Genetic dissection of two wild emmer QTLs conferring drought tolerance

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Drought, one of the major factors limiting global wheat (*Triticum* spp.) production, is expected to increase in severity and frequency in the future, as a result of climate change. The genetic diversity concerning genes responsible for tolerance to drought or other abiotic and biotic stresses has been depleted due to domestication and modern wheat breeding. Therefore, wild relatives offer a valuable source for improving drought tolerance in domesticated wheat.

In previous work QTL regions conferring drought tolerance in wild emmer on chromosome 2BS and 7AS (*T. diccocoides*) have been identified and were transferred into elite wheat cultivars. These near isogenic lines were shown to be more tolerant to drought than their recurrent parents but suffer from linkage drag.

The main aim of this ongoing project is to narrow down the size of these QTL-regions and to re-introgress the shortest fragments bearing drought tolerance into Israeli and German elite wheat cultivars. For that purpose 151 F_7 plants of the original F_6 mapping population were genotyped with the 15k i-Select chip, a high resolution map with 4118 polymorphic marker was constructed and validation of both QTL-regions conducted.

Few candidate genes for both QTL-regions were identified. QTL-region 2BS shows synteny to a genomic region in wheat that is known to contain genes involved in ABA perception and calcium signaling. 15.67 and 26.02 cM intervalls of QTL-regions on chromosome 2BS and 7AS were selected for fine mapping. iSelect-SNP markers mapping in the regions of the QTL-intervals were converted into different types of PCR based molecular markers, such as kompetitive allele specific PCR markers (KASP), cleaved amplified polymorphic PCR-markers (CAPS) and simple sequence repeats (SSR).

Currently 82 and 159 heterozygous segmental recombinant F_2 inbred lines of QTL-region 2BS and 7AS, respectively, are subjected to genotyping. Specific F_2 heterozygote recombinants, showing recombination events in the targeted intervals are going to be selected and F_3 progenies of these plants will be screened to identify homozygous recombinant plants. Next, F_4 progenies of these plants will be phenotyped and the QTL interval reduced in length.