



Blackleg Resistance Stewardship: Improving Our Management of Host Resistance

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*Genetic resistance to blackleg in canola varieties has been widely used in disease control. However, breakdown of host genetic resistance due to population shifts and the emergence of new races of the pathogen is a growing concern. A study was conducted across western Canada to understand the structure of fungal populations in the field and host resistance carried by the canola varieties. Overall, the findings showed that the *L. maculans* population is diverse and consists of dozens of races. As well, although Canadian canola varieties carry resistance genes, most of them carry the same gene, *Rlm3*, which is not effective any more in most canola growing regions in Western Canada. Therefore, in future blackleg resistance breeding programs, using multiple sources of *Rlm* genes with the combination of *APR* will be a better choice.*

Blackleg of canola (*Brassica napus*) is caused by the devastating fungal pathogen *Leptosphaeria maculans*, which is prevalent across canola growing regions in Western Canada, and is the major limiting factor of canola production. Genetic resistance to blackleg in canola varieties has been widely used in disease control. However, breakdown of host genetic resistance due to population shifts and the emergence of new races of the pathogen is a growing concern in disease control. To achieve better disease management, it's very important to understand the structure of fungal populations in the field and host resistance carried by the canola varieties.

Researchers with the University of Manitoba and Agriculture and Agri-Food Canada in Saskatoon conducted a three-year study across Western Canada to gain extensive knowledge of the *L. maculans* pathogen population in terms of frequency of avirulence (*Avr*) genes, race structure, and site to site variation. The objectives of this study were to identify race structure and frequency of avirulence genes in the Western Canadian *L. maculans* populations; to characterize resistance (*R*) genes in Canadian canola varieties/lines; and to understand host defense mechanisms. (Resistance occurs when the *Avr* and *R* genes match.)

For the population study, researchers examined 674 *L. maculans* isolates derived from stubble collected in 2010 and 2011 across the provinces of Alberta, Saskatchewan, Manitoba, and 256 isolates collected from Manitoba in 2012. A total of 930 *L. maculans* isolates were examined for 10 avirulence genes: *AvrLm1*, *AvrLm2*, *AvrLm3*, *AvrLm4*, *AvrLm6*, *AvrLm7*, *AvrLm9*, *AvrLepR1*, *AvrLepR2*, and *AvrLmS*. Researchers also used a set of *L. maculans* isolates with known avirulence genotypes to characterize the presence of 13 major resistance genes (*Rlm* genes) in 206 Canadian canola

varieties/lines. Of these, 104 were further evaluated for adult plant resistance (APR) to blackleg under controlled conditions.

Overall, the findings of this study indicated that the *L. maculans* population in western Canada is diverse and consists of dozens of races, although two are dominant (AvrLm 6 and AvrLm7 comprising > 85%). Among 674 isolates collected in 2010 and 2011, a total of 55 different races of the pathogen were detected and the average isolate carried 4 avirulence genes.

The results of the resistance characterization showed that *Rlm1*, *Rlm2* and *Rlm3* were the top three Rlm genes present in canola varieties/lines, almost none of the rest of the known Rlm genes were detected. In more than 50% of the tested varieties/lines, APR to blackleg was identified. Researchers also observed differences in *Avr* gene frequency across the Prairie Provinces. The regional and provincial variation demonstrates that a single specific resistance gene would not provide effective control of blackleg at all sites across the Prairie Provinces except *Rlm6* and *Rlm7*, which appear at high frequencies in all regions and would be effective against all races examined in Western Canada.

Overall, researchers found that although Canadian canola varieties carry resistance genes, most of them carry the same gene, *Rlm3*, and this gene is not effective any more in most canola growing regions in Western Canada, mainly due to the presence of the virulent allele *avrLm3* in most locations. This resistance gene has been known to breakdown in Manitoba and many other regions, most probably due to the over use of this single resistance gene in disease control. Therefore, in future breeding programs, using multiple sources of Rlm genes with the combination of APR will be a better choice.

It's now very important for Canadian canola breeders to develop blackleg resistant varieties with diversified Rlm genes and quantitative resistance. An alternate strategy of rotating resistance genes similar to rotating fungicides or herbicides would more likely increase the longevity of *Rlm1* and *Rlm2*. This knowledge is essential in selecting resistance sources that are effective against the majority of the pathogen population, and in developing strategies for maintaining durable resistance.

Scientific Publications

Liban SH, Cross DJ, Fernando WGD, Kutcher HR, Peng G. Race structure and frequency of avirulence genes in the Western Canadian *Leptosphaeria maculans* pathogen population. Plant Pathology, submitted 2015.

Zhang X, Liban SH, Peng G, Kutcher HR, Fernando WGD. Breakdown of *Rlm3* resistance in the *Brassica napus* - *Leptosphaeria maculans* pathosystem. European Journal of Plant Pathology submitted 2015.