Studying Microbial Stress Responses in Soil Ecosystems

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Project goal: Using metatranscriptomics, characterize the community response to temperature and resource limitation. This is part of the broader project goal of studying how growth, death, and C use efficiency of individual microbial taxa and whole communities is affected by temperature and changes in substrate availability and regulates whole community and ecosystem responses to changes in temperature.

Introduction: The overall project goal is to relate changes of growth, death and C use efficiency of individual microbial taxa in response to temperature to whole community and ecosystem responses. As part of this overall goal, we will study the response of gene-expression to temperature stress and resource limitation.

In vitro pure culture studies have demonstrated that, when substrate availability falls below or temperature rises above a critical level, microbial cells respond with alterations in gene-expression. These responses have been observed for different taxa, and the responsible genes, sigma factors, transcription factors and regulators, are distributed widely across the bacterial domain. We propose to study the effects of temperature stress and resource limitation in real, complex and diverse soil ecosystems.

Results: Preliminary work was done comparing microbial communities in a litter layer and mineral soil, a marsh sediment, and a marine community (Wemheuer et al 2015). Our analysis focused on sigma factors, transcription factors and regulators that control gene-expression.
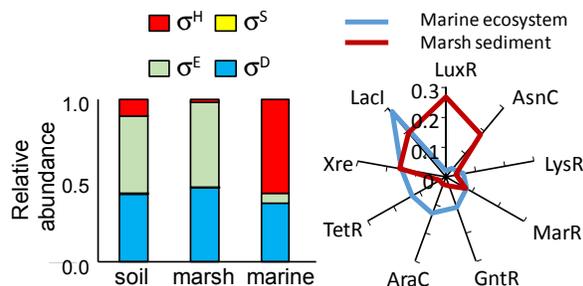
Our findings show that

Fig. 1. Relative transcript abundance of sigma factors and main transcription factor and regulator families for a soil (Paul Dijkstra and Petr Baldrian, unpublished results), marsh (Paul Dijkstra and Galya Orr, unpublished results), and marine ecosystem (Wemheuer et al., 2015). Note the low abundance of transcripts for σ^S in soil, while no σ^S transcripts were observed in marsh and marine ecosystems.

Fig. 2. Transcription factors and regulators in mineral soil and litter layer of a Bohemian Norway spruce forest (Žifčáková et al., 2016) for Acidobacteria and alpha-Proteobacteria (Paul Dijkstra and Petr Baldrian, unpublished results). A shared set of transcription factors and regulators were sorted from high to low abundance in Acidobacteria (soil).
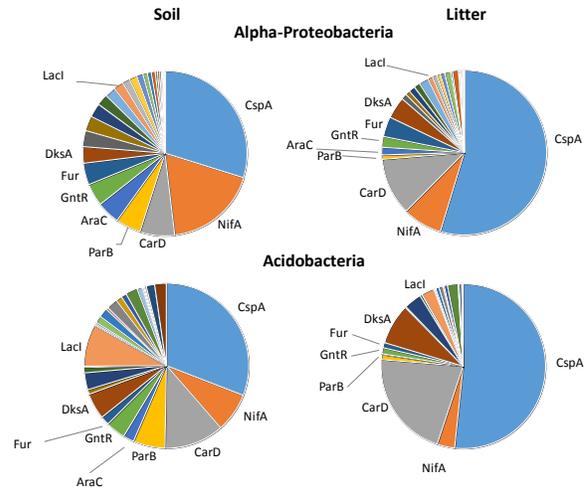
1- Many of the known sigma factors, transcription factors and regulators, responsible for active growth and responses to stress are observed in metatranscriptomes (Fig. 1). For example, sigma D (σ^D), the sigma factor responsible for gene-expression during active growth, is found in all environmental samples, and individual taxa within each community (Fig. 1, 2).

2- The relative abundance of sigma factors, transcription factors and regulators differs between a mineral soil, marsh sediment and marine ecosystem (Fig. 1). For example, sigma H (σ^H), the sigma factor controlling gene-expression under heat stress, was much higher in the marine than in soil or marsh ecosystems. Similar differences are observed for transcription factors and regulators (Fig. 1B). The low abundance of sigma S (σ^S), the general stress sigma factor and involved in the starvation response, contradicts the paradigm that microbes in soil are C-starved.

3- Within the same community, individual microbial taxa can differ in the relative abundance of sigma factors, transcription factors and regulators. For example, Acidobacteria in mineral soil and marsh sediment have high levels of sigma E (σ^E), an indication of extracellular or envelop stress. At the same time, different microbial taxa respond similarly to (long-term) changes in their environment. For example, Acidobacteria and alpha-proteobacteria decrease the relative abundance of NifA, but increase the abundance of CarD and CspA.

Conclusion

Many of the regulators of gene-expression can be recognized in metatranscriptomes and are a rich source of information to understand responses of individual taxa and entire communities to environmental change. Research thus far has been focused on comparing ecosystems which may be characterized by parallel changes in gene abundance and gene-expression. Changes in gene-expression, as a response to altered environment, are likely most important over the short term, while changes in gene abundance is more important in the long-term. This project aims to determine the dynamics of gene-abundance versus gene-expression, and its effect on growth and death and C use efficiency of individual microbial taxa and entire community activities. The data will also be used to study the regulons, that is the genes that are controlled by the sigma factors, transcription factors and regulators, for entire communities and individual taxa. Finally, this dataset will be used to describe the ecological responses to temperature and C availability. For example, we will study the transcript abundances of ecologically relevant processes such as motility, chemotaxis, dormancy and microbe-microbe interactions.