

Physiological Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice.

J.E. Rosas^{a,b}, S. Martinez^b, P. Blanco^b, F. Perez de Vida^b, V. Bonnacarrere^b, G. Mosquera^c, M. Cruz^d, S. Fernandez^b, S. Garaycochea^b, E. Monteverde^e, S. McCouch^e, S. German^b, J.-L. Jannink^e, L. Gutierrez^{a,f}

^a College of Agriculture, University of the Republic, Uruguay jrosas@inia.org.uy

^b National Institute of Agricultural Research (INIA), Uruguay smartinez@inia.org.uy, pblanco@inia.org.uy, fperez@inia.org.uy, vbonnacarrere@inia.org.uy, sfernandez@inia.org.uy, sgaraycochea@inia.org.uy, sgerman@inia.org.uy

^c Rice and Beans Project, International Center for Tropical Agriculture (CIAT), Colombia g.m.mosquera@cgiar.org

^d Latin American Rice Fund (FLAR), Colombia maribel.cruz@cgiar.org

^e School of Integrative Plant Science, Cornell University, USA em638@cornell.edu, srm4@cornell.edu, jj332@cornell.edu

^f College of Agricultural and Life Sciences, University of Wisconsin-Madison, USA gutierrezcha@wisc.edu

ABSTRACT

Stem rot and Aggregated sheath spot of rice are the two major stem and sheath diseases affecting rice in temperate areas. Sheath blight is a major rice disease in tropical areas. Resistance to these diseases is a key objective in rice breeding programs, hindered by its challenging phenotyping and the confounding effects of phenological and morphological traits. The purpose of this study was to find quantitative trait loci (QTL) for resistance to these three major stem and sheath diseases of rice. A population of 316 tropical japonica and 325 indica advanced breeding lines was evaluated in field and greenhouse trials for resistance to the diseases. Field and greenhouse disease resistance phenotypic means adjusted by phenology and plant height were analyzed for association with 29K GBS tropical japonica single nucleotide polymorphisms (SNP), and with 50K GBS indica SNP. Resistance-associated SNP were fit in Multi loci analysis to estimate their reciprocal effect on the other diseases, flowering time (FT), plant height (PH) and yield (YLD), showing that resistant alleles for one disease improved the resistance to the others, and had little impact on agronomic traits. Multiple disease resistance QTL were found in chromosome 9, accounting for more than 15% of the phenotypic variance of the three diseases.