

Genomic selection in Chickpea using Whole Genome re-sequencing data

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Chickpea production in Australia has increased dramatically in the recent years, mainly due to the fast growing demand from the Indian subcontinent. Additionally, chickpea plays an important role in the Australia farming system, serving as a disease break crop and nitrogen fixer. Achieving yield potential in chickpea is limited by many yield constraints such as biotic and abiotic stresses. Phytophthora root rot (PRR) is one of the major root diseases of chickpea in NSW and QLD which are the major chickpea production areas in Australia. Next-generation sequencing technology together with advanced statistical modelling have promising potential to increase genetic gain more efficiently.

We re-sequenced 310 PBA chickpea advanced breeding lines using Illumina next-generation sequencing technology. More than half million SNPs were discovered with a genome coverage of 5-10X. There was a big difference among genomic regions in term of SNP density and linkage disequilibrium. Analysis of population structure revealed a distinct group of ~70 breeding lines with many unique alleles difference from the PBA varieties released recently. Genome-wide association studies (GWAS) identified several SNPs significantly associated with Phytophthora root rot resistance and grain yield evaluated in seven field locations. Reduced level of nucleotide diversity and the long extent level of linkage disequilibrium suggested some regions in the chickpea genome may have gone through selective sweeps probably caused by selective breeding of PRR. We further investigated the effect of genotype by environment interaction on genomic prediction, which is another approach to deal with complex traits. We found that the training set should be phenotyped in the environments relevant to the targeted environments. We also investigated the effect of SNP function on prediction accuracy using different subsets of SNPs based on their annotation such as SNP located in regulatory, exon, and alternative splice site regions. These results have important implication for implementing genomic selection into plant breeding programs.