**Acknowledgements**

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**Introduction**

Climate change can be viewed as humanity’s defining problem of the 21st century (citation needed). Due to the multi-faceted nature of the problem, tackling this issue involves multiple interdisciplinary approaches in terms of both solutions and effects of climate change. For one, the different feedbacks between climate and the rest of the Earth system needs to be considered in order to understand and project the pace at which the climate is changing (citation needed). Multiple feedbacks are at play with some being positive feedbacks while others are negative feedbacks (citation needed). It is also worthwhile to compare the sizes of different reservoirs of carbon in the Earth system. As soil carbon is larger than either land plants or the atmosphere combined, a small change in this reservoir, depending on the direction of the change, can either greatly exacerbate or curb climate change (citation needed). Therefore, the stability of soil as a reservoir of carbon needs to be studied.

The flux of carbon from soils to the atmosphere is mediated primarily by microbes via the sum of processes known as “decomposition” (citation needed). Historically, studies of decomposition primarily considered climatic abiotic factors – such as precipitation, temperature, evapotranspiration – in studying decomposition while neglecting the role of microbial community composition and function (citation needed). Only more recently, towards the beginning of the 21st century, did biogeochemists consider the role of soil microbes in carbon cycling in terrestrial ecosystems. This bias was seen not just in empirical studies (citation needed) but also models that range from the ecosystem scale to the global scale (citation needed). Even to this day, amongst the Earth system models from CMIP6, only one explicitly considers soil microbes in decomposition (citation needed).

This study aims to fill some of the knowledge gaps regarding the role(s) of microbes in biogeochemistry and climate change. Responses of microbes based on their physiology and ecology will influence the nature of feedbacks between soils and climate (citation needed). As a result, studying the responses of microbes to the varying effects of climate change (e.g. from drought, rising temperatures, increasingly intense precipitation) is crucial in projecting future climate change. Microbial-explicit ecosystem models predict fairly different results from microbial-implicit ecosystem models (citation needed). On the one hand, the response of microbes depend on their temperature sensitivity, with soils predicted to sequester more carbon as temperatures increase if microbes have high temperature sensitivity and so microbial mortality increases with temperature; however, if microbes have low temperature sensitivity, then as temperature increases, soils will store less carbon due to lower microbial mortality and, hence, increased decomposition (citation needed). However, what is still lacking in the literature is the influence of drought on soil microbial community functioning.

In addition, as microbial communities vary across ecosystems (citation needed), responses of microbial communities to certain climatic effects might also vary across ecosystems (citation needed). This experiment studies how extracellular enzyme activity in leaf litter varies across ecosystems and by precipitation. Microbes decompose organic matter via the secretion of extracellular enzymes (citation needed), which have been modeled by microbial ecologists using Michaelis-Menten kinetics (citation needed, although see Tang and Riley 2013 or so for a different formulation of microbial enzyme kinetics). The Michaelis-Menten enzyme parameters are Vmax – defined as the maximum reaction velocity when the amount of substrates are abundant – and Km – Michaelis-Menten constant. Vmax, in the context of biogeochemistry and microbial ecology, is a measure of the amount of a particular enzyme where higher values indicate higher enzyme amounts (citation needed). Km, on the other hand, is used as a measure of the amount of enzymatic products due to products having been shown to be competitive inhibitors of substrates for the same enzyme (citation needed).