Harnessing Metagenomic Stable Isotope Probing to Uncover the Carbon Cycling Capacity of Soil Microbes

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Project goals: We aim to recover metagenome assembled genomes of bacteria active in soil carbon cycling by enriching for isotopically labeled DNA from ^{13}C-labeled substrate treated soils with metagenomic-SIP. The goal of this project is to investigate these genomes for signatures of bacterial life history strategies that drive dynamic function in soil carbon cycling.

Soil dwelling microorganisms are an essential part of soil carbon cycling yet their biology and ecology are still poorly understood. There is a lack of representative, cultured isolates from this system and diverse, high-quality genomes are only now being recovered from large metagenome studies. DNA-stable isotope probing (DNA-SIP) has recently allowed us to more thoroughly explore the ecology of bacteria active in the soil carbon cycle. Previously, we ran a high-resolution DNA-SIP experiment to characterize bacteria involved in breaking down nine chemically distinct carbon substrates mimicking natural components of plant litter. By analyzing ^{13}C-labeling patterns of community members over 48 days, we uncovered discrete ecological groups which we believe define important life history strategies. We hypothesize that these ecological groups have distinct genome characteristics explaining their carbon assimilation dynamics.

To elucidate the biology behind these ecological groups and better understand their functional potential, we performed metagenomic-SIP on a subset of samples. Metagenomic-SIP enriches for isotopically labeled genomic DNA from treated environmental samples and has been shown to improve assembly and binning of ^{13}C-labeled genomes from diverse communities. Preliminary analysis indicates that metagenomes were enriched for taxonomic groups corresponding to ^{13}C-labeled OTUs. For example, we observed an enrichment of genes from the *Verrucomicrobia* genus *Chthoniobacter*, a prominent assimilator of carbohydrates, with few cultured representatives. By comparing abundance of COG orthologues between ^{13}C-treatment and ^{12}C-control samples, we also observed substrate and timepoint specific enrichment of relevant gene categories and pathways. For instance, cell mobility genes were highly enriched in early timepoint samples but less so in later timepoints. Similarly, mobile elements including prophages and transposons were enriched in early timepoint samples and those treated with highly labile substrates. We further found characteristic enrichment of CAZy-classified glycoside hydrolases families across samples. Through assembly and binning of metagenome assembled genomes (MAGs) we aim to further identify genomic signatures of life history strategies important to soil carbon cycling. This study is part of ongoing research with the goal of unearthing the role of the soil microbial community in global carbon cycling.

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