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Application of Genomic Selection and Association Mapping to Breeding for Resistance to Rice Blast and Bacterial Blight of Rice (Oryza sativa L.)

ABSTRACT

Rice blast (RB) and bacterial blight (BB) are rice diseases that can cause yield losses of up to 90% respectively if proper preventive and control measures are not adopted at the right time. RB and BB are complex traits and this has caused their genetic improvement using traditional breeding methods to be inefficient. However, marker-assisted selection (MAS) and genomic selection (GS) may be good approaches to achieve genetic improvement of rice varieties against these two devastating diseases. Study objectives were to evaluate the use of GS to improve RB and BB resistance and to identify quantitative trait loci (QTL) for BB resistance. A population of 162 rice lines from the USDA germplasm collection and a set of 237 African rice lines were tested for resistance to eight and six RB isolates respectively. Evaluations were done in a growth chamber. The RB isolates were from Africa and were selected for their virulence and genetic diversity. Each population was genotyped with SNP markers. A subset of 160 Africanrice lines was evaluated for resistance to BB in a field study. Association analysis was used to identify QTL for BB resistance. Genomic estimated breeding values (GEBVs) were obtained using the Ridge regression best linear unbiased prediction (rrBLUP) model.

For RB there were significant genotype, isolate, and genotype by isolate interactions. Lines with resistance to all tested isolates were observed in each set. The accuracy of GS for RB resistance varied by isolate and germplasm set and ranged from 0.29 to 0.59. For BB several lines with good BB resistance in the African set were identified. Twenty-nine QTL in the African set were identified. The analyses indicated that the population structure was likely to have had a large impact on the QTL results despite modeling structure effects in the analysis. In the set of 160 African rice lines there was a pronounced population structure and both phenotypic and marker variations were strongly confounded with the structure causing considerable linkage disequilibrium among markers from different chromosomes. The accuracy of GS for BB was 0.45 over all lines, but only 0.17 when 11 lines from one outlier cluster were removed from the analysis.

Phenotypic analyses identified potential sources of multi-isolate resistance for RB and some sources of resistance to BB. Genomic selection would appear to have potential as a breeding tool to introgress RB resistance into elite germplasm. The genetic analyses for BB were inconclusive as the confounding of phenotypes and allele frequencies with population structure made it difficult to draw definitive conclusions about QTLs and the utility of GS for BB in this population.