**Genetics of Ascochyta Blight Resistance in Chickpea**

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Ascochyta blight (AB) in chickpea, caused by the fungus *Ascochyta rabiei,* is a major endemic disease resulting in significant crop loss and management cost for growers. Limited genetic gains have been achieved through conventional breeding due to the complexity of genetics underlying AB resistance. To identify genetic regions associated with resistance, a diverse chickpea germplasm comprised of domestic x wild introgression material, Vavilov collections, ICARDA FLIP (Food and Legume International Program) lines, and Chickpea Breeding Australia (CBA) material was genotyped using a Multispecies pulse SNP chip and evaluated for resistance to AB. Two phenotyping environments were utilised i) an outdoor netted pot-based screening facility at the Waite campus, Adelaide, known as SARDI and ii) a field disease nursery at Horsham. A total of 1640 genotypes were phenotyped at the SARDI terraces and 1870 genotypes in the Horsham field nursery. Disease Index (%) and stem breakage (%) were used to rate disease severity in the SARDI terraces and in the field nursery. Broad genetic variation in AB disease severity was observed in both environments. Resistant and partially resistant lines, significantly better than the currently released moderately susceptible variety, Genesis™090, were identified. The SARDI terraces and Horsham field assays were highly correlated (r=0.7). GWAS conducted in GAPIT identified significant marker-trait associations for AB resistance in the field and in the SARDI terraces. Genomic regions on chromosomes 2, 4 and 5 were common between the two phenotyping platforms. Sequence capture of the significant regions has identified candidate genes potentially linked to AB resistance.