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# Comparison of Conventional and GBLUP Genome-Wide Association mapping of cold tolerance in advanced rice breeding populations

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## Introduction

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 the trait's genetic architecture in the breeding population is.

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 Single Nucleotide Polymorphism (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 (BLUP) of all the SNP simultaneously overrides these limitations. One approach is to use the marker-based G matrix of realized genotypic relationships (GBLUP) and this strategy has scarcely been explored in plants.

## Objectives

- Detect Quantitative Trait Loci (QTL) associated with cold tolerance at seedling stage.
- Compare GBLUP and CGWAS methodologies.

## Material and Methods

Phenotypic information: With a complete random blocks design with three blocks, 306 ssp. indica lines and 302 ssp. tropical japonica lines were evaluated. At 21 days post seedling, lines undergone a 5 °C ± 0,5 during 32 h treatment. Seven days after the treatment, damage was registered, relative to cold sensitive and tolerant witnesses.

Genotypic information: 50K SNP of the 306 ssp. indica lines and 29K SNP of the 302 ssp. tropical japonica lines, obtained by Genotyping By Sequencing.

CGWAS was implemented using the following model:

vector of fixed effects

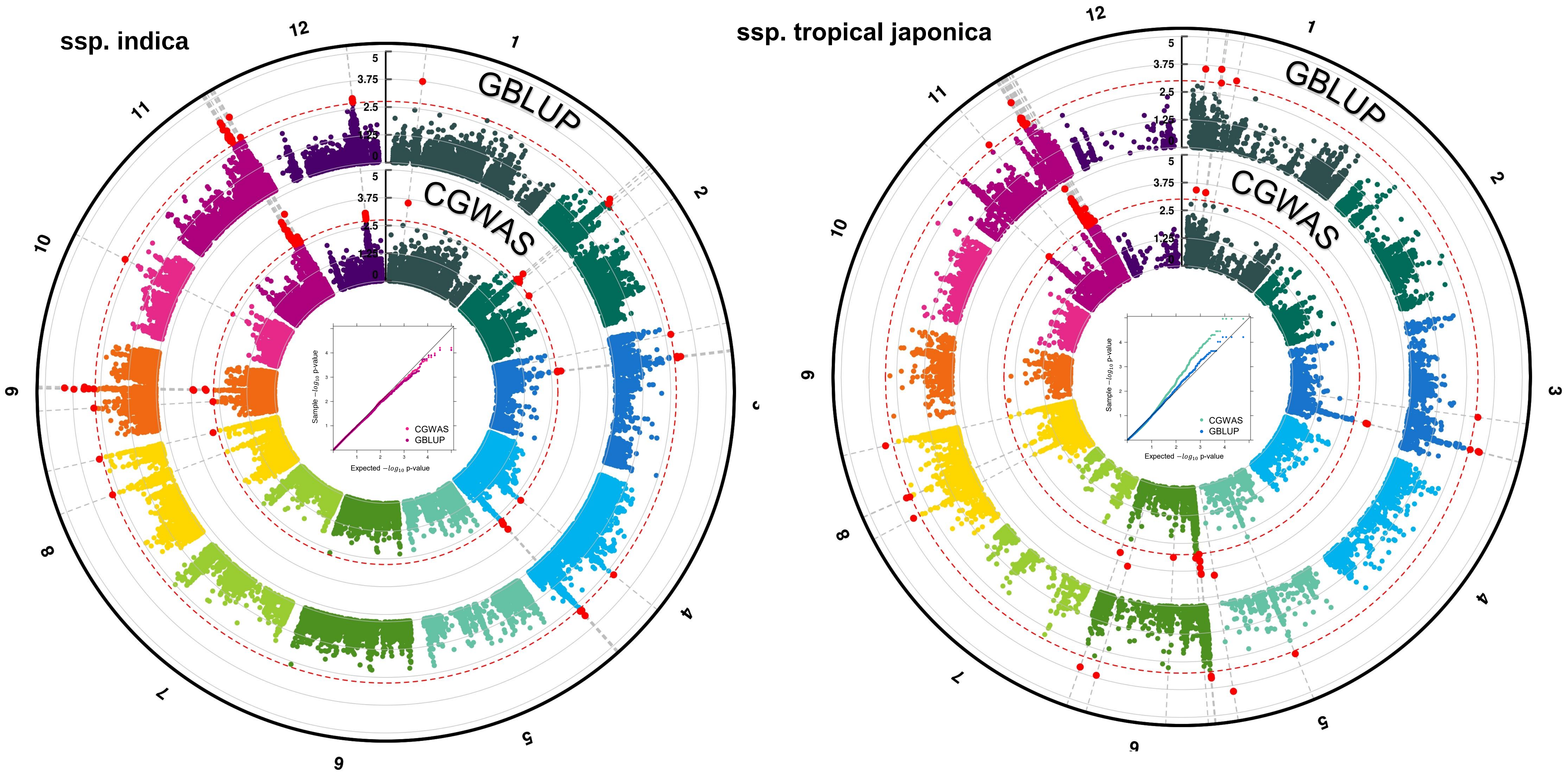
random genotypic effects with $u \sim N(0, Gu2)$ where $G$ is the realized genotypic relationship matrix

$$\text{vector of adjusted phenotypic means for each line} \longleftarrow y = Xb + Zu + e \longrightarrow \text{residual effects vector with } e \sim N(0, I_e^2 2)$$

incidence matrices that relate $y$ with $b$ and $u$

In CGWAS, fixed effects are the general mean and each SNP separately while in GBLUP fixed effects are only the general mean. In GBLUP, SNPs effects and the significance of associations was be derived from genomic breeding values (u), following the methodology used by Gualdrón Duarte et al. (2014) and the calculations proposed by Aguilar et al. (2019) to obtain p-values.

Figure 1. Ciruclar Manhattan Plots and QQ-plots of GWAS for each ssp. and methodology: indica (left) and tropical japonica (right), Manhattan Plot of CGWAS (inner circle), Manhattan Plot of GBLUP (outer circles), QQ-plots (inside the circles).


ssp. indica

ssp. tropical japonica

## Results

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.

## Conclusions

Both methodologies allowed the identification of novel QTL for cold tolerance in seedling stage but GBLUP better revealed the full genetic complexity of the cold tolerance in both breeding populations.

## References

Aguilar, I. et al. 2019. DOI:https://doi.org/10.1101/555243
Gualdrón Duarte, JL. et al. 2014. DOI: https://doi.org/10.1186/1471-2105-15-246.