

RESISTANCE TO MULTIPLE TEMPERATE AND TROPICAL STEM AND SHEATH DISEASES OF RICE

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INTRODUCTION

Stem rot and aggregated sheath spot of rice are the two major stem and sheath diseases affecting rice (*Oryza sativa* L.) in temperate areas and sheath blight is a major disease in tropical areas. Resistance to these diseases is a key objective in rice breeding programs, but phenotyping is complicated by the confounding effects of phenological and morphological traits such as flowering time (FT) and plant height (PH).

OBJECTIVES

This study sought to identify quantitative trait loci (QTL) for resistance to the three major rice stem and sheath diseases after removing the confounding effects of FT and PH.

MATERIALS & METHODS

Mapping population: 643 Uruguayan rice advanced inbred lines (327 *indica* and 316 tropical *japonica* ssp.)

Genotyping: two separate sets of GBS SNPs (49.6K for *indica* and 28.9K for tropical *japonica*) were used.

Phenotyping: Resistance was measured in four years of field trials (2010 to 2013) in Eastern Uruguay and in two (for SCL) and three (for ROS) greenhouse (GH) trials with a 0-9 scale. Phenotypic means were spatially and phenologically corrected, and weighted based on each trial heritability.

Association analysis: GWAS and multi locus analyses were tested by fitting the mixed linear model $y = X\beta + Zu + e$, where y is a vector of adjusted phenotypic means, β is a vector of fixed effects (single SNPs for the GWAS scan, and multiple selected SNPs for the multi locus analysis), u is a vector of random genotypic effects with $u \sim N(0, K\sigma_G^2)$, e is a vector of residual effects with $e \sim N(0, K\sigma_e^2)$, X and Z are incidence matrices that relate y to β and to u respectively, K is the realized genotypic relationships matrix calculated as the variance-covariance matrix of the PCA from SNP data.

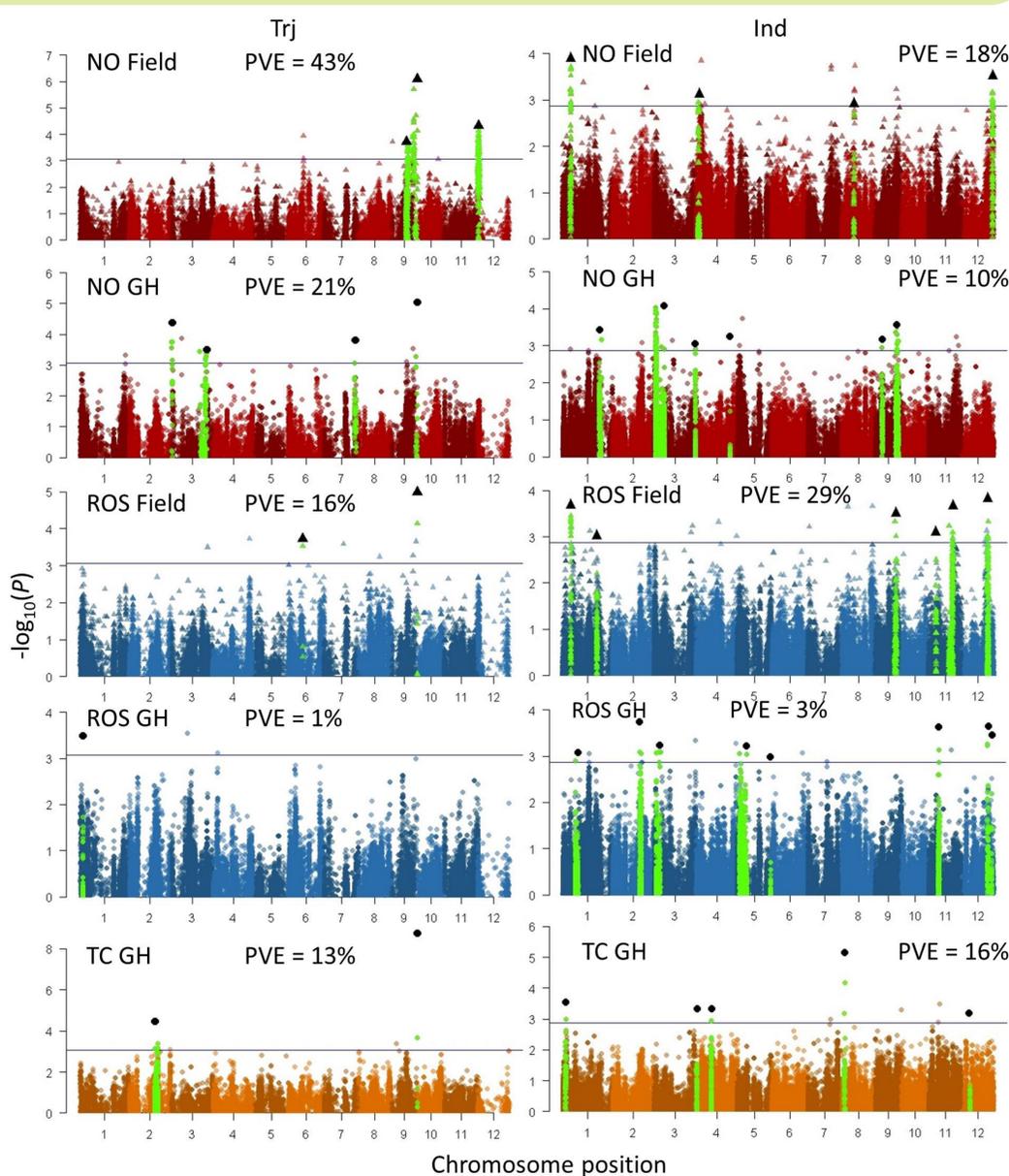


Figure 1. Manhattan plots of the GWAS scan for resistance to *Nakataea oryzae* (NO, red), resistance to *Rhizoctonia oryzae-sativae* (ROS, blue), resistance to *Thanatephorus cucumeris* (TC, orange) in field (triangles) and greenhouse (circles) trials for tropical japonica (Trj, left panel) and indica (Ind, right panel) populations. All SNP in the region of defined QTL are highlighted in light green, and the SNP with highest $-\log_{10}(P)$ in each QTL is colored in black. Percentage of phenotypic variance (PVE) explained by the identified QTL is reported.

RESULTS AND CONCLUSION

A total of 29 QTL were found for resistance and not associated with FT or PH. A QTL on chromosome 9 accounted for more than 15% of the phenotypic variance for the three diseases. When resistance-associated SNPs at this locus from both the tropical japonica and indica populations were incorporated into the model, resistance was improved for all three diseases with little impact on FT and PH.

The confounding effect of some phenological and morphological traits on resistance to stem and sheath diseases can be efficiently controlled using appropriate phenotyping and analytical methodologies. When confounding factors are removed from the analysis, QTL associated with disease resistance have little effect on FT and PH. The effects of the disease resistance QTL found in this work suggest the existence of common physiological mechanisms for resistance to sheath blight, stem rot and aggregated sheath spot, three of the main fungal diseases affecting rice in temperate and tropical areas worldwide.

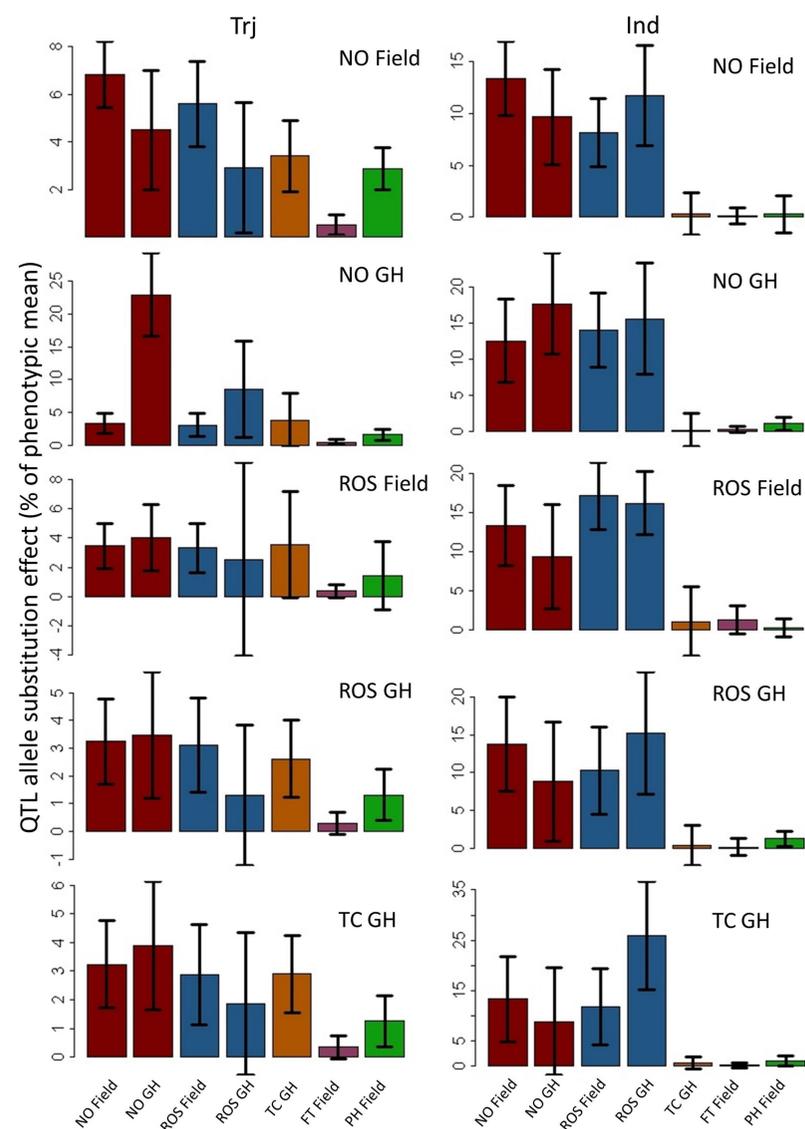


Figure 2. Effects of QTL for resistance to *Nakataea oryzae* (NO), *Rhizoctonia oryzae-sativae* (ROS), and *Thanatephorus cucumeris* (TC) in field and greenhouse (GH) on diseases, flowering time (FT), and plant height (PH) in tropical japonica (Trj) and indica (Ind) populations, estimated with a multi-loci model with all the QTL found in this study for each disease. Allele substitution effect are reported as the percentage of the phenotypic mean.

FUNDING

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