Breeding pea for improved disease resistance

Warkentin TD1, Gali KK1, Jha AB1\*, Dhillon L1, Awodele S1, DeSilva D1, Sivachandra N1\*\*, Breitkreutz C1, Abdelmagid A2, Chatterton S3, and Banniza S1

[tom.warkentin@usask.ca](mailto:tom.warkentin@usask.ca)

1 Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada

2 Agriculture and Agri-Food Canada, Morden, Canada

3 Agriculture and Agri-Food Canada, Lethbridge, Canada

\*Current address: School of Life Sciences, Central University of Gujarat, Gujarat, India

\*\* Center for Crop and Disease Management, Curtin University, Perth, Australia

Improving biotic stress resistance is a key objective in the University of Saskatchewan pea breeding program. From ~1990-2015 our main emphasis was on improving resistance to the ascochyta blight complex. Putative sources of resistance to this quantitative trait were evaluated and used in crosses. Allele diversity for ascochyta blight score and associated single nucleotide polymorphisms were explored. Newer varieties tend to be more resistant than older pointing to gradual progress after recurrent selection. Since ~2015 our emphasis has shifted to improving resistance to root rot with key pathogens being *Aphanomyces eutieches*, *Fusarium avenaceum*, and *F. solani.* We utilized marker-assisted backcrossing to pyramid known quantitative trait loci (QTL) associated with *Aphanomyces* resistance into locally adapted cultivars. The first cohort of arising lines has improved field root rot resistance. We conducted genome wide association analysis for *A. eutieches* and *F. avenaceum* with the objective of identifying new sources to build durable resistance. Recombinant inbred lines arising from one promising accession gave rise to new insights into the relative importance of Aphanomyces QTL for resistance against western Canadian isolates. We developed a multi-parent advanced generation inter-cross (MAGIC) population of 850 F7:8 lines which are being assessed in field trials. Our current goal is to pyramid and fine map the QTL associated with root rot resistance. A synergistic goal is the improvement of nitrogen fixation. We developed lines from crosses with nodulation mutants that have improved nitrogen fixation capacity and have discovered marker-trait associations for nitrogen fixation traits in the GWAS-2 panel.