Enhancing the Durability of Clubroot Resistance with Multiple Genes

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Clubroot continues to spread on the Canadian prairies, posing a serious threat to canola production. Cultivar resistance is the key to clubroot management, but the 17 "new" pathotypes identified recently in Alberta all appeared virulent to current resistant cultivars in the marketplace. Researchers investigated the efficacy and durability of canola lines carrying single and multiple clubroot resistance (CR) genes against 'new' and 'old' pathogen pathotypes under simulated intensive canola-growing conditions. The study results highlight the value of using stacked CR genes of different modes of action for resistance performance and durability. Overall, the study provided valuable information for development of new management strategies against clubroot on the prairies.

Clubroot, caused by *Plasmodiophora brassicae* (Pb), continues to spread on the Canadian prairies, posing a serious threat to canola production. Cultivar resistance is the key to clubroot management, but the 17 "new" pathotypes identified recently in Alberta all appeared virulent to current resistant cultivars in the marketplace. New resistance sources, as well as strategies, are required to address this challenge. Researchers are looking at the potential to use a multi-genic approach for potentially broader spectrum and greater durability of resistance. However, the advantages/disadvantages with this multi-genic approach are largely unknown, especially in terms of the resistance efficacy and longevity in clubroot management.

Researchers at Agriculture and Agri-Food Canada in Saskatoon, Saskatchewan initiated a unique three-year study in 2016 to investigate the efficacy and durability of canola lines carrying single and multiple clubroot resistance (CR) genes against 'new' and 'old' Pb pathotypes under simulated intensive canola-growing conditions. The research also studied the resistance durability under heavy (Alberta) and lighter (Saskatchewan and Manitoba) infestation situations against the predominant pathotype 3H to better understand the risk of resistance erosion in recommending a CR canola cultivar in regions with a lower clubroot pathogen inoculum load on the prairies. The mechanisms of resistance associated with CR genes were examined using transcriptome analysis to differentiate the efficacy of CR gene(s) behind the multi-genic approach.

For the study, 20 canola-quality *B. napus* inbred and hybrid lines carrying single, double and triple CR genes were produced in collaboration with Nutrien Ag Solutions. All of the genotypes selected were resistant to the predominant pathotype 3H and other 'old' Pb pathotypes (2, 5, 6, 8), but the efficacy against some of the newly identified pathotypes had not been determined. Westar and 45H29 (resistance to old pathotypes), both susceptible to the newly identified pathotype 5X, were included as controls. The lines were assessed for resistance against three field populations of the 5X, i.e. L-G1, L-G2 and L-G3 using the inoculum from Dr. Strelkov's lab at University of Alberta. Clubroot symptoms were assessed at about 35 days post inoculation (dpi) for L-G2 and L-G3, but at 42 dpi for L-G1 due to slightly less aggressiveness of this population. Symptoms were photographed and disease severity index (DSI) calculated for each line. The experiment lasted about 18 months for each pathotype and repeated once.

The study results showed that CR genes on chromosome A8 (*CRB*) are effective to old pathotype 3H, but susceptible to L-G3 of the new pathotype 5X. However, moderate resistance was achieved against all 5X populations, as well as the old pathotypes 2, 3, 5, 6 and 8, when combining *CRB* with one of the CR genes on chromosome A3 (*Rcr1* or *CRM*). This indicates that the range of resistance can be increased by stacking two CR genes with different modes of action. The study also showed that in response to 5X infection, many genes involved in pathogen immunity pathways were more strongly activated in lines carrying these two CR genes, relative to those controlled by either of the single CR genes alone.

The study also showed that higher inoculum loads tend to accelerate the resistance erosion, especially for canola varieties carrying only a single CR gene. This highlights the importance of extended crop rotation (a >2-year break from canola) to reduce the load of resting spores in heavily infested fields to assist in the performance and durability of clubroot resistance.

Overall, the study provided valuable information for development of new management strategies against clubroot on the prairies. The results highlight the value to use stacked CR genes of different modes of action for resistance performance and durability. More work is warranted to look at resistance against additional new pathotypes (2B, 3A, for example) to confirm the validity of this multi-genic strategy for enhanced resistance efficacy and durability.