

Identification of genomic regions involved in drought stress tolerance in winter barley by association genetics

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In the face of global warming drought stress tolerance is becoming an important goal in barley breeding. So far there have been no comprehensive studies on genotypic differences in drought stress tolerance in German winter barley cultivars. Therefore, the project aims at determining diversity on the phenotypic and genotypic level in order to identify genomic regions involved in drought stress tolerance by genome wide association studies (GWAS).

For this purpose 113 German winter barley cultivars and 15 accessions of the Spanish Barley Core Collection (SBCC) were grown in rain-out shelter trials under end terminated drought stress conditions initiated at BBCH 45 and well irrigated field conditions (control) for three growing seasons. Furthermore, a pot trial has been conducted in a growth chamber applying end terminated drought stress from BBCH 45 ongoing. In parallel the cultivars were genotyped using the 9k iSelect SNP-chip.

First results obtained in rain-out shelter trials revealed significant differences between the stressed and the control variant and between genotypes in response to drought for yield and yield components, the content of chlorophyll, free proline and soluble sugars as well as for osmotic adaptation, photosynthetic activity and quality parameters.

Similar results were obtained in the growth chamber experiment.

By analysing of 6073 polymorphic SNPs a large genetic variation was detected within the set of genotypes. Based on the phenotypic results and the genotypic data association genetics studies will be conducted. First results show SNPs significantly associated to drought stress tolerance, which will be converted into easy to handle CAPS or pyrosequencing marker. These will allow the effective marker-assisted selection for drought stress tolerance in barley.