

Using a trait-based approach to link microbial community composition and functioning to soil salinity

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Our knowledge of the dynamics structuring microbial communities and the consequences this has for soil functions is rudimentary. In particular, predictions of the response of microbial communities to environmental change and the implications for associated ecosystem processes remain elusive. Understanding how environmental factors structure microbial communities and regulate the functions they perform is key to a mechanistic understanding of how biogeochemical cycles respond to environmental change.

Soil salinization is an agricultural problem in many parts of the world. The activity of soil microorganisms is reduced in saline soils compared to non-saline soil. However, soil salinity often co-varies with other factors, making it difficult to assign responses of microbial communities to direct effects of salinity. A trait-based approach allows us to connect the environmental factor salinity with the responses of microbial community composition and functioning. Salinity along a salinity gradient serves as a filter for the community trait distribution of salt tolerance, selecting for higher salt tolerance at more saline sites. This trait-environment relationship can be used to predict responses of microbial communities to environmental change.

Our aims were to (i) use salinity along natural salinity gradients as an environmental filter, and (ii) link the resulting filtered trait-distributions of the communities (the trait being salt tolerance) to the community composition.

Soil samples were obtained from two replicated salinity gradients along an Australian salt lake, spanning a wide range of soil salinities (0.1 dS m^{-1} to $>50 \text{ dS m}^{-1}$). In one of the two gradients salinity was correlated with pH. Community trait distributions for salt tolerance were assessed by establishing dose-dependences for extracted bacterial communities using growth rate assays. In addition, functional parameters were measured along the salt gradients. Community composition of sites was compared through 16S rRNA gene amplicon sequencing.

Microbial community composition changed greatly along the salinity gradients. Using the salt-tolerance assessments to estimate bacterial trait-distributions we could determine substantial differences in tolerance to salt revealing a strong causal connection between environment and trait distributions. By constraining the community composition with salinity tolerance in ordinations, we could assign which community differences were directly due to a shift in community trait distributions. These analyses revealed that a substantial part (up to 30%) of the community composition differences were directly driven by environmental salt concentrations. Even though communities in saline soils had trait-distributions aligned to their environment, their performance (respiration, growth rates) was lower than those in non-saline soils and remained low even after input of organic material.

Using a trait-based approach we could connect filtered trait distributions along environmental gradients, to the composition of the microbial community. We show that soil salinity played an important role in shaping microbial community composition by selecting for communities with higher salt tolerance. The shift toward bacterial communities with trait distributions matched to salt environments probably compensated for much of the potential loss of function induced by salinity, resulting in a degree of apparent functional redundancy for decomposition. However, more tolerant communities still showed reduced functioning, suggesting a trade-off between salt tolerance and performance.