

## **The dynamic responses of biological soil crust communities revealed by wetting experiments coupled with metagenomics**

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**Project Goals: Understanding the contributions of microorganisms to soil nutrient cycling and organic matter turnover are priorities of the Department of Energy missions. Within this framework, our projects aim to resolve *in situ* microbial activity through the combination of pioneering approaches that link microbial community structure and functional attributes within critical desert biocrust communities.**

Abstract:

The frequency and intensity of rainfall events in dryland ecosystems is predicted to become more variable against the milieu of a warming climate scenario. The southwestern USA is predicted to experience alterations in the timing of rainfall events with concomitant increases in soil surface temperatures. In arid lands, precipitation pulses are rare, yet their timing, intensity and duration dictate biological activity. A significant avenue of recent microbial ecology research has been to elucidate the consequences of climatic change on microbial communities and how these responses in turn affect critical ecosystem processes such as organic matter turnover. Biological soil crust communities, also referred to as biocrusts, will be some of the most impacted systems, and serve as ideal models to explore the effects of changes in rainfall.

Biocrust communities are dominant covers in deserts and occupy more than 14% of the Earth's terrestrial surface. Biocrusts are typically comprised of cyanobacteria, mosses, lichens, fungi, and heterotrophic bacteria that together colonize and stabilize the soil surface. Moreover, biocrusts provide critical functions in deserts by controlling water retention, fixing both carbon (C) and nitrogen (N), and stabilizing surface sediment. The activity of biocrusts hinges upon hydration pulses, and these moisture inputs also impart challenges to dehydrated communities that face rapidly changing osmotic pressure and surface microtopology. We sought to track the responses of biocrust community traits to a hydration event using shotgun metagenomics. We compared biocrust communities that represent a successional maturity gradient and found that the effect of wetting on microbial community structure and functional potential is greater than that of ecological succession.

We observed a dramatic increase in the proportion of *Alphaproteobacteria*, which became central to food web structure by the end of the wet-up. The upturn in gene abundance for these bacteria was linked to significant increases in their ribosomal copy number, as well as genes for sporulation and DNA replication. Thirty-seven draft population genomes of heterotrophic bacteria were reconstructed to explore their nutrient cycling and stress avoidance strategies. Our genomic exploration of abundant microorganisms such as *Bacillus*, *Brevibacillus*

and *Hymenobacter* spp. revealed many pathways for nutrient acquisition, and especially nitrogen metabolism, implicating them as central drivers of nutrient turn-over in this extreme environment. These genomes also offer evidence as to the metabolic mechanisms by which microorganisms persist in this extreme environment, whereby the accumulation of compatible solutes and capacity to transport salt from the cell appears to be critical.

Next we set out to quantify the proportion of microbial taxa that became active following a precipitation event by identifying the spectrum of active and inactive biocrust community members using labelled amino acid probing coupled with cell sorting and click chemistry. This approach highlighted clear differences between translationally-active and -inactive bacterial guilds. Overall, we found evidence that ~61% of biocrust community members become active following wetting, with a very high proportion of those belonging to the nitrogen-fixing *Alphaproteobacteria*, which increased from 42% after 4 hours of wetting, to 53% relative abundance by the end of our wet-up experiment (21 hours after wetting). This pioneering work in a model soil system provides initial evidence of the dynamic responses of biocrust microorganisms to a rainfall event, and has the potential to reveal the key drivers of nutrient cycling in arid ecosystems.

Altogether, our analyses show that most biocrust microorganisms are sensitive to sporadic wetting events, and immediately prepare for anticipated moisture loss through preservation mechanisms such as sporulation, the accumulation of compatible solutes and a switch from anabolic to catabolic metabolism. These adaptations have the potential to dramatically impact carbon fixation through the reduction in cyanobacterial abundance and the facilitation of nitrogen cycling through heterotrophic bacteria in biocrusts.

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