



The “Who” and “How” of Microbial Control over Soil Carbon Dynamics: The Genomic Basis of Soil Microbial Efficiency

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Soil microorganisms are the engines of organic matter cycling in soils. The growth, turnover and efficiency of soil microbes are important controls of organic matter decay and soil C storage. The amount of soil organic matter lost through decomposition is a consequence of tradeoffs between microbial growth rate and carbon use efficiency (CUE; the fraction of assimilated C a microbe incorporates into new biomass). Yet how microbial growth, turnover, and CUE respond to environmental factors is still poorly understood. The genetic basis of microbial growth and efficiency is particularly underexplored. The goals of our research were to (1) define the genes, metabolic pathways, and phylogenetic signals associated with microbial efficiency that drive soil microbial community responses to key global change drivers, and (2) improve predictions of soil C by incorporating genomics-informed microbial efficiency data into ecosystem C models. We isolated a phylogenetically diverse group of microbial taxa (bacteria and fungi) from a temperate forest soil and performed whole-genome sequencing on all taxa. We then measured CUE across all taxa in response to differing temperature and N availability. Carbon use efficiency generally declined with increasing temperature, but the direction and degree of response was species dependent. CUE did not respond to altered N availability. There was a phylogenetic signal for CUE for soil fungi, with fungal phyla showing average efficiencies in the order of Ascomycota (0.86) > Basidiomycota (0.71) > Mucoromycotina (0.59). rRNA copy number was significantly negatively correlated with CUE, while significant genomic predictors of CUE included lipid biosynthesis, carboxylic acid biosynthesis, and sporulation-related genes. We are incorporating our physiological and genome-informed results into the MIMICS soil biogeochemical model. Preliminary modeling results will be discussed.