GWAS and QTL analyses identify genomic regions associated with resistance to Ascochyta blight in chickpea

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Ascochyta blight (AB) - a major endemic disease of chickpea, caused by the fungus, *Ascochyta rabiei* (Pass.) can cause high production losses in all chickpea growing regions worldwide. Deployment of resistant varieties in combination with cultural practices are required for effective management and for long-term sustainability and profitability. Only a few landrace accessions resistant to AB have been identified in the global chickpea germplasm and were subsequently used to introgress resistance in commercial chickpea varieties. The Australian chickpea germplasm is mainly reliant on resistance derived from an Iranian landrace ICC3996. The recent increase in aggressiveness of Australian *Ascochyta rabiei* isolates has resulted in erosion of resistance in current commercial chickpea varieties such as PBA HatTrick. Some of these isolates have also been shown to cause severe disease on ICC3996 as well as the most resistant kabuli variety Genesis™090.

The Pulse Breeding Australia (PBA) Chickpea program has made a concerted effort for continued improvement in resistance, by incorporating diverse sources in the breeding pool. As a result, the breeding germplasm has improved levels of resistance to aggressive *Ascochyta rabiei* isolates compared to commercial varieties. The aim of this study was to identify Quantitative trait loci (QTL) and candidate genes associated with AB resistance in the breeding germplasm. We utilised two genome-wide association study (GWAS) panels comprising breeding lines, varieties and landraces and two F_3 populations derived from PBA Drummond/CICA1841 and CICA1521/CICA1841 to identify marker-trait associations. The breeding line CICA1841 was identified as moderately resistant to the most aggressive isolates in disease screening nurseries.

All populations were genotyped using genotyping-by-sequencing based DArTseq approach. These populations were evaluated for resistance under field/ glasshouse/shade house conditions using the most aggressive isolates. The disease severity was measured as percent main stem breakage (MSB), 0-9 rating scale and a disease index (an average of MSB, percent of stems with lesions, side branches with lesions and affected leaf area). QTL and genome wide association analyses identified several genomic regions associated with resistance that were located on all chromosomes with the exception of Ca8. We compared the QTL identified in our study with the previous reports on the basis of the physical locations on the reference CDC Frontier genome assembly v2.6.3. Common genomic regions were identified on chromosomes Ca1, Ca2 and Ca4. In addition to these, we have identified ‘new loci’ on Ca3, Ca4, Ca5, Ca6 and Ca7. A number of potential candidate genes underlying AB-QTL were

also identified. Our study has provided an insight into the genetic basis of AB resistance and identified favourable alleles. The SNP markers associated with AB resistance will increase the selection efficiency of the PBA chickpea program.