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W433: Plant Molecular Breeding

Identification And Validation Of Molecular Markers For Marker-Assisted Selection Of *Wsm2* In Wheat

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Marker-assisted selection (MAS) or breeding (MAB) has become an important tool for improvement of plant traits in many plant breeding programs worldwide. Usefulness of a marker in MAS depends on the marker polymorphism in nature population and the genetic distance between the marker and the gene of interest. The *wheat streak mosaic virus* (WSMV) resistance gene *Wsm2* was identified in hard winter wheat line CO960293-2 developed by the Hard Winter Wheat Breeding Program at Colorado State University in Fort Collins, CO, USA. *Wsm2* was mapped to the short arm of chromosome 3B with simple sequence repeat (SSR) and sequence-tagged site (STS) markers. A SSR marker *Xbarc102* was 3.6 cM proximal to *Wsm2* in the population CO960293-2/Yuma consisting of 142 F_{2:3} families and 1.6 cM distal to *Wsm2* in an integrated map constructed from two populations. Among four markers evaluated for suitability for MAS, *Xbarc102* correctly predicted the presence or absence of *Wsm2* in all 22 advanced breeding lines developed from crosses of CO960293-2 or RonL (carrying *Wsm2*) with other germplasm lines. In addition, the marker allele *Xbarc102-219-bp* associated with *Wsm2* was present in *Wsm2*-carrying wheat genotypes CO960293-2, CO960293-w133, and Snowmass, but absent in KS96HW10-3 (*Wsm1*), Karl92, TAM 107, and N96L9970, indicating sufficient polymorphism for *Xbarc102* in nature. We therefore conclude that *Xbarc102* is a useful marker in MAS for accelerating transfer of *Wsm2* from CO960293-2 or its derivatives to adapted wheat cultivars.