

Association mapping of root-lesion nematode *Pratylenchus thornei* resistance in *Cicer reticulatum*, the wild progenitor of chickpea.

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Root-lesion nematodes (*Pratylenchus thornei*) are migratory endoparasites that cause substantial damage to a wide range of cereal and pulse crops. Damage caused to roots during feeding and movement of the nematodes through the root cortex leads to poor uptake of water and nutrients by the plant, ultimately reducing plant growth and yield. In the sub-tropical northern grains region of Australia, where 90% of Australia's chickpea (*Cicer arietinum*) production occurs, yield losses of up to 25% have been reported for *P. thornei* intolerant chickpea cultivars. Moreover, high nematode populations build up in the soil to infect and cause yield loss to subsequent susceptible crops. Integration of resistant crops in farming systems is recognised as the most practical, effective and economical management strategy for plant-parasitic nematodes. However, plant breeding for resistance to *P. thornei* is hindered by the lack of genetic diversity in *C. arietinum*. The immediate wild progenitor of chickpea, *C. reticulatum*, offers a means to broaden genetic diversity and reintroduce traits to the *C. arietinum* genepool. Using replicated glasshouse experiments, sources of resistance to *P. thornei* were recently identified in a collection of *C. reticulatum* accessions originating from 15 sites in SE Turkey, spanning the species natural geographic range (Reen *et al.* 2019). From this collection, 125 *C. reticulatum* accessions were used in a preliminary genome-wide association study (GWAS) to identify markers associated with *P. thornei* resistance. Single nucleotide polymorphisms (SNPs) generated using genotyping-by-sequencing on the wild *Cicer* collection were obtained from the NCBI database (von Wettberg *et al.* 2018). After stringent filtering, a dataset of 22,802 high quality SNPs across the 125 *C. reticulatum* accessions was used for association mapping. To minimize the occurrence of false positive marker-trait associations, two statistical models were tested (i) a general linear model (GLM) taking into account population structure, and (ii) a mixed linear model (MLM) taking into account population structure and genetic relatedness. This exploration into the potential of GWAS to identify markers associated with *P. thornei* resistance has revealed the first insights into the chromosomal regions determining *P. thornei* resistance in chickpea. The number of accessions in the association panel is currently being expanded to increase the statistical power of GWAS to identify significant marker-trait associations. The SNPs associated with *P. thornei* resistance identified by GWAS are candidates for genomics-assisted breeding to introgress *P. thornei* resistance from wild *Cicer* into commercial chickpea cultivars.