Saturation Mapping of a Major Fusarium Head Blight QTL in Tetraploid Wheat. (C07-osenga165107-Oral)

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Abstract:

Fusarium head blight (FHB) has posed a major economic threat to the wheat and barley industry. Resistant varieties are needed to combat this problem. Generating a saturated map of a region is the first step toward eventual isolation of resistant gene(s). Analysis of 83 LDN(Dic-3A) recombinant inbred chromosome lines identified a single major QTL, Qfhs.ndsu-3AS, which explains 55% of the genetic variation for FHB resistance. Thirty-six individuals showing recombination in this chromosomal region have been selected and are being re-screened to formulate a more accurate phenotypic characterization. The information available from the NSF Wheat EST project is being used to generate markers for saturation mapping of this region. Twenty-nine primers have been designed from the individual ESTs assigned to chromosomal bin 3AS4-0.45-1.00; 22 primers have been designed using the consensus contig sequence information. Markers showing polymorphism in the population are currently being mapped.

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