

Understanding genome architecture and genome dynamics of elite Canadian chickpea varieties for facilitating molecular breeding

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| SPG Contributions | Project Status | Duration/Timeline of Project (Year to Year) | Co-funders | Total Project Cost |
|-------------------|----------------|---|---|--------------------|
| \$299,705.00 | Completed | March 2014 – February 2016 | Saskatchewan Ministry of Agriculture – Agriculture Development Fund (ADF) | \$560,318.00 |

Project Description

Chickpea is the world's second most important pulse crop, supporting the livelihoods of millions of small-holder farmers in the semi-arid tropics, including several countries from sub-Saharan Africa and Asia. In Western Canada, chickpeas have emerged as an important pulse crop in cereal based rotations, especially in southwest Saskatchewan. Chickpea production, however, has been adversely affected by several abiotic and biotic stresses. The availability of the genome sequence facilitates molecular breeding approaches for chickpea improvement. In this context, it is desirable to re-sequence the leading chickpea varieties, elite breeding lines, and selected germplasm lines to mine alleles and haplotypes for agronomically important traits.

Outcome

The CDC assembled a panel of 109 elite lines that are important for the Canadian environment and carry superior alleles for a range of agronomic traits. This research focused on the re-sequencing and analysis of these 109 Canadian lines. A whole genome resequencing approach generating approximately 4.8 billion reads after filtering, with an average genome coverage per accession of 7.8x, was completed. Alignment of the re-sequence data with the reference genome showed an average alignment of each accession of 98.8%, which demonstrated that the resequencing effort covered most of the genome. These alignments were used to identify sequence variants. A total of 2,900,063 SNPs were identified in the current panel. These SNPs are well distributed across all chromosomes, with chromosomes 4, 1, and 6 harbouring the largest number of SNPs. Concurrently, all 109 lines were phenotyped under field conditions in two consecutive years for agronomic traits important for chickpea production in Saskatchewan. The phenotypic data, along with the re sequenced data, were used to identify superior alleles using genome-wide association studies (GWAS). In summary, the research provided the basis for large scale discovery of superior alleles that will accelerate chickpea improvement efforts at the Crop Development Centre.

Research Objective

OBJECTIVE 1

To resequence elite Canadian chickpea varieties.

OBJECTIVE 2

To identify structural variations in elite Canadian chickpea varieties.

OBJECTIVE 3

To understand genetic relationships of Canadian chickpea varieties.