

Molecular mapping of a major stem rust resistance gene in oat

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Abstract

Stem rust caused by the fungus *Puccinia graminis* Pers. f. sp. *avenae* Eriks. and E. Henn., is an important disease of cultivated oat. Control of this disease has been through the use of host resistance genes, but changes in pathogen virulence provide a continuing threat to oat production. Currently, the predominant race of *P. graminis* f. sp. *avenae* in the eastern prairie region of western Canada is TJJ (NA67). A recombinant inbred line (RIL) population consisting of 226 lines, derived from the cross OT7030 × Leggett, was phenotyped for stem rust seedling reaction to TJJ (NA67) in glass house experiments during 2012 and 2013. Segregation results indicated the presence of a single resistance gene. Genotyping of the parents, along with resistant and susceptible bulks, with the 6K oat SNP array identified three polymorphic markers. These markers were located on the oat Mrg8 linkage group. Genotyping of the entire RIL population identified GMI_EB05_c13908_354 as the most closely linked SNP marker, at a genetic distance of 0.5 cM from the postulated *Pg12* resistance gene. In addition to these SNPs, GBS markers identified additional SNPs near the gene. Currently, these SNPs are being validated on the entire population. The linked markers will also be validated on a second RIL population derived from CDC Weaver × Stainless. Interestingly, the identified stem rust resistance gene co-segregates with markers linked to the *PcKM* (*Pc45*) crown rust resistance gene, which is found on the same linkage group (Mrg8).

Key words: Oat stem rust, NA67, Mrg8, SNP, Kompetitive allele-specific PCR (KASP)