Improving Phytophthora root rot resistance in Chickpea using genomic selection

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Introduction

Phytophthora root rot (PRR) is one of the major diseases of chickpea in NSW and Queensland, the major chickpea production areas in Australia. A recent study had identified many QTL with relatively small effect sizes, probably due to the quantitative nature of PRR resistance (Amalraj et al., 2019). This poses a challenge for marker-assisted selection. Therefore, we are applying an alternative approach, genomic selection.

Methods and materials

A set of ~250 chickpea lines representing the diversity of the PBA chickpea breeding program was genotyped based on DArTseq genotyping technology resulting in ~4000 SNP markers. This diversity set was phenotyped for PRR resistance, measured as percentage survival in a irrigated field trial at Hermitage research station, QLD. Three RIL mapping populations (9001, 9008, and 9024) previously genotyped and phenotyped were used as training populations.

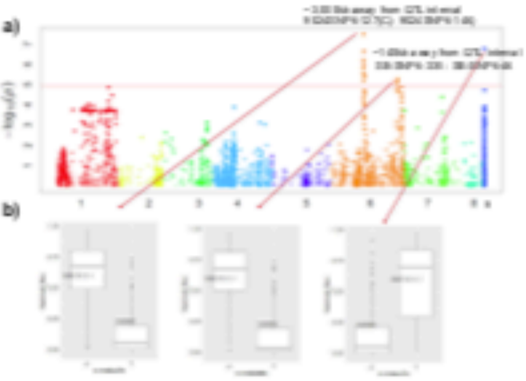

Fig.1 a) Manhattan plot of genome-wide association studies. Each SNP is represented by a dot. The physical locations of SNPs are in order according to chromosome which number 1 to 8, while 9 represents all unassembled contigs. The red line is significant threshold of p-value= 1.22E-05, equal to alpha level of 0.05 after Bonferroni correction. **b) Allelic effects of the three top significant SNPs from the signals.** The Y axis represents PRR resistance as measured by percentage of plant survival. The X axis shows the two alleles of the SNPs.

Results

Genome-wide association study identified two regions on Chr6 significantly associated with PRR resistance in the diversity set. The two regions were located close to two QTL for PRR resistance in a recent published study (Amalraj et al., 2019). This indicates that the effect of these two QTL are consistent in different genetic backgrounds.

Reference:

1. Amalraj A, Taylor J, Bithell S, Li Y, Moore K, Hobson K, Sutton T (2019) Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (Cicer arietinum L.) and wild (Cicer echinospermum P.H. Davis) chickpea. TAG 132:1017-1033

Table 1 **Prediction accuracies for the diversity set**: Correlation of predicted and actual PRR resistance

	2015 irrigated trial					2015 rainfed trial					2016 rainfed trial			
Training populations	GBLUP	BL	BRR	sBLUP		GBLUP	BL	BRR	sBLUP		GBLUP	BL	BRR	sBLUP
9001	0.29	0.24	0.29	0.69		-0.21	-0.25	0.21	0.17		-0.08	0.11	-0.07	-0.21
9008	0.73	0.72	0.52	-0.07		0.72	0.68	0.71	-0.16		0.73	0.73	0.73	0.45
9024	0.71	0.68	0.46	0.66		0.71	0.67	0.72	0.68		0.72	0.60	0.62	-0.08
9008+9024	0.73	0.71	0.53	0.66		0.70	0.69	0.70	0.66		0.62	0.62	0.58	0.28
9001+9008+9024	0.65	0.63	0.38	0.66		0.71	0.71	0.60	0.53		0.70	0.63	0.71	0.49

GBLUP: genomic best linear unbiased prediction. **BL**: Bayesian LASSO (least absolute shrinkage and selection operator). **BRR**: Bayesian ridge regression. **sBLUP**: BLUP model with QTL-linked markers.

To predict PRR resistance of the diversity set, training populations consisting of different combinations of three RIL populations were tested using irrigated and rainfed field trials with four models. Population 9008 (with wild species background) based on the GBLUP model had the highest prediction accuracies (r=0.72-0.73) in each combination of environment and population (Table 1). Model sBLUP increased prediction accuracies significantly only in population 9001 which was the worst training population based on other models. Increasing the training population size (9001+9008+9024) did not increase prediction accuracies. The training populations with rainfed trials had similar prediction accuracies as that with irrigated trial, even thought the diversity set was evaluated under irrigation. This points to lack of genotype by environment interaction in these datasets.

Table 2 Prediction accuracies of PRR resistance based on cross-validation approach

	2015 irrigated trial				2015 rainfed trial				2016 rainfed trial		
Populations	GBLUP	BL	BRR		GBLUP	BL	BRR		GBLUP	BL	BRR
9001	0.06	0.05	0.11		0.19	0.19	0.20		0.12	0.07	0.06
9008	0.46	0.47	0.48		0.57	0.57	0.58		0.57	0.57	0.58
9024	0.38	0.35	0.39		0.49	0.49	0.48		0.20	0.18	0.17
9008+9024	0.45	0.42	0.43		0.76	0.76	0.75		0.60	0.60	0.60
9001+9008+9024	0.42	0.41	0.42		0.78	0.78	0.78		0.65	0.65	0.65
Diversity set	0.60	0.65	0.58		n.a	n.a	n.a		n.a	n.a	n.a
9001+9008+9024+Diversity set	0.72	0.72	0.72		n.a	n.a	n.a		n.a	n.a	n.a

Note for cross-validation: A five-fold cross-validation was performed to evaluate the prediction performance of the three models. The whole dataset was randomly divided into five mutually exclusive subsets, four of which formed the training set for fitting the model and the fifth was used as a test set. This process was repeated ten times, resulting in 50 cross-validations. Prediction accuracy was calculated as Pearson's correlation coefficient between the predicted values and observed phenotypic values of the test set.

Prediction accuracies differed amongst combinations of populations based on the cross-validation approach (Table 2). The highest prediction accuracy (r=0.78) was achieved using population 9001+9008+9024 with 2015 rainfed PRR trial whereas the lowest prediction accuracy was always observed with population 9001. The three models have very similar prediction accuracies.

Conclusion

We have validated two QTL for PRR resistance discovered previously in three RIL mapping populations. We further tested the possibility of using those populations as a training population to predict PRR resistance. The results are promising and can be applied to the PBA chickpea breeding program.