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## Linking microbial communities to soil carbon cycling under anthropogenic change using a trait-based framework

Ashish Malik<sup>1</sup>, Robert Griffiths<sup>2</sup>, and Steven Allison<sup>3</sup>

<sup>1</sup>University of Aberdeen, Aberdeen, United Kingdom (ashish.malik@abdn.ac.uk)

<sup>2</sup>Centre for Ecology & Hydrology, Bangor, United Kingdom

<sup>3</sup>University of California, Irvine, United States of America

Microbial physiology may be critical for projecting future changes in soil carbon. Still, predicting the ecosystem implications of microbial processes remains a challenge. We argue that this challenge can be met by identifying microbial life history strategies based on their phenotypic characteristics, or traits, and representing these strategies in models simulating different environmental conditions. By adapting several theories from macroecology, we define microbial high yield (Y), resource acquisition (A), and stress tolerance (S) strategies. Using multi-omics and carbon stable isotope probing tools, we empirically validated our Y-A-S framework by studying variations in community traits along gradients of resource availability and abiotic conditions arising from anthropogenic change. Across a Britain-wide land use intensity gradient, we used isotope tracing and metaproteomics to show that microbial resource acquisition and stress tolerance traits trade off with growth yield measured as carbon use efficiency. Reduced community growth yield with intensification was linked to decreased microbial biomass and increased biomass-specific respiration which subsequently translated into lower organic carbon storage in such soil systems. We concluded that less-intensive management practices have more potential for carbon storage through increased microbial growth yield by greater channelling of substrates into biomass synthesis. In Californian grass and shrub ecosystems, we used metatranscriptomics and metabolomics to infer traits of in situ microbial communities on plant leaf litter in response to long-term drought. This experimental set-up provided gradients of resource availability and water stress. We observed that drought causes greater microbial allocation to stress tolerance. The most discernable physiological adaptations to drought in litter communities were production or uptake of compatible solutes like trehalose and ectoine as well as inorganic ions to maintain cellular osmotic balance. Grass communities also increased expression of genes for synthesis of capsular and extracellular polymeric substances possibly as a mechanism to retain water. These results showed a clear functional response to drought in grass litter communities with greater allocation to survival relative to growth that reduced decomposition under drought. In contrast, communities on chemically complex shrub litter had smaller differences in gene expression and metabolite profiles in response to drought, suggesting that the drought stress response is constrained by litter chemistry which also reduces decomposition rates. Overall, our findings suggest trade-offs between drought stress tolerance, resource acquisition and growth yield in communities across different ecosystems. These

empirical studies demonstrate how trade-offs in key microbial traits can have consequences on soil carbon decomposition and storage. We recommend the use of our Y-A-S framework in experimental and modelling studies to mechanistically link microbial communities to system-level processes.