

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Pre-breeding
Keyword 2	: Germplasm Enhancement
Keyword 3	: Marker-assisted selection
Title of Entry	: Identifying Panicle Architecture Traits for Rice Improvement: A Treasure Hunt from Genome-wide Association Studies to QTL Validation, Marker Development and Germplasm Release
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Abstract : The Rice Diversity Panel 1 (RDP1) was developed for genome-wide association (GWA) studies to explore the five diverse rice (*Oryza sativa*) subpopulations (indica, aus, aromatic, tropical and temperate japonica). RDP1 was genotyped with 700,000 SNPs and evaluated for over 30 agronomic traits, including the panicle architecture traits (panicle traits) panicle length, primary panicle branch no., percent fertility, no. of florets, seeds and sterile florets per panicle. Most rice grown in the Southern USA is tropical japonica, thus this subpopulation is of interest to U.S. rice breeders. Objectives of this study were to 1) validate panicle trait GWA-QTL identified in RDP1 using a bi-parental recombinant inbred line (RIL) population developed from tropical japonica RDP1 accessions, 2) develop markers useful for marker assisted selection (MAS) based on GWA-QTL SNPs, and 3) select RILs with diverse panicle traits for germplasm release. ‘Estrela’ and NSFTV199 are phenotypically and genotypically divergent, thus excellent parents for developing a population to validate GWA-QTL by overlaps with RIL-QTL, especially for Japonica subpopulations. The Estrela/NSFTV199 population was evaluated for 15 of the same agronomic traits as RDP1 and genotyped with 137 SSR markers. QTL analyses revealed ~100 GWA-QTL that overlapped with the 70 RIL-QTL. Of the 24 panicle trait RIL-QTL, 14 had overlapping GWA-QTL with underlying candidate genes, and eight of these had R² values above 0.13. Significant SNPs, in the overlapping GWA-QTL with high R² values, were further examined for marker development. These regions, on chromosomes 1, 4, 7 and 8, were associated with known genes, GN1A, RFL, FZP and ASP1 which affect seed number, panicle branching and/or spikelet formation. Based on 27 significant SNPs, Kompetitive Allele Specific PCR (KASP) markers were designed for potential use in MAS, with about half the KASP markers validated to reliably differentiate the SNPs in diverse accessions. To capture the phenotypic variation in panicle traits for rice improvement, a subset of 38 RILs was evaluated for yield, grain shape and percent chalk in replicated plots. Six of the most promising RILs are being evaluated in a replicated yield trial to identify high yielding RILs with diverse panicle architecture useful for rice improvement.

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