

Genomic selection of *Phytophthora* root rot resistance in the PBA chickpea breeding program

yongle Li¹

Amritha Amalraj¹, Kristy Hobson², Sean Bithell², Kevin Moore² and Tim Sutton^{3,1}

¹ The University of Adelaide

² NSW DPI

³ SARDI

Phytophthora root rot (PRR) is one of the major fungal diseases of chickpea in NSW and Queensland which are the major chickpea production area in Australia. we have identified more than 10 QTLs for PRR resistance using three RIL mapping populations. Subsequently, we have developed and validated nine KASP markers flanking seven major QTL. The KASP markers were used to screen two F2 populations and ~500 advanced chickpea lines for recurrent selection.

Although we have successfully implement marker-assisted selection (MAS) in the project, we noticed many QTL have relatively small effect size which limited the efficacy of MAS. Therefore, we also investigated the value of an emerging alternative method called genomic selection (GS). GS used all marker across the genome to estimate the breeding value of individual plants and thus shift the focus of marker identification to parent selection. This approach is more relevant to breeding programs as it can select the best parents for crossing, reduce the cost and time of a breeding cycle.

We used the three RIL mapping population to predict the PRR resistance of a set of chickpea germplasm with divers genetic background and the result was promising with a prediction accuracy of up to 0.7. The work is still in progress with the aims of assisting parent selection from F2 populations and advanced lines selection with the purpose of releasing new varieties.