

Prolonged drought alters plant-litter decomposition  
via changes in bacterial communities and substrate availability

Sarai S. Finks<sup>1\*</sup>, Claudia Weihe<sup>2\*</sup>, Eoin L. Brodie<sup>3</sup>, Michael L. Goulden<sup>4</sup>, Adam C. Martiny<sup>5</sup>,  
Kathleen K. Treseder<sup>6</sup>, Jennifer B.H. Martiny<sup>7\*</sup>, and **Steven D. Allison**<sup>8</sup>

\*sfinks@uci.edu, cweihe@uci.edu

<sup>1-2, 4-8</sup> University of California Irvine

<sup>3</sup> Lawrence Berkeley National Laboratory

Microbial decomposers of plant litter play an important role in carbon and nitrogen cycling in terrestrial systems. Past research has focused on the direct effects of global changes, such as increased temperature, added nitrogen, and reduced water, on microbial abundance and composition. However, there is limited understanding of the indirect effects that plant communities may have, via plant-microbe interactions, on the microbial response to climate change. Here we investigated how drought impacts bacterial communities: directly through abiotic changes in water availability to the microbes and/or indirectly through changes in plant communities. To do this, we first surveyed the bacterial communities on plant litter within a decade long global change experiment applied to two adjacent ecosystems (a grassland and coastal sage scrub, CSS). The Loma-Ridge Global Change Experiment (LRGCE) employs a split-plot design where a nitrogen addition treatment is nested within plots receiving either ambient rainfall or a ~50% reduction in rainfall. Bacterial composition was characterized for each treatment over 2.5 years ( $n = 214$ ) by 16S rRNA sequencing. We then conducted a reciprocal transplant experiment ( $n = 192$ ) over 1.5 years to disentangle the abiotic effects of drought versus plant community effects on microbial composition. The cages contained sterile plant litter from grassland or CSS ambient plots and were inoculated with grass or CSS microbial communities exposed to ambient or drought conditions. To assay the response of the bacterial communities to the separate factors, we characterized composition and their functioning (mass loss) over time. Within the LRGCE, bacterial community composition differed greatly between the grassland and CSS ecosystems (explaining 12% of compositional variation), indicating a strong effect of the plant-litter substrate on the decomposer community. Drought also significantly altered bacterial community composition across both ecosystems (4% of the variation). However, drought had a much stronger effect on bacterial communities in the grassland than the CSS, suggesting that the influence of drought might be mediated by the plant community. The main taxonomic drivers to microbial drought response were among the most abundant genera overall in grassland or CSS, namely, *Curtobacterium*, *Janthinobacterium*, *Pedobacter*, and *Methylobacterium*. The reciprocal transplant experiment confirmed an indirect role of the plant community in the bacterial response to prolonged drought. Lastly, decomposition of the litter substrate was strongly dependent upon water availability and the ecosystem the plant-litter was taken from. This work highlights the importance of considering plant-microbial interactions on the microbial response to climate change.