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Historical precipitation regimes structure the growth of soil microorganisms in three California annual grasslands

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Earth system models project altered precipitation regimes across much of the globe. Soil microorganisms in Mediterranean climates must withstand both direct physiological stress during prolonged periods of low soil moisture and be able to compete for resources when seasonal rains return and plant growth resumes⁵. However, we do not have a mechanistic understanding of how altered soil moisture regimes affect microbial population dynamics and in turn how this will affect soil carbon (C) persistence.

We used quantitative stable isotope probing (qSIP) to compare total and growing soil microbial communities across three California annual grassland ecosystems with Mediterranean climates that span a rainfall gradient and have developed from similar parent material. Sampling was conducted during the wet season, when environmental conditions were most similar across the sites. We assessed multiple edaphic variables, including the radiocarbon (¹⁴C) age of soil C. We hypothesized that the long-term legacy effect of soil water limitation would be reflected in lower community growth capacity at the driest site. We also predicted that actively growing communities would be more compositionally similar across the gradient than the total (active + inactive) microbiome.

Community and phylum mean bacterial growth rates increased from the driest site to the intermediate site, and rates were similar at the intermediate and wettest sites. These differences were persistent across major phyla, including the Actinobacteria, Bacteroidetes, and Proteobacteria. Additionally, soil C at the driest site was younger than the wet or intermediate sites. The microbial families that grew fastest at the driest site include taxa that have been described as having traits that are advantageous for surviving dry spells, such as spore formation, polyhydroxyalkanoate accumulation, carotenoid biosynthesis, extracellular polymeric substances production, and trehalose synthesis. Microbial communities at the driest site displayed phylogenetic clustering, suggesting environmental filtering for slow-growing microbial taxa that can withstand water stress at this site. Taxonomic identity was a strong predictor of growth, such

that the growth rates of a taxon at one site predicted its growth rates at the others. We think this finding reflects the influence of genetic and physiological constraints on growth which appear to persist across rainfall gradients, edaphic properties, and biological communities. Lastly, we found that actively growing taxa represented (28-58%) of the taxa comprising total communities and that the composition of growing and total communities were similar. The finding that the growing communities were just a subset of the total microbiome, despite environmental conditions being favorable for growth, raises questions about the mechanisms maintaining soil microbial diversity in ecosystems with Mediterranean-type climates.