

## **BRE1204: Integrating Genetic and Genomic Resources for Lentil Improvement**

The objective of this project was to combine the use of wild relatives and genomic tools to broaden genetic variability in cultivated lentil with a focus on disease resistance and agronomic traits. Several wild x wild (intraspecific) and wild x cultivated (interspecific) populations were generated and a sub-set were phenotyped and genotyped to better understand the genetics of both the beneficial and potential negative traits coming from the wild relatives in interspecies crosses. We found sources of tolerance to ascochyta blight, anthracnose races 1 and 0 and stemphylium blight in the wild relatives. Crosses between these and cultivated lentil resulted in populations segregating for disease resistance as well as phenological traits such as days to emerge, days to flower, vegetative period, reproductive period, plant height, and seed-related traits such as seed weight and carbohydrate content. There was no improvement in Group 14 herbicide tolerance to be gained from the wild lentils and no simple genetic solution within cultivated lentil, but we now have a much better understanding of the mechanism of increased tolerance and will be incorporating this information into future work on increasing the level of tolerance.

Phenotypic variability from the wild parents was both positive and negative when viewed in the context of cultivated lentil production. Through the use of sequencing technology, we determined the genomic regions carrying genes controlling some of the key traits. These will be useful for tracking the introgression of the 'good' genes and avoiding the 'bad' ones when using wild lentil as a source of increased variation for lentil breeding.