

Toward cloning of a major QTL for preharvest sprouting resistance in white wheat.

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Preharvest sprouting (PHS) is a major constraint to white wheat production. Previously, we mapped a major quantitative trait loci (QTL) for preharvest sprouting resistance in the U.S. white wheat Rio Blanco and located the QTL in the distal end of 3AS using a recombinant inbred line (RIL) population derived from the cross 'Rio Blanco/NW97S186'. To validate and fine map the QTL, a new segregation population consisting of 1,874 F₂ lines was developed by selfing the progenies of a RIL (RIL25) that was heterozygous for the three SSR markers in the QTL region. The segregation ratio of PHS resistance in the population fits monogenic inheritance. Plants with all Rio Blanco marker alleles at the three marker loci were resistant to PHS, whereas those with all NW97S186 alleles were susceptible. The additive effect of the QTL played major role on PHS resistance with dominant effect was also observed. Fifty-six recombinants among the three SSR markers were identified in the population to produce homozygous recombinants. Fine mapping delimited the QTL in the region close to *Xbarc57* flanked by *Xbarc321* and *Xbarc12*. The QTL region was further saturated by 11 AFLP and seven wheat EST-derived markers. Microcolinearity was established between the QTL region and the corresponding region on rice chromosome 1 according to the EST information. The QTL was narrowed down to a region about 0.4 cM after analyzing the PHS resistance of the homozygous recombinants. A physical map of the QTL region was constructed by screening a Chinese Spring chromosome 3AS arm-specific BAC library with markers flanking the QTL. Two contigs were identified to span the QTL region. Sequence analysis of these contigs is underway.

POSTER SESSION ABSTRACTS

Poster 1. Saturation and comparative mapping of the Tsc2 region in hexaploid wheat.

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Ptr ToxB is a proteinaceous, host-selective toxin produced by the tan spot fungus, *Pyrenophora tritici-repentis*, capable of causing chlorosis in susceptible wheat (*Triticum aestivum* L.) cultivars. Sensitivity to Ptr ToxB is governed by the *Tsc2* gene located at the distal end of wheat chromosome arm 2BS. *Tsc2* was initially mapped in the International Triticeae Mapping Initiative (ITMI) mapping population, which was derived from the synthetic hexaploid wheat W-7984 and the hexaploid variety Opata 85. The main objectives of this study were to validate the chromosomal location of *Tsc2* and its effects in an intervarietal hexaploid wheat population, develop or identify user-friendly PCR-based markers suitable for marker-assisted selection (MAS) against toxin sensitivity conferred by the *Tsc2* locus, and determine the utility of rice and *Brachypodium* genomic sequences for fine-mapping of the *Tsc2* region. A population consisting of 121 F_{2:7} recombinant inbred lines derived from a cross between the Ptr ToxB-sensitive hexaploid wheat cultivar Katepwa and the Ptr ToxB-insensitive hexaploid landrace Salamouni was used for mapping and phenotypic analysis. SSR markers known to map to 2BS and sequence tagged site (STS) primers developed for 2BS-bin mapped ESTs were mapped in the 'Salamouni/Katepwa' (SK) population. Monomorphic EST-STs were further mapped as RFLPs. To date, the 2BS map developed in the SK population consists of 32 SSR, 9 EST-STs, and 3 RFLP markers. The SSR marker *Xmag681* and RFLP marker *XBE444541* flanked the *Tsc2* locus at distances of 2.8 cM and 2.6 cM, respectively. *Xmag681* will be suitable in MAS schemes and efforts are underway to convert *XBE444541* to a PCR-based marker as well. Results regarding the effects of the *Tsc2* locus on conferring tan spot susceptibility, comparative analysis of the *Tsc2* region with rice and *Brachypodium*, and discussion regarding the usefulness of using the genomic information from rice and *Brachypodium* for developing additional markers, genomic analysis, and map-based cloning of *Tsc2* will be presented.