Sclerotinia stem rot, caused by Sclerotinia sclerotiorum, is a serious disease problem of canola worldwide. The long term objective for researchers at Agriculture and Agri-Food Canada is to provide the canola industry with specific resistance genes and molecular markers as a selection tool used by plant breeders for selection of stem rot resistant canola cultivars. The researchers are using a genomics approach to characterize sclerotinia resistance in resistant Brassica napus lines identified in a previous project. In a three-year study initiated in 2007, researchers identified candidate resistance genes using genomics methods and examined the contribution of selected genes to resistance. As a result of the project, genes expressed in B. napus cultivars resistant to S. sclerotiorum have been identified and genetic markers that will allow their introduction into elite canola varieties are being developed.

Sclerotinia stem rot, caused by Sclerotinia sclerotiorum, is a serious disease problem of canola worldwide. Canola breeders and producers have a long-term goal of obtaining sclerotinia resistant canola crops. The objective of the research was to identify specific resistance genes and to design molecular markers to support plant breeders in the development of stem rot resistant canola cultivars. The molecular markers will be used selecting resistant lines from crosses between resistant and agronomically optimal cultivars in breeding programs.

The objectives of the three-year project initiated in 2007 at the Agriculture and Agri-Food Canada Saskatoon Research Centre were to identify candidate resistance genes using genomics methods, such as expressed sequence tags (ESTs) and gene arrays, to examine the contribution of selected genes to resistance, and to develop a better understanding of the factors employed by the fungus to cause disease and to determine how the plant inactivates these factors.

Figure 1. Phenotypes of B. napus Zhongyou 821 and Westar 21 days after inoculation of stems with S. sclerotiorum.
In the first component, researchers at AAFC used a genomics approach to identify putative defense genes that were responsible for sclerotinia resistance in certain *B. napus* lines. The winter-type *B. napus* Zhongyou 821 developed in China was one of the first cultivars with resistance to stem rot, and the research was mainly carried out with this line. Using powerful techniques, such as DNA sequencing and DNA micro-arrays, researchers identified the genes expressed in Zhongyou 821 in response to *S. sclerotiorum* infection. Several putative resistance genes were introduced into a susceptible *B. napus* line to determine their individual contribution to resistance.

In a parallel project, several mapping populations of doubled haploid (DH) lines were developed from crosses between Zhongyou 821 x susceptible lines. Several quantitative trait loci (QTL) contributing to resistance were identified in these populations. Some of the defense related genes identified by the genomics approach were mapped to these resistance loci. Vice versa, some of the QTL were shown to contain defense related genes identified in the DNA microarray study.

In addition, the researchers examined how *S. sclerotiorum* causes disease and the mechanisms used by the plant to prevent this. Five polygalacturonases (enzymes that break down plant cell walls) and two necrosis-inducing proteins were found to be the principal factors responsible for the development of necrotic lesions. Using a genomics approach, genes in *B. napus* encoding polygalacturonase inhibiting proteins were identified. This study provided new insight into aspects of the defense response to necrotrophic pathogens using an experimental design that resembles the interaction between *S. sclerotiorum* and *B. napus*.

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