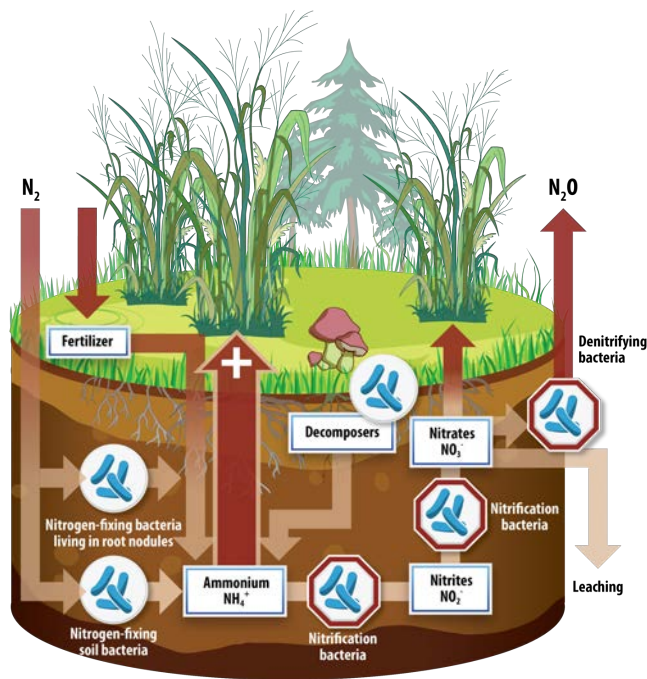


Fig 1. Conceptual illustration of the Bio-Scales concept to understand how plant chemotypic traits may influence rhizosphere biological nitrification and denitrification processes and microbiomes, and how these in turn may feedback to affect plant N availability and other critical ecosystem N cycle processes.