

Mapping the oat stem rust resistance gene *Pg13*

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Compared with the transfer of a dominant gene, the transfer of a recessive gene into elite oat cultivars through conventional breeding is a complicated and lengthy process. *Pg13* is one of the most effective race-specific stem rust resistance genes in North America, but it is recessive. Identification of effective molecular markers that are tightly linked to this gene would increase the efficiency of oat breeding. The objectives of the current study were to construct a high density genetic map for *Pg13* using three bi-parental populations (an F₃ and two recombinant inbred line [RIL] populations), to identify highly predictive SNP markers, and to design a SNP-based KASP assay for future use in marker assisted selection. Based on the three populations, *Pg13* was mapped to the 7C-17A translocation between 46.5 and 72.6 cM on Mrg18 of the oat genetic consensus map. This result was validated using linkage maps constructed from two additional bi-parental RIL populations and a genome-wide association of SNP markers on a set of elite oat lines (CORE lines). *Pg13* was tightly linked to the crown rust resistance gene *Pc91*, which was also mapped to this linkage group in earlier studies. The usefulness of selected SNPs was tested in diverse oat lines and effective markers were identified for use in oat breeding programs.