



## **The effect of elevated atmospheric CO<sub>2</sub> concentration on gross nitrogen and carbon dynamics in a permanent grassland: A field pulse-labeling study**

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To predict ecosystem reactions to elevated atmospheric CO<sub>2</sub> (eCO<sub>2</sub>) it is essential to understand the interactions between plant carbon input, microbial community composition and activity and associated nutrient dynamics. Long-term observations (> 14 years) within the Giessen Free Air Carbon dioxide Enrichment (Giessen FACE) study on permanent grassland showed next to an enhanced biomass production an unexpected strong positive feedback effect on ecosystem respiration and nitrous oxide (N<sub>2</sub>O) production. The overall goal of this study is to understand the long-term effects of eCO<sub>2</sub> and carbon input on microbial community composition and activity as well as the associated nitrogen dynamics, N<sub>2</sub>O production and plant N uptake in the Giessen FACE study on permanent grassland. A combination of <sup>13</sup>CO<sub>2</sub> pulse labelling with <sup>15</sup>N tracing of <sup>15</sup>NH<sub>4</sub><sup>+</sup> and <sup>15</sup>NO<sub>3</sub><sup>-</sup> was carried out in situ. Different fractions of soil organic matter (recalcitrant, labile SOM) and the various mineral N pools in the soil (NH<sub>4</sub><sup>+</sup>, NO<sub>3</sub><sup>-</sup>), gross N transformation rates, pool size dependent N<sub>2</sub>O and N<sub>2</sub> emissions as well as N species dependent plant N uptake rates and the origin of the CO<sub>2</sub> respiration have been quantified. Microbial analyses include exploring changes in the composition of microbial communities involved in the turnover of NH<sub>4</sub><sup>+</sup>, NO<sub>3</sub><sup>-</sup>, N<sub>2</sub>O and N<sub>2</sub>, i.e. ammonia oxidizing, denitrifying, and microbial communities involved in dissimilatory nitrate reduction to ammonia (DNRA). mRNA based analyses will be employed to comparably evaluate the long-term effects of eCO<sub>2</sub> on the structure and abundance of these communities, while transcripts of these genes will be used to target the fractions of the communities which actively contribute to N transformations. We quantified the contribution of mycorrhizae on N<sub>2</sub>O emissions and observed the phenological development of the mycorrhizae after the labeling.