

INTRODUCTION

Stem Rot and Aggregated Sheath Spot are among the major diseases affecting temperate rice worldwide, and are caused by the fungi *Sclerotium oryzae* (SCL) and *Rhizoctonia oryzae-sativae* (ROS), respectively. Resistance to these diseases is quantitatively inherited and has low heritabilities in field trials, making conventional breeding difficult. Furthermore, reports on QTL for resistance to both diseases are scarce. Thus, identification of QTL is needed for marker assisted breeding for these traits.

OBJECTIVES

Identify QTL for resistance to SCL and ROS in temperate advanced rice germplasm, and quantify its effects and proportion of phenotypic variance explained by them.

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 trials with a 0-9 scale. Phenotypic means were spatially and phenologically corrected, and weighted based on each trial heritability.

Association analysis: Two mixed models, one with P (PCA scores) for tropical *japonica*, and another with K (kinship) matrices for *indica*, were used for GWAS scan accounting for different levels of relatedness.

Multiloci Mixed Models correcting for population structure where fit with selected associated SNP for each trait, and the best set of SNP (highest R² of the multiloci model) was identified with a stepwise procedure.

CONCLUSIONS

High proportions of phenotypic variance of both diseases were explained by the selected SNP. This highlights the usefulness of GWAS in advanced breeding populations and its ability to capture the relevant genetic variants for quantitative traits.

REFERENCES

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RESULTS

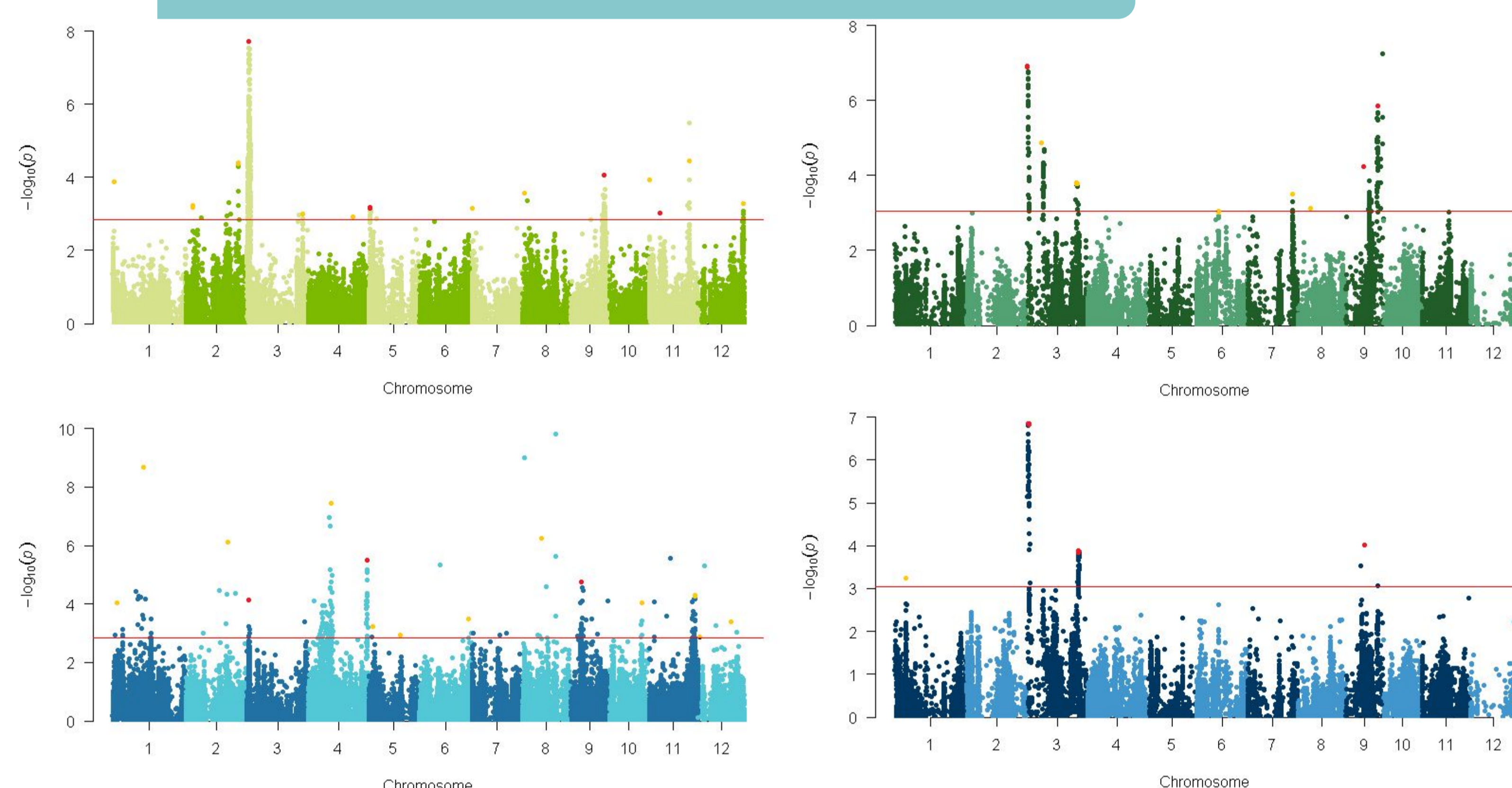


Figure 1. GWAS scans of averaged resistance to: A) SCL in *indica*; B) ROS in *indica*; C) SCL in tropical *japonica*; and D) ROS in tropical *japonica*. Significance threshold adjusted by effective independent tests. Dots in yellow are the selected SNP for full multi loci models, and in red are the SNP in the optimal multiloci models.

Associated SNP were found for both traits and in both rice subspecies. Two QTL (in chr. 3 and 9) were consistent across pathogens and subpopulations (Figure 1 and Table 1). The best multiloci models from the stepwise analysis had three to four SNP. Additive effects of the relevant SNP explained high proportions of the phenotypic variance (Table 1).

Table 1. Best multi loci model for each subpopulation and trait.

Ssp.	Trait	SNP	Effect	-log ₁₀ (p)	R ²
Indica	SCL	S3_1227543	-0.35	9.69	0.32
		S5_872081	0.31	2.50	
		S9_20009406	-0.23	2.93	
		S11_6934652	0.40	4.24	
Indica	ROS	S3_1204281	-1.47	11.65	0.48
		S4_13154793	0.56	2.76	
		S9_6450665	-0.29	0.94	
Tr. Japonica	ROS	S3_1299562	-0.70	5.53	0.36
		S3_31256588	-1.07	3.61	
		S9_19586603	0.38	3.12	
Tr. Japonica	SCL	S3_579022	-1.65	7.95	0.23
		S9_14394903	0.48	2.68	
		S9_22544543	0.68	8.80	

FUNDING



MONSANTO'S
Beachell-Borlaug
International Scholars Program



Instituto Nacional de Investigación Agropecuaria
URUGUAY



AGENCIA NACIONAL
DE INVESTIGACIÓN
E INNOVACIÓN