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Plant resource history effects on contemporary microbial processes

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Background/Questions/Methods
Soil microbial communities play a pivotal role in providing ecosystem services, given that they are key drivers of biogeochemical processes such as carbon and nitrogen cycling. As species-rich communities, made-up of populations with short generation times, it is commonly assumed that there is a high degree of functional redundancy within soil communities with respect to broad-physiological processes, such as organic carbon decomposition. This assumption underlies the majority of terrestrial ecosystem models, where relationships between processes and controlling factors are parameterized using statistical relationships generated from measurements across space. However, microbial communities display biogeographic patterns, even at fine scales and it is possible that these patterns extend to influence their function.

I first present experiments that combine common garden and reciprocal transplant approaches to test whether microbial communities sourced from distinct habitats across the contiguous United States exhibit functional similarity (i.e. redundancy) or dissimilarity in common environments. The environments are experimental microcosms composed of leaf litters differing markedly in recalcitrance. Following inoculation with the microbial communities, decomposition rates are followed across 300 days. Next, using a similar experimental microcosm design, I present experiments that test whether a common resource history might cause communities, which are initially dissimilar, to converge functionally. Distinct microbial communities are introduced into a fresh litter environment every 100 days for 300 days total. Finally, I present an experiment to test whether functional convergence (either partial or complete) is associated with a reduction in function in alternate environments (essentially a functional 'trade-off'). In this last experiment decomposition rates are measured for 100 days in alternate environments following 300 days of successive exposure to a single litter type.

Results/Conclusions
I show in the first experiment that rates of carbon dioxide production from litter decomposition are strongly dependent on the microbial inoculum, with differences in the microbial community alone accounting for substantial (up to 85%) variation in total carbon mineralized. Communities that share a common history with a given foliar litter exhibit higher decomposition rates when compared to communities foreign to that habitat, suggestive of local adaptation. In the second experiment, decomposition rates (measured as cumulative carbon dioxide values per 100-day run) converge partially in the second 100-day run, and cumulative values for all six inocula increase toward the highest values observed in the initial 100-day run. Convergence continues but at a reduced rate in the third 100-day run; yet increases in function appear to asymptote. The increasing similarity in cumulative values between inocula, observed in the successive 100-day runs, is consistent with partial functional convergence of communities exposed to a common environment. In the final experiment, microbial inocula crossed to an alternate environment (e.g. those communities maintained in a grass environment then inoculated into a hardwood litter environment) results in cumulative values in the alternate environments that are approximately half those observed for communities inoculated into the same environment.

Collectively, our results suggest that the implicit assumption in ecosystem models (i.e. microbial communities in the same environment are functionally equivalent) is incorrect. The increasing similarity across time in function in common environments of inocula sourced from different resource habitats shows the potential for function to converge. Yet this convergence is only partial and is associated with "apparent' trade-offs in the ability to decompose substrates from the original environments from which the inocula were sourced. To predict accurately how biogeochemical processes will respond to global change may require consideration of the community composition and/or adaptation of microbial communities to past resource environments and the consequences of their (partial) adaptation to new ones.