



Introgression of the highly effective *Brassica rapa* blackleg resistance gene *Rlm11* into spring-type *Brassica napus*

Hossein Borhan and Nicholas Larkan, Agriculture and Agri-Food Canada, Saskatoon SK

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Researchers with Agriculture and Agri-Food Canada recently completed the genetic mapping of the blackleg resistance gene Rlm11. Rlm11 is effective against the L. maculans isolates carrying the avirulence gene AvrLm11, which is found in 95 percent of L. maculans isolates collected from western Canadian canola farms. In the project, researchers also incorporated Rlm11 into a spring-type B. napus, and generated molecular markers linked to the resistance gene. The canola lines with Rlm11 that were successfully developed in this project, combined with the blackleg race determination markers developed by this research team, will enable canola farmers to effectively control the blackleg disease.

Genetic resistance is the most cost-effective, efficient and environmentally safe approach for protecting crops such as canola against various pathogens, particularly for blackleg fungus *L. maculans* that does not respond to late applied – after cotyledon or early true leaves – foliar fungicides. To date, 19 resistance (R) genes in Brassica have been identified (named as *Rlm* or *LepR*) that confer resistance to various isolates of *L. maculans* with matching Avirulence (*Avr*) genes.

However, tight crop rotations and the rapid emergence of new virulent isolates of *L. maculans* have led to resistance breakdown, forcing researchers to search for new sources of R genes. Field surveys across western Canadian canola farms found that blackleg races with the avirulence (*Avr*) gene *AvrLm11* were highly prevalent at greater than 95 percent of fields across the prairies. This makes the matching R gene, *Rlm11*, a highly relevant and effective gene used in canola cultivars in western Canada. *Rlm11* was identified in a *Brassica rapa* accession; however, the genome location of the gene and associated markers were unknown, and incorporation of *Rlm11* from *B. rapa* is challenging and time-consuming for canola breeders.

Researchers with Agriculture and Agri-Food Canada (AAFC) have recently addressed these issues in a four-year project initiated in 2016. The objectives were to complete the genetic mapping of the blackleg resistance gene *Rlm11*, to incorporate *Rlm11* from the winter-type *B. rapa* to a spring-type *B. napus* and to generate molecular markers linked to *Rlm11*.

Researchers first identified a *B. rapa* line that contained the race-specific resistance gene *Rlm11*. This homozygous *Rlm11* line named BR-11 was used to generate inter-species (*B.*

napus x *B. rapa*) mapping populations by crossing BR-11 to the double haploid, blackleg susceptible *B. napus* line Topas DH16516. DNA from 96 F₂ lines was applied to the Brassica 60K Illumina single nucleotide polymorphism (SNP) genotyping marker array and a genome scale SNP map was generated. *Rlm11* was found to be positioned on the lower arm of chromosome A07 in a region between the previously mapped *Rlm1* and the *Rlm3-4-7-9* gene cluster.

To generate the spring type *B. napus Rlm11* introgression lines, the *B. napus* susceptible line Topas DH16516 was chosen as the recipient parent. Several resistant individuals were selected for successive backcrossing to the susceptible Topas DH16516 parental line. Plants with a normal spring-type growth habit and good seed set were selected at each back-cross generation. Researchers advanced the generation of Topas-*Rlm11* introgression lines through further back-crossing to produce and phenotype advanced back-cross populations. These advanced populations were screened using the KASP markers to generate and identify further recombination in the *Rlm11* region. In the fall of 2021, advanced generations of Topas-*Rlm11* introgression lines were harvested. These lines will be used to produce bulk seeds for distribution among canola breeders and agronomists in the near future.

As a result of the project, researchers have completed the genetic mapping of the blackleg resistance gene *Rlm11* and successfully developed Topas-*Rlm11* introgression lines. Researchers also generated molecular markers linked to *Rlm11*. These markers will be shared with the industry and canola breeders. *Rlm11* markers and Topas-*Rlm11* introgression lines will allow canola breeders to offer a new and effective resistance gene to farmers. Canola cultivars with *Rlm11* combined with the blackleg race determination markers developed in this project will enable canola farmers to continue to effectively control the blackleg disease in the future when new varieties incorporate *Rlm11* resistance.

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