

Identification of SNP markers linked with known oat stem rust resistance genes using bulked segregant analysis

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Oat stem rust, caused by *Puccinia graminis* f. sp. *avenae* Eriks. & E. Henn. (*Pga*), can reduce yield and quality in oat, *Avena sativa* L. (Roelfs and Long 1980). Resistance breeding has been used as a cost-effective strategy to prevent these losses. There are currently 17 numbered oat stem rust resistance genes (*Pg*), and one gene complex known as *Pg-a*. Twelve of the numbered *Pg* genes are used as standard differentials to identify pathogenic races of *Pga* (Fetch Jr. and Jin 2007). While RFLP and RAPD markers for *Pg9* and *Pg13* have been previously reported (O'Donoghue et al. 1996), there has been no systematic search for markers linked to all known *Pg* genes. Objectives of this study were to 1) generate crosses of each standard differential and the *Pg-a* complex in two susceptible genetic backgrounds, and 2) find SNP markers linked to resistance using bulked segregant analysis.

Accessions with *Pg8* (CIav 9321; with Rodney 0 background) and the *Pg-a* complex (CIav 9339) were crossed to the susceptible *A. sativa* cultivars 'Marvellous' and 'Otana'. *A. strigosa* accession CIav 6956 with *Pg6* was crossed with the susceptible *A. strigosa* accessions CIav 2524 and PI 573582. Populations were advanced to F_{2:3} and 10 seedlings from each of 70 families, parents, and F₁s were inoculated with *Pga* race KBD (virulent to *Pg2*, *Pg3*, *Pg4*, and *Pg15* and avirulent to *Pg1*, *Pg6*, *Pg8*, *Pg9*, *Pg10*, *Pg12*, *Pg13*, *Pg16* and the *Pg-a* complex). Homozygosity in the F_{2:3} families was verified in the F_{2:4}. F₁s obtained from crosses with the *Pg6*, *Pg8* and *Pg-a* complex were resistant, indicating dominant inheritance. A 1:1 segregation ratio of homozygous F_{2:3} families in the 'Otana'/*Pg6* and 'Otana'/*Pg8* crosses indicated the presence of a single dominant resistant gene. The segregation ratio of 2 resistant to 1 susceptible F_{2:3} families in the 'Otana'/*Pg-a* was not consistent with previous work that concluded the *Pg-a* complex consisted of the recessive *Pg12*, and at least one other recessive *Pg* gene (Fetch Jr. 2006). The parents, F₁s, and families that were homozygous for susceptibility from the 'Otana'/*Pg8*, 'Otana'/*Pg-a*, and PI 573582/*Pg6* crosses were genotyped with the Illumina Oat Consortium 6K SNP BeadArray. Markers linked to resistance will be identified when genotyping data are available. Marker information obtained from this project can be used to identify new *Pg* resistance (Steinberg et al. 2005), and facilitate selection of progeny with multiple resistant genes.

References

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