

Comparison of Conventional and GBLUP Genome-wide association mapping of cold tolerance in advanced rice breeding populations

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ABSTRACT

Rice cold tolerance at seedling and reproductive stage is crucial for high yield stability in subtropical and temperate rice growing areas. Field phenotyping for this traits is often confounded by phenology, seeding date, and weather conditions. Therefore, marker assisted or genomic selection could be useful depending on how complex is the trait's genetic architecture in the breeding population. Genome-wide association studies (GWAS) enable to dissect the genetic architecture in breeding populations. The conventional GWAS method commonly used in plant breeding (CGWAS) tests the association between the phenotype and each SNP separately, which has some drawbacks such as the need of multiple-testing correction and low power due to correlation between markers. Fitting a mixed model to get the best linear unbiased prediction of all the SNP simultaneously overrides these limitations. One approach is to use the marker-based G matrix of realized genotypic relationships (GBLUP). The GBLUP strategy is usually employed for GWAS in animal breeding but has been scarcely explored in plants. This work compares GBLUP with CGWAS for cold tolerance at seedling stage in two rice breeding populations (306 indica and 302 tropical japonica inbred lines, genotyped with ~50K and ~30K SNP, respectively) adapted to the subtropical Uruguayan rice growing area. The correlation between the p-values of CGWAS and GBLUP was 0.988 and 0.925 for the indica and tropical japonica population respectively. A total of 14 QTL were found in the indica population, and 18 in the tropical japonica population. There was 1 QTL in indica and 2 in tropical japonica that were detected with CGWAS but were not significant with GBLUP. Conversely, there were 3 QTL for indica and 8 for tropical japonica that were detected only with GBLUP. This suggest that GBLUP better reveals the full genetic complexity of the cold tolerance in both breeding populations.

Key words: Genomic selection, mixed models, *Oryza sativa*, cold tolerance at seedling stage.