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| Title of Entry                       | : Sucrose and starch stem storage at heading in rice: A trait to increase yield potential?  |
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| Abstract                             | : A high capacity for accumulation of non-structural carbohydrates in stem after heading is a desirable trait to increase yield potential in rice. However, the value of metabolomics in rice has been poorly explored in rice breeding programs. This study aims at studying an indica diversity panel (244 acc) to (i) validate a phenotyping platform for starch (STA) and sucrose (SUC) quantification in rice stems, (ii) identify across different years and management conditions (transplanting (TR) and wet direct seeding(WDRS)) the source-sink background where SUC and/or STA accumulation in stem at heading favors yield potential, and to (iii) dissect the genetic control for SUC and STA at heading applying Genomic Wide Association Studies (GWAS) based on 83.374 SNPs. Two experiments were set up at CIAT, Palmira, in 2013 and 2014 dry seasons. A total of 1464 stem samples were analyzed using Near Infrared reflectance. STA concentrations varied from 3.26 to 157.18 mg/g dw in 2013-TR and from 8.12 to 169.15 mg/g dw in 2014-WDRS. SUC concentrations ranged from 23.12 to 146.24 and from 26.72 to 140.76 mg/g dw, for 2013-TR and 2014-WDRS respectively. STA and SUC concentrations in the main stem and Grain yield (GY) were significantly higher for 2013-TR than 2014-WDRS. For both environments, higher SUC and STA concentrations were observed in medium and late maturity groups. However, SUC and STA only contributed to GY in the medium maturity group with high Grain Number (GN). Although there was a significant environmental effect on both STA and SUC, GWAS analysis resulted in the identification of 17 loci for STA and 7 loci for SUC across environments, different from loci controlling cycle length. We found only 13 loci related to both NG and STA or SUC, indicating the complexity to find out a relation between metabolic and agronomic traits. A total of 18 loci associated to cloned genes were related to abiotic-biotic |

stress tolerance, panicle formation, grain size, cell division or cell wall biosynthesis. The potential use of these associations as markers to increase yield potential and the use of the NIRS as a phenotyping platform for NSC is discussed.

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