

A reverse introgression and genomics strategy to develop and characterize chickpea germplasm for yield and climate-resilience traits

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Co-funders	Total Project Cost
\$197,183.60	Completed	January 2014 – January 2018	Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF); Western Grains Research Foundation	\$565,832.60

Project Description

To substantially leverage the resources and expertise of the world's major chickpea improvement programs including the CGIAR's pulse program at ICRISAT (Hyderabad, India) and its mandate country (Ethiopia) and the National Programs in Turkey, Australia and Canada.

Chickpea is well known to have a narrow genetic base which, consequently, limits our ability to expand the cultivation of the crop into new environments such as Western Canada, and limits our breeding efforts to improve stress tolerance as well as other economically important traits. Wild species of chickpeas are an important, but underutilized resource for crop improvement. Exploitation of chickpea wild relatives offers opportunities for identifying genetic variations for simple, as well as for more complex, traits.

This research addressed three main objectives: 1) introduce wild diversity into phenology normalized backgrounds suitable to the Western Canadian environment so that it is suitable for trait assessment and use in breeding; 2) characterize the material by systematic phenotyping under the Western Canadian environment; and, 3) develop genotype-phenotype associations.

Outcome

This research is part of a larger research collaboration coordinated by UC Davis, USA, involving partners from other universities and research institutions in USA, Turkey, Australia, India and Ethiopia. The research at the Crop Development Centre (CDC) started with the development of 40 F2 populations from crosses between elite cultivars (CDC Leader and CDC Consul) with each of the 20 accessions of the newly collected *Cicer reticulatum*. The F2 populations derived from crossing with CDC Leader were screened for cultivated alleles for early flowering and upright growth habit. The most diverse F2 plants within each of 20 populations that had a fixed flowering and growth habit for the cultivated type were selected and intercrossed to create diverse progeny lines. A total of 600 F5' diverse families were selected and characterized for important agronomic and nutritional traits under field conditions in 2017. The project team also developed unselected F2 populations for studying the genetics of micronutrient accumulation in seeds, and developed some additional lines from intercrossing the F2 plants across different populations (inter-populations), creating a wealth of genetic resources for breeding applications. The project team completed a systematic evaluation of the parental lines and their progeny for a series of agronomic and nutritional quality traits and identified accessions of the *C. reticulatum* and their progeny with better cold tolerance than the cultivated lines, as well as high iron and other nutrient content in the seeds. The diverse genetic materials and the information on SNP-trait associations are invaluable for selection for continuing genetic improvement in the chickpea breeding program at the Crop Development Centre (CDC).

Research Objective

OBJECTIVE 1

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