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How relevant are microbial traits to understand soil biogeochemical cycles?

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Our knowledge about the role of microbial organisms as drivers of soil biogeochemical cycles is mainly based on soil analyses, and the physiological information that exists for few microbial model organisms. In soil, measurements of process rates and element contents can be related to the apparent activity of the microbial community, though conclusions are often indirect - actual microbial physiology and diversity remains hidden. By contrast, analyses of microbial physiology under controlled conditions are hardly representative of the vast diversity of microorganisms in soil, and a transfer of these findings to complex soil systems is challenging. Thus, we argue that a better exchange among these ecological disciplines will lead to a valuable transfer of relevant questions, knowledge and improved understanding of the role of microbes in soil and its responses to environmental change.

Here, we provide examples of an evaluation of microbial parameters relevant in soil biogeochemical cycles, analysing traits in a collection of 31 saprobic fungi in response to varying substrate conditions. The large dataset allowed to test several assumptions and conclusions derived from soil system analyses exemplarily for soil fungi. Specifically, we (1) evaluated the optimum C:N:P (carbon:nitrogen:phosphorus) substrate ratio for fungal growth and activity, (2) assessed the responses in carbon-use efficiency and enzyme activity to N deficiency, (3) analyzed the relevance of C versus N supply for fungal growth and activity under varying substrate conditions and (4) tested the assumption of microbial stoichiometric homeostasis, that represents a basic principle in soil ecological stoichiometry.

Fungal responses to changes in N and C availability were partly consistent with expectations, e.g. regarding general nutrient demands, though as often discussed C availability appeared more relevant for growth especially in complex substrates. Enzymatic activity and respiration also positively correlated with N availability, resulting in decreased carbon-use efficiency at high N supply. These findings, for example, contradict certain conclusions in soil analyses, namely that N limitations will result in "N mining" (high enzymatic activity), while the excess of C causes "overflow respiration" and reduced CUE. Regarding fungal C:N:P ratios, those were only related to nutrient demands when growing in simple media, while in soil substrate such relations seem more complex. Contradicting the assumption of microbial homeostasis in soil, fungal individuals showed more flexible C:N:P ratios than expected, though the degree of flexibility varied among isolates. In general, the results also reveal a large trait variation among different isolates, with several traits

showing a phylogenetic signal, indicating variations in microbial activity depending on community composition.

Finally, we want to raise and discuss several emerging questions: How relevant is a deeper understanding of microbial physiology to understand soil biogeochemical processes? How do we include the variability of traits in diverse soil communities – are average values informative, or can we proceed with useful categories? And how can methods in soil science and microbial ecology be merged best to allow fruitful knowledge transfer?