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REVEALING THE PREDOMINANCE OF *SACCHARUM SPONTANEUM* ALLELES FOR ORANGE RUST RESISTANCE IN SUGARCANE USING GENOME-WIDE ASSOCIATION

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Sugarcane orange rust (SOR) is a threatening emerging disease in many sugarcane industries worldwide. Improving the genetic resistance of commercial cultivars remains the most promising solution to control this disease. In this study, an association panel of 568 modern interspecific sugarcane hybrids (Saccharum officinarum x S. spontaneum) from Réunion's breeding program was evaluated for its resistance to SOR under natural conditions of infection. Two Genome-Wide Association Studies (GWAS) were conducted between disease reactions and 183,842 Single Nucleotide Polymorphism (SNP) markers obtained by targeted genotyping-by-sequencing. Five resistance Quantitative Trait Loci (QTLs), named Oru1, Oru2, Oru3, Oru4 and Oru5, were identified using a Single-Locus GWAS (SL-GWAS). These five QTLs all originated from the species S. spontaneum. A Multi-Locus GWAS (ML-GWAS) uncovered an additional but less significant resistance QTL named Oru6, which originated from S. officinarum. All six QTLs had a moderate to major phenotypic effect on disease resistance. Prediction accuracy estimated with linear regression models based on each of the five QTLs identified by SL-GWAS was between 0.16-0.41. Altogether, these five QTLs provided a relatively high prediction accuracy of 0.60. In comparison, accuracies obtained with six genome-wide prediction models (i.e. GBLUP, Bayes-A, Bayes-B, Bayes-C, Bayesian-Lasso and RKHS) reached only 0.65. The good prediction accuracy of disease resistance provided by the QTLs and the predominant S. spontaneum origin of their resistance alleles pave the way for effective marker-assisted breeding strategies.

Keywords: Genome Wide Association Study (GWAS); genomic prediction; sugarcane orange rust (SOR); resistance alleles; sugarcane; *S. spontaneum*

