

## Grain size QTL region *QTgw.ipk-7D* in wheat: sequence analysis and synteny to related grass species

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The previously described QTL for thousand-grain weight *QTgw.ipk-7D* associated with microsatellite marker *Xgwm1002-7D* was originally detected in a BC<sub>2</sub>F<sub>3</sub> advanced backcross population of the winter wheat variety ‘Prinz’ and the synthetic wheat line W-7984 (lab designation: M6) (Huang et al., 2003). We developed nearly-isogenic lines (NILs) carrying introgressions of M6 in the genetic background of ‘Prinz’ with varying size on chromosome 7DS. The BC<sub>4</sub>F<sub>3</sub> NILs had a 10% increase in thousand-grain weight compared to the control group and the recurrent parent ‘Prinz’. The same QTL was detected in another population of winter wheat ‘Flair’ and synthetic wheat ‘XX86’ (Huang et al. 2004). By using homozygous recombinant lines developed from both populations, it was possible to fine-map *QTgw.ipk-7D* to an interval of approx. 1 cM flanked by markers *barc126*, *wmc405* and *gwm44* on wheat chromosome arm 7DS. From a chromosome arm 7DS-specific BAC library, BACs covering the region of *QTgw.ipk-7D* were isolated and their sequences were obtained by 454 sequencing. Of the sequenced BACs, new microsatellite markers were developed and used for anchoring the BACs to the genetic map. Finally the region of *QTgw.ipk-7D* was delimited to 6 BACs carrying ca. 12 predicted genes. A good synteny to the genomic sequences of rice, *Brachypodium* and *Sorghum* was observed. A BAC contig covering the respective genomic region in barley was identified and also completely sequenced. A detailed comparison of the barley sequence to the wheat sequence with respect to genome evolution is currently conducted.

For verification of possible candidate genes, sequencing of the genes from parental lines and various NILs aiming to identify SNPs is ongoing. In addition, sequence capture technology will be used for detecting new SNPs in this region. In general, our data support the concept of using nearly isogenic introgression lines for validating and dissecting QTL into single Mendelian genes and open the gateway for map-based cloning of a grain size QTL in wheat.