

Identification of QTLs for drought stress induced leaf senescence in barley using genome wide association studies

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Due to climate change tolerance to drought stress has become an important goal in plant breeding. Therefore, the aim of this project is to identify genomic regions involved in drought stress induced leaf senescence in early developmental stages in barley by applying genome wide association studies.

In pot experiments (three replications each) 156 barley genotypes including 64 six-rowed, 49 two-rowed German cultivars and 43 accessions of the Spanish Barley Core Collection (SBCC) are tested for their response to early drought stress and induction of leaf senescence under control (70% water capacity) and stress conditions (20% water capacity).

During the stress period physiological parameters, e.g. the photosystem II

efficiency, the chlorophyll content, the content of proline and soluble sugar and the aboveground biomass production were determined.

First results revealed significant differences between the treatments and between genotypes concerning the parameters mentioned above.

In parallel this set of genotypes was analysed with the 9k iSelect chip available for barley. In summary 6807 SNPs turned out to be polymorphic. Those being mapped and showing a minor allele frequency >5% were used for whole genome association studies taking into account population structure and kinship. Based on this procedure significant associations were observed for all traits analysed.