Coordination of species roles during chitin decomposition in a model soil microbial consortium

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Project Goals: PNNL's Phenotypic Response of Soil Microbiomes SFA aims to achieve a systems-level understanding of the soil microbiome's phenotypic response to changing moisture. We perform multi-scale examinations of molecular and ecological interactions occurring within and between members of microbial consortia during organic carbon decomposition, using chitin as a model compound. Integrated experiments address spatial and inter-kingdom interactions among bacteria, fungi viruses and plants that regulate community functions throughout the soil profile. Data are used to parametrize individual- and population-based models for predicting interspecies and inter-kingdom interactions. Predictions are tested in lab and field experiments to reveal individual and community microbial phenotypes. Knowledge gained provides fundamental understanding of how soil microbes interact to decompose organic carbon and enable prediction of how biochemical reaction networks shift in response to changing moisture regimes.

Abstract: Soil microorganisms are the drivers underpinning key ecological functions, including plant growth promotion and nutrient cycling. These important processes rely on metabolic interactions between individual populations of the soil microbiome. Despite the importance of microbial interaction networks to the emergent properties of decomposition and nutrient cycling, the complexity of soil makes analysis and data interpretation difficult. Here, we focused on a simplified, defined, and representative community of eight bacterial species, MSC-2, as they interact to metabolize chitin, an abundant carbon source in soil.

Using a multi-omics approach we show that both species and community level processes during chitin decomposition were distinct when comparing monocultures of individual members to co-culture growth of the complete MSC-2 community. In addition, emergent properties of both specific species and the community were found. While certain members of MSC-2 showed poor growth on chitin in monoculture our metabolomic and metatranscriptomic analysis suggests that

these same species, when cultured within the context of the complete MSC-2 community, contribute to chitin metabolism. The dominant metabolically active members within MSC-2 were further evaluated to determine their specific roles during chitin breakdown. Intriguingly, the most highly abundant members of MSC-2 were not those that could metabolize chitin, but rather those that could grow best on the resulting breakdown products. The use of multi-omics also allowed us to map the path of chitin through this community, assigning certain species to certain steps of chitin breakdown. This mapping revealed which taxa are critical to different aspects of chitin breakdown and revealed how, in environments where chitin is a major nutrient source, carbon cycling could be disrupted through the loss of certain taxa.

This study not only greatly increased knowledge of how chitin is metabolized by soil microbial communities, but also provided new details underpinning interspecies interactions that are key to global carbon and nitrogen cycling in soil. These conclusions will be critical to our understanding of how native soil microbiomes process C sources, especially those such as chitin that drive interactions and metabolite sharing, and how these processes may shift as community membership changes as a function of both biotic and abiotic pressures. Application of these conclusions to the native soil microbiome will greatly expand our ability to identify what the keystone species are, who may have the greatest advantage for growth and how these communities are organized to promote C cycling in natural settings.

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