

Identification of genomic regions involved in drought stress tolerance in 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 results 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 128 genotypes were analyzed in rain-out shelter trails for drought stress tolerance at flowering and in parallel were genotyped using the newly developed 9k iSelect chip. First results obtained in rain-out shelter trials revealed significant differences between stressed and non

stressed plants and also between genotypes in response to drought stress concerning the content of proline and soluble sugars as well as senescence and yield parameters.

Based on the analysis of 6073 polymorphic SNPs a large genetic variation could be detected within the set of genotypes. Based on these phenotypic and genotypic results association genetics studies will be conducted.

SNPs being significantly associated to drought stress tolerance will be converted into easy to or Pyrosequencing marker. These will allow the effective marker-assisted selection for drought stress tolerance in barley.