

Corrinoids as model nutrients to probe microbial interactions in a soil ecosystem

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Project Goals: The overall goal of this research is to gain a deeper understanding of the microbial interactions that drive soil community structure. This research leverages a model group of key metabolites related to vitamin B₁₂, known as corrinoids, to investigate microbial interactions. Corrinoids are a structurally diverse nutrient class shared between different bacterial species, as they are produced by only a subset of the bacteria that use them. Based on the inherent specificity of bacteria for particular corrinoids, the hypothesis driving this work is that corrinoids are keystone nutrients in shaping soil microbial communities. To test this hypothesis, we will examine the effects of corrinoid addition on community composition and function across multiple levels of complexity. By investigating cycling of a key nutrient in soil at levels spanning the whole community to individual isolates, this work will gain an unprecedented view of metabolic interactions in a soil microbial community.

Microbial communities in soil are key drivers of biogeochemical cycling and plant growth. Current research methods in soil microbial ecology cannot simultaneously analyze all microbe-microbe interactions in situ, making it difficult to identify keystone interactions that could predictably modulate these communities. We aim to overcome this limitation by focusing on corrinoids, a group of structurally diverse metabolites used by a majority of the community. Exemplified by its flagship member, Vitamin B₁₂, corrinoids are essential cofactors produced only by a fraction of the bacteria that use them, and thus are shared metabolites. However, in contrast to many other essential cofactors, over a dozen different structural forms of corrinoids exist, and different groups of bacteria require different corrinoids for metabolic needs that play central roles in bioremediation, plant-bacteria symbiosis, organic matter accumulation, and elemental cycling. Here, we test the hypothesis that corrinoids are a key nutrient family in soil microbial ecosystems. We show that a significant number of bacteria are corrinoid-dependent by performing a pilot phenotype-guided isolation of corrinoid-dependent bacteria from soil. Furthermore, we demonstrate that a bioinformatics-to-experiment pipeline can rapidly predict and verify the corrinoid production capacity of soil isolates.

These results are being used to guide corrinoid-based perturbations of soil samples and soil-derived enrichment cultures. We expect that providing excess corrinoid will remove corrinoid

synthesis or availability as a barrier to growth, leading to increased abundance of microbes capable of using the added corrinoid. At the same time, growth of microbes incapable of using the added corrinoid should decrease if the corrinoid interferes with metabolism. These corrinoid-induced changes in the community could potentiate other metabolic networks, leading to differences in the growth of community members that are not directly affected by the corrinoid amendment. Our proposed holistic approach to understanding corrinoid cycling in soil addresses a key issue in soil microbial ecology, namely that soil is too complex to simultaneously understand all microbe-microbe interactions in a whole-community context and the metabolites involved in those interactions. However, by focusing on one key shared, yet structurally diverse, metabolite used by a majority of the community, we can pinpoint key interactions for further study.

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