

Control of flowering time in cultivated lentil

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SPG Contributions	Project Status	Duration/Timeline of Project (Year to Year)	Total Project Cost
\$100,000.00	Completed	July 2015 – March 2018	\$100,000.00

Project Description

To develop molecular marker(s) to predict flowering time response in lentil.

Outcome

The project was set up to assess molecular markers to predict flowering time in lentil. Almost one-third of the lines in the lentil diversity panel were found to carry the mutation in the FTa1-a2 region and most of them were of South Asian origin. The deletion marker was shown to be insufficient in explaining the days to flower results – some lines that were predicted to be early based on genotypic data are not, and vice versa. Targeted re-sequencing of the FTa1-FTa1 region in 81 cultivated lentil accessions revealed three distinct groups. Several of the lines contained a ~4kb insertion of a putative retrotransposon upstream of the start codon of the FTa2 gene. Unfortunately, these differences did not explain differences in days to flower under long days either and we need to look more closely at the less obvious differences. Annotation of the lentil genome for genes that are related with flowering time was done and will help with marker discovery in other projects.

Research Objective

OBJECTIVE 1

To develop molecular marker(s) to predict flowering time response in lentil.