

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

Gwendolin Wehner, Christiane Balko and Frank Ordon

Julius Kühn-Institut, Institute for Resistance Research and Stress Tolerance, Quedlinburg

Email of corresponding author: gwendolin.wehner@jki.bund.de

Premature leaf senescence as one important factor of yield loss is often induced by external stress conditions, e.g. drought stress. So 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 of barley (*Hordeum vulgare* L.) by applying genome wide association studies (GWAS).

In greenhouse pot experiments 156 barley genotypes including 113 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% of maximal soil water capacity) and stress conditions (20% of maximal soil water capacity). At the end of a four weeks stress period physiological senescence parameters chlorophyll content and chlorophyll fluorescence, as well as drought stress parameters e.g. content of free proline, total soluble sugars,

osmotic adjustment and the above-ground biomass production, are determined.

The experiments of two year's trials revealed variability in the parameters representing different and specific adaptation mechanisms to drought stress. Analysis of variance revealed significant genotype and treatment effects for all investigated traits and genotype treatment interactions for biomass production and content of free proline.

In parallel this set of genotypes was analysed with the 9k iSelect SNP-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 GWAS taking into account population structure and kinship. Based on this procedure, significant marker trait associations were observed under stress conditions for chlorophyll content, total content of soluble sugars osmotic adjustment and biomass production.