

Genetic mapping of a seedling resistance QTL effective against the oat leaf blotch pathogen *Pyrenophora avenae*

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Oat leaf blotch diseases are caused by a complex of *Pyrenophora avenae*, *Cochliobolus sativus* and *Stagonospora avenae*. Concern exists as to the potential harm they may pose to oat yield and physical grain quality (i.e. test weight) which can negatively impact production and the potential to meet minimum standards of milling quality. Growing resistant varieties is an effective method of control, but very little is known about sources and effectiveness of resistant oat germplasm. This project was initiated to address these deficiencies through four objectives: 1) to understand the prevalence of these pathogens in commercial oat fields and develop artificial inoculation techniques suitable for evaluating oat germplasm resistance, 2) to study the virulence variability in these pathogens, 3) to identify resistant oat germplasm and, 4) to map resistance quantitative trait loci (QTL).

Over 4 field seasons (2014-2017) *P. avenae* was identified in 59% of 160 fields surveyed, *Cochliobolus sativus* was present in 23% of surveyed fields while *S. avenae* was only identified in 3% of fields. Methods to culture these pathogens on artificial media and to develop an effective inoculation procedure to screen oat germplasm were successful. Critical factors included inoculation of 14 day old oat seedlings, maintenance of 100% relative humidity and total darkness following inoculation for a period of 24 hours, and scoring disease reaction seven days after inoculation. Subsequent work focused on *P. avenae* due to the high prevalence of this pathogen. A set of 15 *P. avenae* isolates were screened across a panel of nine oat lines from diverse origins which revealed a wide range in pathogenicity. A larger panel of 32 oat lines were evaluated with a subset of the *P. avenae* isolates and several oat lines with effective resistance were identified.

Four bi-parental recombinant inbred line (RIL) populations were used to study the genetic inheritance of resistance against three *P. avenae* isolates. One or two gene models explained the inheritance of resistance in four cases with one population being unable to fit any model. QTL mapping using the oat iSelect 6K Genotyping beadchip in the OT3011 x Iowa N2052 population revealed a single major QTL (explaining 67% of the variation) on chromosome 5C that was effective against the two *P. avenae* isolates evaluated. Currently this QTL is being evaluated on a wider set of oat germplasm to determine its utility for incorporating leaf blotch resistance into future oat varieties.