GWAS for Resistance to Stem Rot and Aggregated Sheath Spot of Rice Advanced Breeding Lines

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INTRODUCTION

Stem Rot and Aggregated Sheath Spot are among the major diseases affecting temperate and subtropical 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.

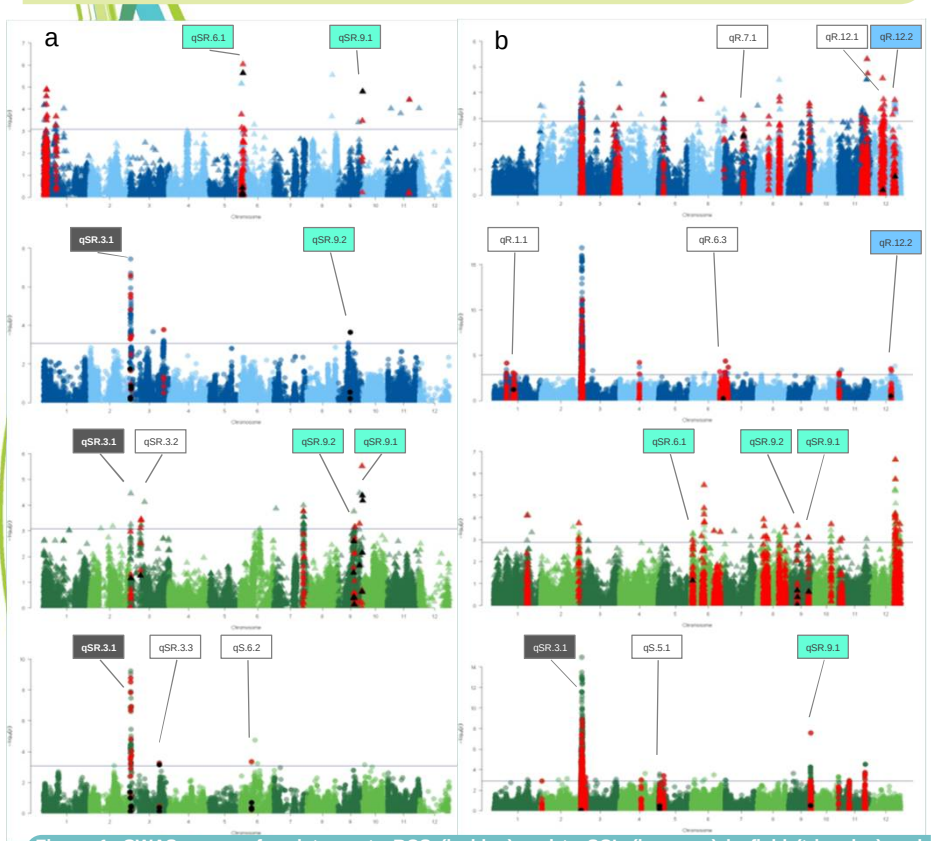

Figure 1. GWAS scans of resistance to ROS (in blue) and to SCL (in green) in field (triangles) and greenhouse (circles) in Japonica population (panel a) and Indica (panel b). Significance threshold adjusted by effective independent tests. Points in red are the non-collinear SNP for the initial full multi loci model. Points in black are the selected SNP in the final multi loci model. Consistent QTL across environment, diseases and populations are highlighted in dark grey; across diseases only in mint green; and across environments only in light blue.

RESULTS AND CONCLUSSION

One QTL in chr. 3 (qSR.3.1) was consistently found across indica and japonica populations, field and greenhouse experiments and for resistance to both ROS and SCL diseases. Three QTL (qSR.6.1, qSR.9.1 and qSR.9.2) were found at least in one environment or in one population for both diseases. QTL qR.12.2 for ROS was found for field and greenhouse environments. QTL x environment and QTL x disease interactions was found.

SNP effects are typically overestimated with the simple linear regression model used for GWAS scan due to the so-called Beavis effect. Our approach with a **multiloci mixed model enable a more conservative estimation of SNP effects** and the proportion of phenotypic variance explained by them. This provides **a more realistic assessment of the usefulness of the SNP for assisted selection**. We found **7% to 51% of phenotypic variance** of the studied diseases explained by the selected SNP. Since both ROS and SCL usually have low heritabilities in field trials, this finding suggests the **convenience of these SNP for molecular breeding**. Furthermore, our results highlight the **usefulness of GWAS in advanced breeding populations** and its ability to capture the relevant genetic variants for quantitative traits.

OBJECTIVES

Identify QTL for resistance to SCL and ROS in subtropical élite rice germplasm, and estimate their 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 (GH) 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 non-collinear SNP belonging to all identified QTL for each trait (in red in Fig. 1). The SNP with significant effect (α=0.05) in the final Multiloci Model were selected with a backward procedure.

Population	Disease	Environment	QTL	SNP	Effect	$-\log_{10}(P)$	R^2
Japonica	ROS	Field	qSR.6.1	S6_1092113	1.2	5	0.51
				S6_1502573	2.8	68	
				S6_1620285	1.7	10	
				S6_1664716	1.4	8	
				S6_1695608	1.4	8	
				S6_2093328	1.3	7	
				S6_2269816	1.1	3	
			qSR.9.1	S9_22544543	0.5	5	
	ROS	GH	qSR.3.1	S3_727102	1.6	10	0.10
				S3_1009844	1.5	5	
				S3_1009847	1.6	13	
				S3_1395351	2.1	22	
				S3_1463198	0.7	1	
			qR.9.2	S9_11361008	1.2	2	
				S9_11361227	2.5	23	
				S9_11406394	1.6	12	
	SCL	Field	qSR.3.1	S3_1147366	0.6	2	0.21
			qSR.3.2	S3_10133802	0.5	4	
			qSR.9.2	S9_14398981	2.5	8	
				S9_14409367	1.1	5	
				S9_14567057	1.2	3	
				S9_14584021	2.6	9	
				S9_14698903	1.5	4	
				S9_14811026	3.9	74	
			qSR.9.1	S9_19737129	0.8	7	
				S9_22091701	0.7	2	
				S9_22275709	1.6	16	
				S9_22395327	0.8	4	
				S9_22544543	1.1	7	
	SCL	GH	qSR.3.1	S3_727102	1.0	2	0.07
				S3_1009844	1.2	3	
				S3_1009847	1.9	9	
				S3_1463198	1.3	3	
				S3_1579415	1.8	8	
			qSR.3.3	S3_27309938	1.0	2	
				S3_27406180	2.1	9	
				S3_27429552	5.2	14	
			qS.6.2	S6_10108766	2.7	4	
				S6_10115242	3.1	6	
				S6_10124510	1.8	4	
				S6_10203048	2.0	2	
Indica	ROS	Field	qR.7.1	S7_16851259	5.9	9	0.08
			qR.12.1	S12_11358117	6.2	42	
			qR.12.2	S12_22513564	5.0	20	
	ROS	GH	qR.1.1	S1_17922741	11.4	93	0.30
			qR.6.2	S6_29086916	10.0	19	
			qR.12.2	S12_18891436	3.6	7	
	SCL	Field	qSR.6.1	S6_909555	2.2	4	0.21
			qS.9.1	S9_7924883	7.3	42	
				S9_7936052	8.1	174	
				S9_7996044	3.1	3	
			qS.9.2	S9_18276737	6.1	88	
	SCL	GH	qS.3.1	S3_555587	1.7	4	0.34
			qS.5.1	S5_891267	7.1	191	
				S5_891285	7.0	186	
			qSR.9.1	S9_19997257	1.5	2	

Table 1. Results of multiloci model analysis with the effect and significance ($-\log_{10}(P)$) of selected SNP grouped by QTL. Proportion of phenotypic variance (R^2) explained by each model is shown.

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INIA Instituto Nacional de Investigación Agropecuaria Uruguay

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