Molecular genetics and genomics approaches to improve phytophthora root rot resistance in chickpea (Cicer arietinum L.)

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Phytophthora root rot (PRR) caused by *Phytophthora medicaginis* is a major soil borne disease of chickpea in the northern region of Australia. With no economical in-crop control available, a genetic approach is the most practical management option. To date, moderate field resistance has been identified and incorporated in the cultivated *Cicer arietinum* variety Yorker, and an alternative source of resistance identified in *C. echinospermum* has also been incorporated in interspecific hybrids. Using these sources of resistance as parents, three recombinant inbred line (RIL) mapping populations were previously generated. We genotyped them using a Genotype-by-Sequencing approach and phenotyped for PRR across three field environments using a mixture of ten *P. medicaginis* isolates. Whole genome QTL analysis identified major QTL on chromosomes 3 and 6 with the resistance source derived from *C. echinospermum.* Major QTL were also identified on chromosomes 5 and 6 with the resistance source derived from *C. arietinum*. The PRR resistance loci from the cultivated and wild species were found to be distinct.

This research also aimed at developing a high-throughput, controlled environment PRR infection system that can be used as a phenotyping tool in breeding. Current PRR phenotyping methods in chickpea are field based, rely on the application of mycelium slurries or oospore inoculum solutions and are impacted significantly by environmental variation. A procedure for *P. medicaginis* zoospore production was standardized and was used to produce the inoculum for a hydroponics based infection method. The system was validated qualitatively based on observations of PRR symptom development and quantitatively based on pathogen DNA quantification in roots. Two of the RIL populations for which resistance QTL from field experiments are known were screened in the hydroponics system. Two traits (plant survival time and canker length) were measured and genetic analysis identified QTL associated with PRR resistance. A model-based correlation analysis demonstrated a high genetic correlation between the field and hydroponics traits, indicating the expression of genetic factors involved in PRR resistance under field and controlled environment is similar.

The findings from this research provide tools for marker assisted selection in chickpea and information to assist the development of populations suitable for fine-mapping of loci associated with PRR resistance. Implementation of the developed method in breeding could facilitate high-throughput screening of new genotypes and elite breeding lines, whilst also assisting with molecular-focussed studies aimed at identifying resistance genes in chickpea and virulence factors in *P. medicaginis*.