

Physiological adaptations of leaf litter microbial communities to drought reduce decomposition rates

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Project Goals: Predictions of carbon cycle processes under environmental change are highly uncertain. Integration of molecular data with process rate measurements remains a challenge, thereby making it difficult to link microbial diversity and carbon cycling processes. We aim to uncover the genomic and cellular mechanisms that underlie microbial traits important for carbon cycling under drought. Traits related to drought tolerance, resource acquisition, and growth yield will be measured with molecular and biochemical approaches. In addition, we will quantify the consequences of these tradeoffs for litter carbon loss. The goal is to implement modeling approaches that use trait relationships as a mechanistic basis for predicting how microbial communities and carbon cycling processes will respond to drought, a critical environmental change driver.

Drought is known to reduce organic matter decomposition in terrestrial ecosystems by causing a decline in microbial growth. This decline is partially attributed to increased microbial investment in physiological adaptations to tolerate or avoid drought stress. However, we still lack a detailed understanding of the stress adaptations that enable microbial decomposers to survive and thrive in such environments. Here we present metatranscriptomic and metabolomic insights into the physiological response of *in situ* plant leaf litter microbial communities to long term drought and pulse wetting in Californian grass and shrub ecosystems. Litter bags with native litter were deployed mid-summer and *in situ* wetting was performed at the end of the dry season to simulate commencement of seasonal precipitation. Legacy of reduced precipitation (long-term simulated drought treatments) leads to decreased decomposition rates in grass but not in shrub litter, and overall decomposition rates were higher in grass than shrub litter. Taxonomic and functional responses of active communities to pulse wetting and subsequent drying were smaller compared to the legacy effect of drought and vegetation type. Fungi dominated both litter communities. In shrub communities, functional diversity was higher than in grass communities but there were only small differences in gene expression profiles in response to either pulse wetting or long-term drought treatment. However, in grassland drought and ambient communities had significantly distinct functional profiles, and genes for membrane transporters and flagellar motility were upregulated in response to wetting while those coding for biomolecular repair were downregulated. The most significant discernable physiological adaptations to drought across both litter

communities were production or uptake of various compatible solutes like trehalose and ectoine as well as inorganic ions to maintain cellular osmotic balance. Drought communities also increased expression of genes for capsular and extracellular polymeric substance synthesis possibly as a mechanism to retain water. The magnitude of stress tolerance traits was much bigger in grass than shrub communities. These stress adaptations highlight the metabolic tradeoffs with growth that lead to reduced decomposition under drought, thereby directly linking microbial physiology to ecosystem function.

Figure: Impact of drought legacy on microbial physiology. Frequency of significant transcript indicators in the upper level functional groups (level 1 in KEGG Subsystems classification). These indicators were unique to communities in either ambient or reduced precipitation treatments across both grass and shrub litter types and therefore represent global functional indicators of drought or control ecosystems.

