The impact of increased atmospheric carbon dioxide on microbial community dynamics in the rhizosphere

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Summary

Carbon dioxide is the most important anthropogenic greenhouse gas. The global atmospheric concentration of carbon dioxide has increased markedly as a result of human activities since 1750 and now far exceeds the pre-industrial values determined from ice cores spanning many thousands of years. The global increases in carbon dioxide concentration are due primarily to fossil fuel use and land use change.

Rising atmospheric CO_2 levels are predicted to have major consequences upon carbon cycle feedbacks and the overall functioning of terrestrial ecosystems. Photosynthetic activity and the structure of terrestrial macrophytes is expected to change, but it remains uncertain how this will affect soil-borne communities dependent on plant-derived carbon, and their feedbacks on ecosystem function.

The main objective of this thesis is to assess the impact of increased atmospheric carbon dioxide on microbial community dynamics in the rhizosphere**.** This objective is pursued via two complementary experimental approaches:

1. A detailed description of the plant-driven impacts of elevated CO_2 concentrations on shifts within both broad microbial groups as well as the dynamics of specific groups in mycorrhizal and non-mycorrhizal plants (Chapters 3 and 4).
2. Three CO_2 pulse labelling studies to track the fate of plant-assimilated C in mycorrhizal and non-mycorrhizal plants to the belowground microbial community, and to examine the impact of elevated atmospheric CO_2 levels on these processes in the short- (6 months; chapters 5 and 6) and long-term (3 years; chapter 7).

The combination of RNA-based stable isotope probing, biomarkers, community fingerprinting analysis and real-time PCR allowed us to examine the effects of increasing atmospheric CO_2 concentration on the size and structure of rhizosphere communities and to trace plant-fixed carbon to the affected soil-borne microorganisms.

Using a controlled growth system, we examined the short-term (chapters 3-6) and long-term (chapter 7) impact of elevated atmospheric CO_2 on soil-borne microbial communities by comparing belowground community responses associated with plants grown under ambient (350 ppm) versus double ambient (700 ppm) CO_2 environments. Results on the structure and dynamics of broad and specific microbial groups provide insight into the plant-microbe interactions of the rhizosphere under elevated CO_2. These experiments also showed that the specific microbial groups are affected by elevated CO_2 and demonstrate that presumably rhizo-competent bacteria and fungi are most highly affected by increased atmospheric CO_2. These patterns were consistent with observed changes in the density of antibiotic production genes as well as changes in exudation patterns. The results demonstrate that elevated CO_2 influenced different parts of the soil microbial community, but that the effects depend on the plant species and soil type. Pulse labelling studies demonstrates that elevated atmospheric CO_2 increases translocation of plant-fixed carbon, via arbuscular mycorrhizal fungi (AMF), and that distinct microbial populations incorporate plant-derived carbon under different levels of atmospheric CO_2. As opposed to simply

increasing the activity of soil-borne microbes resident at ambient CO_2 conditions, elevated atmospheric CO_2 clearly selects for opportunistic plant-associated microbial communities, with a shift in dominant AMF species, as well as rhizosphere bacterial and fungal populations. These experiments also showed that AMF are the main conduit in the transfer of carbon between plants and soil.

The microbial carbon dynamic model derived from our results provides a general framework for reappraising our view of carbon flow paths in soils and their effects on soil biodiversity under elevated atmospheric CO_2 concentration.