**RNA-seq analysis of the molecular changes underlying defense responses in chickpea to infection by *Phytophthora medicaginis***

Amalraj A1, Baumann U1, Hayes JE1, Sutton T1,2

*julie.hayes@adelaide.edu.au*

*1School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide Waite Campus, Adelaide SA, Australia*

*2South Australian Research and Development Institute (SARDI), Adelaide SA, Australia*

In this study, we generated and analysed an RNA-seq dataset from biological replicate samples of chickpea roots, including treatments infected with phytophthora root rot (PRR), and without infection [1]. Chickpea genotypes were chosen representing sensitive and moderately-resistant cultivated chickpea, and a resistant genotype containing a wild *Cicer*-derived source of PRR resistance that is extensively utilised in the Australian chickpea breeding program. The genetic determinants underlying this critical source of resistance remain unknown, but our selected genotypes have previously been used for genetic studies to identify regions associated with PRR resistance.

The data were explored for potential mechanisms and gene candidates contributing to PRR resistance. We found limited evidence to support involvement of annotated R-genes. Different gene expression responses were observed between the wild *Cicer*-derived resistance source and the cultivated source, and supported earlier hypotheses that resistance derived from wild *Cicer* involves an ability to maintain primary root elongation and minimise initiation of lateral or adventitious roots in the presence of the pathogen [2]. We interrogated defined sets of differentially expressed genes for resistance gene candidates, by comparing their genomic locations with previously reported genetic regions. A number of candidates of interest were identified, providing a foundation for future research aimed at resolving the genetic basis of chickpea resistance to PRR.

***References:***

[1] Amalraj A. et al, ‘Using RNA sequencing to unravel molecular changes underlying the defense response in chickpea induced by Phytophthora medicaginis’, Physiol. Plant., vol. 176, no. 4, 2024, e14412.

[2] Dron N. et al, ‘Phenotyping for waterlogging tolerance as a proxy for Phytophthora medicaginis resistance in chickpea’, Plant Health Progress, vol. 22, no. 3, 2021, p. 287.