

The biogeographic distribution of genomic traits between soil microbial communities

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Project Goals: Microorganisms play key roles in soil carbon turnover and stabilization of persistent organic matter via their metabolic activities, cellular biochemistry, and extracellular products. Microbial residues are the primary ingredients in soil organic matter (SOM), a pool critical to Earth's soil health and climate. We hypothesize that microbial cellular-chemistry, functional potential, and ecophysiology fundamentally shape soil carbon persistence, and are characterizing this via stable isotope probing (SIP) of genome-resolved metagenomes and viromes. We focus on soil moisture as a 'master controller' of microbial activity and mortality, since altered precipitation regimes are predicted across the temperate U.S. Our SFA's ultimate goal is to determine how microbial soil ecophysiology, population dynamics, and microbe-mineral-organic matter interactions regulate the persistence of microbial residues under changing moisture regimes.

Abstract:

Linking microbial communities to broad ecosystem scale processes is a central focus in microbial ecology. Here, we analyzed over 500 metagenomes to examine how fundamental microbial characteristics relate to environmental parameters, primarily in soil microbial communities. Our study combines traditional statistical analyses and a machine-learning approach to determine the environmental factors which most strongly control the genomic traits in soil microbial communities. This work provides valuable insight into the forces dictating microbial life-strategies in soil, which could assist in determining the environmental services soil microbes may provide.

Environmental conditions exert selective pressure on bacteria in microbial communities, and these pressures are often exhibited in the genomic traits of these bacteria. Traits such as genome size, GC content, and amino acid and codon frequency can lend valuable insight into the relationship between environment pressures and bacterial life-strategy [1]. For example, bacteria in nutrient limited environments often exhibit smaller genomes in order to curb the cost of reproduction, and lower GC content in order to conserve nitrogen (as the GC base pair has a higher nitrogen content than the AT base pair) [2]. While genomic traits could be used in the assessment of microbial communities across broad scales, little work has been done to examine how genomic traits are distributed among different environments. Further, the factors which

shape traits in soil microbial communities remains especially understudied. Here we present findings from two studies which look at the distribution of genomic traits between microbial communities. In the first, we compared 100+ publicly available metagenomes from the Joint Genome Institute [3] which were collected from soils, oceans, animal microbiomes, and hot springs, to evaluate how genomic traits were distributed across fundamentally different systems. We found that the relationships between genomic traits were unique among these different ecosystems and notably, that the relationship between the GC content and average genome size of communities was different between soil and marine environments. The GC content and average genome size of ocean microbial communities were positively correlated—consistent with results from previous studies examining individual bacteria taxa. However, in soils we found that larger genomes demonstrated comparatively lower GC content, indicating that a different set of environmental constraints are dictating the traits of soil bacteria. In our second study we examined this relationship more closely and compared the genomic traits of soil microbial communities across 400 metagenomes and assessed how these traits were related to numerous environmental parameters. These data, accessed from the National Ecological Observation Networks [4], showed that the genomic traits of soil bacteria were most closely related to pH. In low pH soils, soil microbial communities tended to have larger genomes with a lower GC content, and communities in high pH soils often had smaller genomes with higher GC content. We suggest that this reflects the several environmental parameters which are reflected in soil pH, specifically: soil carbon to nitrogen ratios, moisture availability, and physiological stress.

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