Metabolic modeling of a rhizosphere microbial community

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Project Goals:

The goal of this project is to integrate novel systems biology-based tools and genome-scale metabolic modeling with laboratory ecosystems (EcoFABs), plant genetics, and integrated field trials to gain insights into the dynamic plant-microbe interactions governing nitrogen exchange to improve plant productivity in marginal soils. The vast complexity of plant-microbe interactions and their dynamic nature renders elucidation of the underlying mechanisms of these interactions. Thus, we are developing a predictive metabolic model of plant root and rhizosphere community to guide experimental designs and generate hypotheses that are then tested in laboratory and field studies.

Abstract:

Genome-scale metabolic models for microorganisms derived from the rhizosphere can be employed as a framework to unravel microbe-microbe and host-microbe interactions. Here, we present manually-curated genome-scale metabolic models for 17 bacteria of the rhizosphere. These bacteria were isolated from switchgrass rhizospheres, and represent dominant members commonly found in the rhizosphere of grasses belonging to the genera *Arthrobacter, Bacillus, Bosea, Bradyrhizobium, Brevibacillus, Burkholderia, Chitinophaga, Lysobacter, Methylobacterium, Mucilaginibacter, Mycobacterium, Niastella, Paenibacillus, Rhizobium, Rhodococcus, Sphingomonas,* and *Variovorax.* Genome-scale models were generated using standard pipelines developed by our lab. Collectively, the models incorporate 3,877 reactions (including exchange reactions that represent uptake and secretion of metabolites) and 2,663 metabolites. Moreover, the individual metabolic models contain 790 to 1,788 genes, covering 15% to 30% of all functionally annotated genes in these microbial genomes. All models were manually curated using information based on literature and public databases, such as KEGG, modelSEED, MetaCyc, UniProt, BRENDA, IntEnz, TCDB, and TransportDB. The curation resulted in the removal of 271 genes and 21 reactions from the models on average, while 131 new genes and 3 new reactions were introduced into the models during curation. We simulated these models on 95 different carbon sources and compared predicted phenotypes with experimental measurements. This practice helped to validate the prediction capabilities of these models and provided information on pathways absent in the models. Subsequent gap-filling added 288 new reactions to the models. We are currently validating growth predictions under hundreds of different conditions experimentally. Collectively, the study will lay the foundation to

advance our understanding of dynamic plant-microbe interactions in the rhizosphere and how these interactions contribute to nitrogen use efficiency.

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