

Diversity key to blackleg resistance stewardship



KEY PRACTICE: Diversity of cultivar resistance, crop rotation and fungicide usage can prevent both infection and breakdown of blackleg resistance.

PROJECT TITLE, LEAD RESEARCHER: “Blackleg Resistance Stewardship: Improving our management of host resistance,” 2010-14, Dilantha Fernando, University of Manitoba

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Leptosphaeria maculans, the fungal pathogen that causes blackleg in canola, is a limiting factor of canola production in Western Canada. Although resistant cultivars are widely used to control this disease, the breakdown of canola’s genetic resistance, the emergence of new blackleg races, market restrictions, and economic losses are increasing and important concerns to growers.

The objectives of this study, led by Dilantha Fernando, University of Manitoba Department of Plant Science, were to:

- understand pathogen races on-farm and by region;
- identify blackleg-resistant genes in commercial cultivars and strategies to reduce resistance breakdown; and
- initiate a new blackleg management stewardship program that would optimize grower success with

moderately-resistant and resistant cultivars through rotations designed to maintain genetic resistance.

Between 2010 and 2012, a total of 930 *L. maculans* isolates were collected from field stubble across the Prairies and examined for the presence of 10 different avirulence genes. When these genes are absent, there is the possibility of infection on the corresponding blackleg resistance genes in the host. Summary of these results showed that, on average, three of the avirulence genes were absent in more than 90 percent of the pathogen population (*AvrLm3*, *AvrLm9* and *AvrLepR2*), but two others (*AvrLm6* and *AvrLm7*) were present in more than 85 percent of the population. Blackleg races are composed of combinations of these avirulence genes. In 2010-11, 55 races were detected with each isolate



carrying an average of 4.18 out of the 10 genes examined.

Evaluation of 206 Canadian canola lines found the *Rlm3* gene to be present in the majority, but all other known *Rlm* genes were rarely detected. *Rlm3* corresponds with the *AvrLm3* avirulent gene, which was among the rarest to be found in all tested pathogen isolates. The low frequency of the *AvrLm3* gene coupled with the overuse of *Rlm3* single resistance gene to blackleg in planted Canadian canola varieties is the probable cause of current resistance breakdown in many growing regions.

Among the canola varieties examined, 85 percent showed seedling resistance and eight known *Rlm* genes were found to be present. *Rlm3*, the most common, was found in 57 percent of the samples. Single-gene resistance was found in 36 percent of these canola samples with the *Rlm3* gene again being the clear majority at 92 percent of that subset. All other *Rlm* traits combined were found in only 14 percent of the samples, and a surprising 43 percent showed no *Rlm* genes at all.

Among the tested *L. maculans* isolates, only 8.15 percent carried the *AvrLm3* allele, which would prove to be the lowest risk of blackleg infection to canola cultivars carrying this most common *Rlm3* gene. More than half of the isolates carried either four or five

of the 10 avirulent alleles and a further 11 percent carried three of them.

Indications from these findings are that *L. maculans* diversity is not evenly distributed in Western Canada. Pathogen populations consist of dozens of races and differ greatly from field to field.

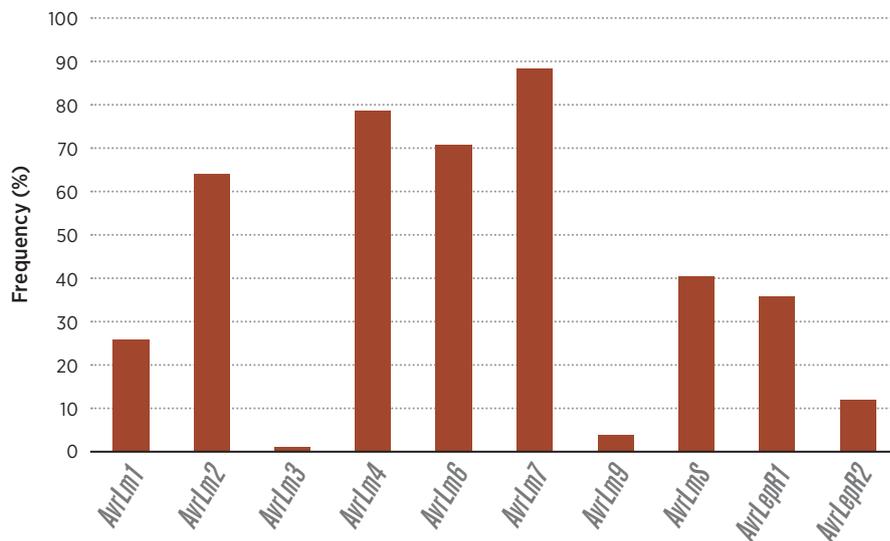
Conclusion

Blackleg management recommendations based on this study are:

- Selecting canola varieties with genetic resistance is the best strategy to control blackleg.

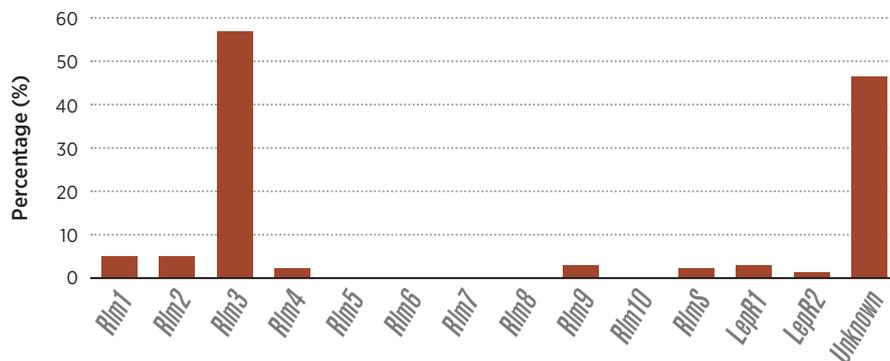
- Frequent monitoring of the *Avr* gene frequency in fungal populations and presence of *Rlm* genes in canola varieties is critical to disease control.
- Diversification of blackleg resistance in commercial cultivars will allow strategies for disease control such as rotation of diverse *Rlm* genes.
- The results of this and earlier studies have shown that selection pressure against some *Rlm* genes may alter the frequency of avirulent genes in *L. maculans*. This could be exploited for future deployment of *Rlm* traits. ●

Frequency of avirulence genes in fungal population *AvrLmS* was assessed in 193 *L. maculans* isolates



As shown in the figure above, the blackleg fungal population has a high level of diversity in Prairie fields. However, the figure below shows that genetic resistance relies primarily on just one gene, *Rlm3*. The low frequency of the *AvrLm3* allele in the fungal population coupled with the overuse of *Rlm3* single resistance to blackleg in planted Canadian canola varieties is the probable cause of current breakdown in many growing regions.

Percentage of *Rlm* genes in 102 canola varieties/lines



Pathogen populations consist of dozens of races and differ greatly from field to field. Early infection, as shown here, could indicate a resistance breakdown for those genetics on that field.

