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Microbial functional traits and life strategies: Bridging physiological and molecular approaches

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The process of transformation of soil organic matter is dependent on functional traits of active microbial decomposers. Microbial functional traits, in turn are selected and driven by the local environmental conditions and can be subdivided into three groups. Microbial traits in the first group are very dynamic, for example, the size of the microbial fraction maintaining activity or alert state (*active* biomass) and the time required for dormant microorganisms to switch to active growth (i.e., *lag time*). The second group represents *intrinsic functional traits* of the microbial population, such as maximal specific growth rate (μ_m), generation time (T_g), and affinity of extracellular enzyme systems (K_m) to soil organic substrates used for microbial growth. The third group refers to phenotypic traits at the level of functional genes, for example, those related to internal microbial metabolism, extracellular resource acquisition, or stress tolerance. Recent developments in molecular approaches have provided potential for microbial trait differentiation based on information regarding genome size, number of ribosomal gene copies per genome, and quantification of functional marker genes or their transcripts by -omics approaches (Li et al., 2019; Malik et al., 2020). This enabled to reconsider the classical concepts of microbial life strategies with the goal of specifying functional groups according to their ecological relevance considering microbial yield, resource acquisition, and stress tolerance (Ho et al. 2017, Krause et al. 2014; Malik et al., 2020). However, it remains challenging to identify proxies for specific traits that can serve as quantitative measures of a category. Based on literature review and own experiments, we compared the specificity of microbial physiological and phenotypic functional traits in contrasting soil environments. We demonstrated that mechanical disturbance of soil structure by tillage rather than chemical properties were responsible for reduction of total biomass and growing microbial fraction, for slower activity of C- and N-acquiring enzymes under conventional versus minimal tillage. High nutrient availability ensured by fertilization generally selected the microbial strategy with low total biomass but high abundance of active microorganisms. Microbial community adapted to resource depletion with soil depth was characterized by low total and growing biomass, retarded activity of enzymes decomposing plant and microbial residues and by accelerated activity and altered affinity of enzyme systems responsible for nutrients acquisition. Thus, environmental selection resulted in the activation of populations with *intrinsic functional traits* that are mostly suited to the individual soil habitat. This calls for the studies linking genetic and metabolic potential with microbial functions. However, synchronization of experimental design by sampling time is required for correct comparisons of microbial growth rates obtained by

different approaches.