

BRE1518: Integration of Aphanomyces Resistance Screening Into Rapid Generation Technology of Lentil and Pea

Aphanomyces euteiches represents the most serious root rot pathogen of several pulse species, including peas and lentils, due to its resilience in field soils for extended periods without host plants, and because management options are currently limited to primarily long crop rotations away from susceptible hosts. No resistance has been identified in lentil and pea cultivars currently cultivated in the Prairies. Population studies on international isolates of the pathogen revealed groups with different levels of virulence, but Western Canadian isolates were not included in these studies. The objectives of this project were therefore to identify the pathotypes of Western Canadian isolates, to screen lentil and pea lines from around the world to identify high *Aphanomyces* root rot (ARR) resistance, to develop an efficient and effective breeding platform and to develop varieties with improved ARR resistance.

We spent a significant time and effort on developing methods to work with this pathogen, which is as difficult in the laboratory as it is in the field. Once protocols were established for growing the pathogen and for disease screening, we were able to initiate experiments to study the virulence of isolates and screen for disease resistance. The population study revealed that the Western Canadian community of the pathogen consists primarily of highly virulent isolates, probably explaining the severity of disease symptoms encountered in commercial pea and lentil fields. This study also showed that our field isolates are more virulent than isolates used in USA for the screening of pea and lentil germplasm. As a result, lentil germplasm identified by US colleagues as having good partial resistance proved to be susceptible when challenged with Saskatchewan isolates. As a result, we have systematically screened our collection of wild lentils and found good partial resistance in close relatives.

In peas we were able to access two major sources of resistance from French and US colleagues, and based on data published by these colleagues, could develop molecular markers to complement traditional disease screening to speed up the transfer of these resistance genes into adapted pea lines. Within three years, through a combination of back-crossing, molecular markers and conventional disease screening, we have combined resistance of these two sources into the genetic backgrounds of five pea varieties, while a sixth cross is still underway. Offspring from those will have to undergo one more round of molecular marker and disease screening before we can select final candidates for seed increase. Once enough seed is available, we will conduct field experiment to a) assess the level of resistance under field conditions (either in our own ARR disease nursery currently under development, or in the AAFC Morden or AAFC Lethbridge ARR disease nursery) and to assess agronomic traits in yield trials. We anticipate that we will have sufficient seeds for replicated field trials in 2021. The selected lines will then have to go through two years of coop testing before registration.