

Integrating genetic and genomic resources for lentil improvement

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| SPG Contributions | Duration/Timeline of Project (Year to Year) | Co-funders | Total Project Cost |
|-------------------|------------------------------------------------|------------------------------------------------------------------------------|--------------------|
| \$341,100.00 | March 2012 – March 2017 | Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF) | \$856,845.00 |

Project Description

To combine the use of wild relatives and genomic tools to broaden genetic variability in cultivated lentil with a focus on disease resistance and agronomic traits.

Several wild x wild (intraspecific) and wild x cultivated (interspecific) populations were generated and a sub-set were phenotyped and genotyped to better understand the genetics of both the beneficial and potential negative traits coming from the wild relatives in interspecies crosses.

Outcome

The research team found sources of tolerance to Ascochyta blight, anthracnose races 1 and 0 and stemphylium blight in the wild relatives. Crosses between these and cultivated lentil resulted in populations segregating for disease resistance as well as phenological traits such as days to emerge, days to flower, vegetative period, reproductive period, plant height, as well as seed-related traits such as seed weight and carbohydrate content. Through the use of sequencing technology the research team determined the genomic regions carrying genes controlling some of the key traits. These will be useful for tracking the introgression of the 'good' genes and avoiding the 'bad' ones when using wild lentil as a source of increased variation for lentil breeding.

Research Objective

OBJECTIVE 1

To combine the use of wild relatives and genomic tools to broaden genetic variability in cultivated lentil with a focus on disease resistance and agronomic traits.