**R-7736-1 Functional Genomics for Canola Traits**

**Background and current progress:**

This project aims to develop functional genomics tools for canola and use them to deliver novel traits for the Australian and global canola industries. A three year project was funded in SIP 2015, the main aim of which was to develop a TILLING population in an Australian variety and develop high throughput methodology to identify mutants in a set of genes predicted to generate useful traits. In addition to TILLING, the population can also be screened for altered phenotypes in forward genetic screens.

To date the project has generated a population of 3000 mutant lines in the NuSeed variety Zircon. We are currently growing M2 lines to bulk seed and sample for DNA. An exon capture method has been developed to allow high throughput screening; a preliminary experiment with 600 lines has identified 600 high confidence premature stop codons in 900 target genes (including potential regulators of phenology, oil, disease and architecture traits). From the data so far 3000 lines are needed to produce a population with a high probability of a useful premature stop codon in any given gene. By the end of the current FY we anticipate having completed DNA extraction and library preparation for half the population. Screening of an additional 600 lines using the existing exon capture targets will also be carried out.

The TILLING population has been included in a potential NuSeed project to generate increased oil content based on the results of the preliminary screening. To carry out this project the extraction and library preparation for the whole population needs to be completed.

**Proposed activities for 2017-18:**

* Complete the DNA extraction and library preparation for the remainder of the population.
* Complete screening for mutants in genes in the existing exon capture set.
* Streamline methods to identify mutant individuals from pools and track mutant loci. This will be done using a set of target genes identified by Louise Thatcher and Jonathan Anderson.
* Use mutants from the exon capture as proof of concept that new traits can be identified from the TILLING population. Potential target traits are: architecture via TFL genes, pod shatter via ADPG genes and phenology via flowering time genes. The aim is to have an example that can be used to demonstrate the utility of the population to external partners.