BRE1715: 50K Single Nucleotide Polymorphisms (SNP) Chip Development for Genomic-Enabling Chickpea Breeding

Chickpea cultivation in Canada has been fluctuating in the past years. Ascochyta blight and late maturity due to cool and wet growing conditions, and unpredictable drought stress are among the major constraints for successful chickpea production in Canada. Improving these traits along with seed quality and nutritional value will help to stabilize crop production, as well as increase the market value for Canadian chickpeas. Complexities of all these traits in terms of genetics, as well as accurate quantification of the traits, pose a great challenge to conventional plant breeding. Next generation genotyping tools, such as DNA chips, have greatly facilitated genetic and genomic studies. Sequence variation (SNP) markers based high-density genetic maps have been successfully used for precise mapping of QTLs and candidate gene identification in many plant species. In the current reporting period, we have developed the Canadian based DNA chip and used it to develop five chickpea genetic maps that will allow high precision mapping of early flowering, disease resistance, and quality traits. A consensus map based on these five maps was developed and will be used in genetic and genomic studies of complex traits. The SNP markers associated with important traits will be used further for selection of important traits through marker-assisted selection. The association mapping panel of 185 lines and the chickpea genome selection testing population of 100 lines were evaluated for multiple agronomic traits at Limerick and Elrose in 2018. The yield-related traits such as 1,000 seed weight, biomass and harvest index of all lines were measured. The seed nutritional value (total protein and oil content) measurement is in progress. Phenotypic data generated during this reporting period together with data from the previous years will be used for genome-wide association mapping analysis. Advancement of nested association mapping (NAM) population to F_6 was completed. The NAM population will be grown in 2019 for field evaluation for QTL mapping.