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Response of microbial extracellular enzyme activities and r- vs. K-selected microorganisms to elevated atmospheric CO_2 depends on soil aggregate size

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Increased belowground carbon (C) transfer by plant roots under elevated atmospheric CO_2 and the contrasting environment in soil macro- and microaggregates could affect properties of the microbial community in the rhizosphere. We evaluated the effect of 5 years of elevated CO_2 (550 ppm) on four extracellular enzymes: ß-glucosidase, chitinase, phosphatase, and sulfatase along with the contribution of fast- (r-strategists) and slow-growing microorganisms (K-strategists) in soil aggregates. We fractionated the bulk soil from the ambient and elevated CO_2 treatments of FACE-Hohenheim (Stuttgart) into large macro- (>2 mm), small macro- (0.25-2.00 mm), and microaggregates (<0.25 mm) using a modified dry sieving. Microbial biomass (C-mic by SIR), the maximal specific growth rate (μ), growing microbial biomass (GMB) and lag-period (t-lag) were estimated by the kinetics of CO_2 emission from bulk soil and aggregates amended with glucose and nutrients. In the bulk soil and isolated aggregates before and after activation with glucose, the actual and the potential enzyme activities were measured. Although C-org and C-mic as well as the activities of ß-glucosidase, phosphatase, and sulfatase were unaffected in bulk soil and in aggregate-size classes by elevated CO_2, significant changes were observed in potential enzyme production after substrate amendment. After adding glucose, enzyme activities under elevated CO_2 were 1.2–1.9-fold higher than under ambient CO_2. In addition, μ values were significantly higher under elevated than ambient CO_2 for bulk soil, small macroaggregates, and microaggregates. Based on changes in μ, GMB, and lag-period, we conclude that elevated atmospheric CO_2 stimulated the r-selected microorganisms, especially in soil microaggregates. In contrast, significantly higher chitinase activity in bulk soil and in large macroaggregates under elevated CO_2 revealed an increased contribution of fungi to turnover processes. We conclude that quantitative and qualitative changes of C input by plants into the soil at elevated CO_2 affect microbial community functioning, but not its total content. An increase in r-selected microorganisms could accelerate C turnover in terrestrial ecosystems under a future CO_2-elevated atmosphere.