



Breeding for oat leaf blotch resistance

CATEGORY [disease](#) | June 25, 2019

A 4-year research project at the University of Saskatchewan's Crop Development Centre set the platform that will assist plant breeders in developing leaf blotch resistant oat varieties. Growing resistant varieties in combination with adequate crop rotation intervals will be the most effective, economical and eco-friendly method of control.

Field surveys identified the pathogens responsible for oat leaf blotch in Saskatchewan. An indoor screening protocol was developed to aid plant breeders in variety development. Resistance was identified in several oat lines among a set of 32, and a molecular marker linked to resistance from two oat lines was identified to aid in the incorporation of leaf blotch resistance into future oat varieties.

Leaf blotch surveys

Leaf blotch diseases of oat are caused by a complex of *Pyrenophora avenae*, *Cochliobolus sativus* and *Stagonospora (Septoria) avenae*. The complex has become more prevalent in recent years.

Thirty-three fields in 2014 were surveyed across Saskatchewan in early August, when the crops were at the milk to soft dough growth stages. An additional 28 fields were surveyed in 2015, 43 in 2016, and 64 in 2017. Across all four years *P. avenae* was identified in 59% of 160 fields surveyed, *C. sativus* was present in 23% of surveyed fields while *S. avenae* was only identified in 3% of fields.

The ranking prevalence of these pathogens was consistent across all four years and differs from prior surveys conducted where *S. avenae* was observed in all years and with greater prevalence than *C. sativus* in most years (2011-2013). The researchers felt that because *P. avenae* was consistently the

most prevalent oat leaf spot pathogen regardless of growing conditions, *P. avenae* may be less impacted by environmental factors.

Indoor screening technique developed

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 7 days after inoculation.

Identification of pathogenic variability

Nine oat lines were screened with 15 isolates of *P. avenae* and 17 isolates of *C. sativus* to assess virulence variability among different isolates. These studies revealed variability in pathogen virulence and infection response in oat lines.

Resistant genes identified

Evaluation of the 32 oat lines with three isolates of *P. avenae* and six isolates of *C. sativus* indicated many lines carried resistance with 10 showing resistance, 11 were intermediate and 11 displayed a susceptible reaction to one of the isolates.

The highest level of resistance to all isolates of *P. avenae* and most isolates of *C. sativus* was found in two oat lines, one from Great Britain and the other from Chile. In general, lines that showed better resistance to one pathogen were also more resistant to the other pathogen. In total, 4 resistant oat lines were found to have potential as parents in breeding programs for resistance to oat leaf blotches.

Genetic mapping of resistance

Based on the results from screening the 32 oat lines, four oat lines were identified to evaluate genetic inheritance of resistance to 3 *P. avenae* isolates. Three oat lines were identified to study resistance against 1 *C. sativus* isolate.

A major resistance gene was identified against multiple isolates of *P. avenae*. Molecular markers linked to this QTL are being developed to allow genotyping of resistant oat breeding lines. This marker will aid in the incorporation of leaf blotch resistance in future oat varieties.

Four additional resistance genes were identified and future work to map these genes will be required to determine their usefulness in resistance breeding.

Resistance to *P. avenae* appears to be more heritable and governed by 1 to 2 genes while resistance to *C. sativus* is moderately heritable and governed by 3 genes.

Collectively these successes will allow oat breeding programs to start breeding for oat leaf blotch resistance, a previously neglected disease of oat, which should lead to improved varieties better able to protect their yield potential from losses caused by leaf blotch pathogens.

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Beattie, A., Grewal, T., Kutcher, R., and Woitas, A. 2018. Breeding for Resistance to Leaf Blotch Pathogens in Saskatchewan Oat. ADF Project Final Report.

[https://poga.ca/images/pdf/research/2018 ADF Project 20140228 \(Oat Leaf Blotch\) - Final Report.pdf](https://poga.ca/images/pdf/research/2018%20ADF%20Project%2020140228%20(Oat%20Leaf%20Blotch)%20-%20Final%20Report.pdf)

Photo courtesy Aaron Beattie