

## **Introgression of clubroot resistance from *B. rapa* into *B. napus* canola and identification of molecular markers for resistance, and pyramiding of this resistance with other resistance genes**

**Category: Pre-Breeding**

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**Term:** 6 years, ending November 2023

**Status:** Complete

**SaskCanola Investment:** \$118,320

**Total Project Cost:** \$696,000

**Funding Partners:** Alberta Canola Producers Commission, Alberta Innovates (AI) and Results Driven Agriculture Research (RDAR).

### **Grower Benefits:**

- Genomic and molecular approaches identified several genes and proteins to be involved in clubroot resistance of the canola lines carrying resistance of the *B. rapa* var. *rapifera* turnip cv. Debra.
- Mapping of the resistances demonstrated that multiple clubroot resistance loci can be transferred from *B. rapa* into canola. Among these, the A09 locus introgressed from turnip proved to be novel in canola, exhibiting resistance to multiple *Plasmodiophora brassicae* pathotypes, including the recently evolved pathotypes 3A, 2B, 3D and 5X.
- Several canola quality lines carrying A09 locus with acceptable agronomic and seed quality traits, and exhibiting resistance to multiple *P. brassicae* pathotypes, were generated.
- The A09 locus has not been reported previously by any other researchers in any other Brassica plants, making it a significant contribution to the canola community. Use of this locus in breeding will diversify the resistance genes in canola cultivars, benefitting canola growers.
- The novel clubroot resistant germplasm and molecular markers developed from this project can be used in breeding to develop improved clubroot resistant *B. napus* canola cultivars.

### **Project Summary:**

Several clubroot-resistant canola cultivars have been developed in Canada, however the newly evolved *Plasmodiophora brassicae* pathotypes have overcome some of the resistances. The long-term objective of this project is to diversify the clubroot resistant genes in Canadian canola for clubroot resistance and develop molecular markers for these resistances.

The objectives of this project were to investigate the prospect of introgression of clubroot resistances from *Brassica rapa* var. *rapifera* turnip cv. Debra and *B. rapa* var. *pekinensis* Chinese cabbage cv. Bilko into *B. napus* canola. Another objective was to map the resistances for using the associated molecular markers in breeding. Researchers also used genomic and molecular approaches to extend knowledge on the resistance and to identify molecular markers for use in marker-assisted breeding.

In this project, resistance to multiple *P. brassicae* pathotypes including pathotype 3A was introgressed from *B. rapa* var. *rapifera* turnip cv. Debra and *B. rapa* var. *pekinensis* Chinese cabbage cv. Bilko into *B. napus* canola through interspecific cross between these two species. Mapping of the resistance was carried out by using the advanced generation canola lines and following multiple approaches. By using the canola lines derived from the Canola × Turnip cross, four clubroot resistance loci were identified on A02, A03, A08 and A09; these loci confer resistance to pathotype 3A. Using canola lines derived from the Canola × Chinese cabbage cross, a single locus conferring resistance to pathotype 3H was identified on chromosome A03.

The resulting mapping demonstrated that multiple clubroot resistance loci can be introgressed from *B. rapa* into canola; with the A09 locus introgressed from turnip proving to be novel in canola. Fine mapping of the turnip-resistance introgressed into canola will be needed to develop gene-based molecular markers, especially from the A02, A03 and A09 loci, for use in breeding, as well as for further understanding of the A02 and A03 loci in relation to the previously reported loci.

Several canola quality lines with acceptable agronomic and seed quality traits, and exhibiting resistance to multiple *P. brassicae* pathotypes, were generated. Advanced generation populations confirmed the resistance both under greenhouse and field conditions. Genomic and molecular methods and tools identified several genes and proteins to be involved in clubroot resistance of the canola lines carrying turnip-resistance, and this laid the foundation for functional validation of these genes and proteins.

In summary, the results demonstrated that multiple clubroot resistance loci can be transferred from *B. rapa* into canola. The clubroot resistance of turnip introgressed into canola plays an important role in resistance to multiple *P. brassicae* pathotypes. Among the mapped loci, the A09 locus is novel in canola. This locus has not been reported previously by any other researchers in any other *Brassica* plants, making it a significant contribution to the canola community. This locus provides resistance to the recently evolved pathotypes 3A, 2B, 3D and 5X. This research also provided a deeper insight into the putative genes and proteins to be involved in clubroot resistance. The novel clubroot resistant germplasm and molecular markers developed from this project can be used in breeding to develop improved clubroot resistant *B. napus* canola cultivars.

#### **Referred journal articles:**

Kaur K, 2023. A Multi-omics approach for genetic and molecular analysis of clubroot resistance in *Brassica napus* canola. PhD thesis, University of Alberta.

Kaur K, Liu Y, Rahman H, 2022. Introgression of resistance to multiple pathotypes of *Plasmiodiphora brassicae* from turnip (*Brassica rapa* ssp. *rapifera*) into spring *B. napus* canola. *Agronomy* 12:1225. <https://doi.org/10.3390/agronomy12051225>

Hasan J, Shaikh R, Basu, U, Rahman H, 2021. Mapping clubroot resistance of *Brassica rapa* introgressed into *Brassica napus* and development of molecular markers for the resistance. *Crop Sci* 61:4112–4127. <https://doi.org/10.1002/csc2.20626>

Kaur K, Megha S, Wang Z, Kav NNV, Rahman H, 2023. Identification and expression analysis of C2H2 zinc finger protein genes reveals their role in stress tolerance in *Brassica napus*. *Genome* 66: 91–107. <https://doi.org/10.1139/gen-2022-0100>

Megha S, Wang Z, Kav NNV, Rahman H, 2022. Genome-wide identification of Biotin Carboxyl Carrier subunits of Acetyl-CoA Carboxylase in *Brassica* and their role in stress tolerance in oilseed *Brassica napus*. *BMC Genomics* 23:107. <https://doi.org/10.1186/s12864-022-08920-y>