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

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Premature leaf senescence induced by environmental stress conditions, e.g. drought stress, is an important factor for growth limitation and yield losses. Drought tolerance is a complex quantitative trait that is controlled by various genes. With genome wide association mapping (GWAS) we got a powerful tool to itemize such complex pathways by the detection of quantitative trait loci (QTL) suited to be used in future plant breeding programs.

In greenhouse pot experiments 113 German barley (*Hordeum vulgare* L.) cultivars and 43 accessions of the Spanish Barley Core Collection were tested for their response to drought stress. At the end of a four weeks stress period (BBCH 33) chlorophyll content which is an indicator of leaf senescence, as well as the chlorophyll fluorescence, content of free proline, content of soluble sugars, osmotic adjustment and the aboveground biomass production indicative for drought stress response were determined in the control and stress variant. The panel showed obvious phenotypic variation for all traits, significantly correlated to drought stress induced leaf senescence.

Association mapping was performed using the genotypic data generated with the Illumina 9k iSelect SNP Chip and the phenotypic data out of the pot experiments. One major QTL for drought stress induced leaf senescence was found on barley chromosome 5H, whereas another strong QTL was found on chromosome 2H. NCBI Blast search of the significant marker sequences pointed out that respective SNPs are in some cases located in genes coding for proteins related to drought stress or leaf senescence eg. serine/ threonin protein kinase (SAPK9), or nucleotide pyrophosphatase (AVP1).
Tolerance ranking of phenotypic data (drought susceptibility index DSI) with the leaf senescence parameter chlorophyll content and the drought stress parameter biomass yield revealed some tolerant and sensitive genotypes reacting in the same way for both traits. Furthermore, tolerance ranking with gene expression data (fold change) with four genes out of the GWAS showed identical sensitive and tolerant genotypes for these genes. By comparing the DSI and fold change ranking two tolerant and one sensitive genotype was found out of the 156 analysed barley genotypes.