

BRE1408: A Reverse Introgression and Genomics Strategy to Develop and Characterize Chickpea Germplasm for Yield and Climate-Resilience Traits

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. 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 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. This selection normalized the phenology of the progeny for flowering time and growth habit characteristics of cultivars. 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 (intra-population), 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. We 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. We have 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. High throughput genotyping using 50K Axiom® *Cicer* SNP chip has identified loci associated with the important traits in the genetic stock. 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 CDC. To date, the project partners simultaneously screened the accessions for other traits such as drought tolerance, root architecture and heat tolerance, interaction with *Rhizobium* and nitrogen fixation, and reaction to root rot and other diseases. All the data will be shared among the project partners, allowing us to use such information to select our materials.