

Identification of genomic regions involved in tolerance to drought stress and drought stress induced leaf senescence in juvenile barley

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Premature leaf senescence induced by external stress conditions, e.g. drought stress, is a main factor for yield losses in barley (*Hordeum vulgare* L.). Research in drought stress tolerance has become more important as due to climate change the number of drought periods will increase and tolerance to drought stress has become an important goal in barley breeding.

Therefore, the aim of this subproject was to identify genomic regions involved in drought tolerance and leaf senescence in early developmental stages of barley. For this purpose phenotyping, genotyping and expression analyses were conducted on 156 genotypes and based on these data genome wide association studies were performed. After a four weeks stress period (BBCH 33) six physiological parameters for drought stress and leaf senescence were determined in the control and stress variant in greenhouse pot experiments.

Significant phenotypic variation was observed for all traits analysed and significant effects of genotype, treatment and genotype x treatment were estimated for most traits analysed. Based on these phenotypic data and 3,212 polymorphic SNPs with a minor allele frequency >5 % derived from the Illumina 9k iSelect SNP Chip, 181 quantitative trait loci (QTL) were detected for all traits analysed. Major QTL for drought stress and leaf senescence were located on chromosome 2H and 5H. Expression analyses of a set of 14 genes involved in drought stress and early leaf senescence on these 156 genotypes resulted in the identification of 13 expression QTL. One of those is located in the same region of chromosome 5H as the QTL for biomass yield and leaf colour under drought stress. Respective markers may be used in future barley breeding programmes for improving tolerance to drought stress and leaf senescence.