



Mapping of crown rust (*Puccinia coronata* f. sp. *avenae*) resistance gene *Pc54* and a novel quantitative trait locus effective against powdery mildew (*Blumeria graminis* f. sp. *avenae*) in the oat (*Avena sativa*) line *Pc54*

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Summary:

Crown rust, caused by the fungus *Puccinia coronata* f. sp. *avenae* (*Pca*), and powdery mildew, caused by *Blumeria graminis* f. sp. *avenae* (*Bga*), are two of the most important foliar diseases of cultivated oats. Crown rust is the main biotic production constraint of oats in North America and is also present in most oat producing countries of the world. Powdery mildew, on the other hand, is mainly common in cooler, humid regions of Europe and South America. The use of fungicides to manage both diseases in oats is not recommended, as it is not economically justifiable or environmentally desirable, and excessive use may lead to the development of fungicide resistance in the pathogen populations. The use of resistant cultivars carrying effective genes against the pathogens is generally accepted as being the best alternative.

The *Pc54* gene, conferring seedling resistance to crown rust, was originally identified in an accession of the wild oat species *Avena sterilis* (CAV 1832) collected in the Mediterranean region of Turkey (<https://pgrc-rpc.agr.gc.ca/gringlobal/accessiondetail?id=35345>, PGRC). The accession was crossed and backcrossed with the *A. sativa* cultivar 'Pendek' to develop the single gene crown rust differential line *Pc54*. In addition to the crown rust resistance gene, this line also carries an unknown gene effective against powdery mildew and the stem rust resistance gene *Pg15*. In this study, two recombinant inbred line (RIL) populations were developed, with the objective of identifying the genomic locations of the two genes and associated molecular markers for use in marker-assisted selection.

The RILs, along with the parents, were phenotyped for crown rust and powdery mildew in a controlled environment and genotyped using the 6K Illumina Infinium iSelect oat SNP chip. Multiple interval mapping placed *Pc54* on linkage group Mrg02 and the novel powdery mildew QTL *QPm.18* on Mrg18 of the hexaploid oat consensus map (Chaffin, *et al.*, 2016). The map locations were validated using a second mapping population. Reactions to crown rust inoculations suggest a separate identity of *Pc54* from other crown rust resistance genes and the QTL that have previously been reported on Mrg02, with the exception of *qPCRFD*. *Pm3* is the only powdery mildew resistance gene previously mapped on Mrg18. However, the *Pm3* differential line 'Mostyn' was susceptible to the oat powdery mildew race used in this study, suggesting that *Pm3* and *QPm.18* represent different genes.



Determining the chromosomal locations of *Pc54* and *QPm.18* is helpful for better understanding the molecular mechanism of resistance to crown rust and powdery mildew in oats. Furthermore, SNPs and SSRs that are closely linked with the genes could be valuable for developing further PCR-based molecular markers and facilitating the utilization of these genes in oat breeding programs. Markers associated with powdery mildew resistance were validated in a survey of 168 oat breeding lines and varieties.

In summary, we find that the *Pc54* and *QPm.18* loci conferring crown rust and powdery mildew resistance in the oat line Pc54 are linked with SNP markers placed on the oat consensus linkage groups Mrg02 and Mrg18, respectively. The identification of validated PCR-based markers will enable the rapid selection of genotypes with *Pc54* and *QPm.18*, as well as the identification of homozygous and heterozygous genes in breeding programs.

Reference:

Chaffin, A. S., Huang, Y. F., Smith, S., *et al.* (2016) A consensus map in cultivated hexaploid oat reveals conserved grass synteny with substantial sub-genome rearrangement. *Plant Genome* 9:plantgenome2015-10. <https://doi.org/10.3835/plantgenome2015.10.0102>