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## Growth and genome-wide association analyses of 100 field-grown barley genotypes exposed to future CO<sub>2</sub> concentrations

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### Abstract

The continuing increase in atmospheric CO<sub>2</sub> concentration will have direct implications for plant growth and agricultural ecosystems, as CO<sub>2</sub> is the most important resource for plant growth. Growth and yield of C3 crops are known to be positively affected by elevated CO<sub>2</sub>. Although recent evidence from studies with a small number of genotypes suggest that intraspecific variability exists among genotypes, a systematic evaluation of a broader set of diverse genotypes under field conditions is still lacking. However, sufficient genetic variation is a prerequisite that would allow breeders to select for CO<sub>2</sub> responsiveness. Results of a 2-years field experiment are presented during which a diversity set consisting of 100 barley genotypes was exposed in open-top field chambers to ambient CO<sub>2</sub> (~400 ppm) and elevated CO<sub>2</sub> (~700 ppm) during the growing seasons. Elevated CO<sub>2</sub> increased yield and above-ground biomass by ~18 % and 16 %, respectively, averaged over years and genotypes. However, there were significant differences between genotypes with some genotypes showing a much larger growth response to elevated CO<sub>2</sub>, indicating a high genetic variability in CO<sub>2</sub> responsiveness in barley. A significant difference was observed in the growth and yield responses between 2-rowed and 6-rowed genotypes, such that growth stimulation by CO<sub>2</sub> was higher in 6-rowed genotypes than in 2-rowed genotypes. The variability among the cultivars within the diversity set points to the fact that no indirect selection of CO<sub>2</sub> responsiveness has been conducted so far in barley. Whole genome-wide association analyses were performed to detect genomic regions involved in the response to elevated CO<sub>2</sub>, using a QK mixed model approach. Based on 3842 polymorphic mapped SNPs from the Illumina 9k-chip and phenotypic data obtained during the two growing seasons, a total of 134 highly associated (-log p values ≥ 3) markers were detected of which 75 were associated with multiple traits.

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