

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Yield: Grain quality and quantity
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Genetics of Yield Grain quality and quantity Keyword 1	: Grain yield
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Title of Entry	: Multi-Environment Database on Rice Yield Traits Generated by GRiSP Phenotyping Network: A Genome-Wide Association and GxE Study
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: The GRiSP Global Rice Phenotyping Network (2011-2016) field-phenotyped an indica-rice diversity panel (300 accessions), in order to detect genomic loci controlling yield potential and adaptation traits through genome-wide association studies (GWAS). A data subset is presented, comprising days from sowing to flowering (DTFL), plant height (PHT), grain yield (GY), % sterility (PCST) and 1000 filled grain weight (TGW) observed under irrigated conditions in 15 environments in the Philippines, Senegal, Colombia, China and India. GWAS was conducted on imputed phenomics datasets by using three approaches: (1) analyses for traits observed at individual sites and for means for all sites; (2) additive main effects and multiplicative interaction (AMMI) analysis, generating GxE terms that were considered as traits for GWAS; and (3) slope and regression coefficients for correlations of trait values vs. climate variables for each genotype, also treated as traits. The panel was genotyped by GBS, providing 17k SNP markers. For all traits, significant GWAS-QTLs were found for individual sites or for global means. QTLs for GxE responses (approaches 2 and 3) were found only for the DTFL trait. A highly significant QTL on chr7 (-log(P)=7.1) for mean DTFL across sites was associated with candidate genes HEN1 (methylates micro-RNA involved in flowering) and GIDL2 (gibberellin receptor). A strictly environment-dependent QTL for DTFL on chr2 (approaches 1 and 2; -log(P)=6.7) was associated with SAP18 (histone deacetylase involved in flowering) and was related to day-length response of flowering. Another such QTL was associated with OsERS1, an ethylene receptor related to

flowering. For GY, a major QTL on chr3 was associated with several cytokinin related genes, including an IPP transferase. GWAS results for PHT were dominated by SD1. QTLs for other traits are awaiting analysis. These first results are encouraging, confirming that (1) multi-E field phenotyping provides added value for gene discovery; and (2) AMMI principal components can serve as proxies for GxE response traits, are meaningful for genetic analysis and can sometimes be related to specific environment factors. This study also provides promising methods for the analysis of new data resources expected from the RICE-CRP phenotyping network, the successor of the GRiSP network.

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