

Category	: 8th Rice Genetics Symposium
Select Theme	: High through-put technologies: Genotyping, Phenotyping and Omics
Endorsement email	:
High through put technologies Genotyping Phenotyping and Omics Keyword 1	: SNPs
High through put technologies Genotyping Phenotyping and Omics Keyword 2	: Phenotype
High through put technologies Genotyping Phenotyping and Omics Keyword 3	: Variants
Title of Entry	: Uniqueness amongst the Indica and Japonica subpopulations within a diverse collection of Vietnamese Rice
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Vietnam is an important country for rice production, both for export and for providing a staple food for circa 100 million people. Vietnam's national seedbank holds a collection of over 9,000 samples which represent the rich diversity of rice germplasm grown in Vietnam. This includes native and local landraces and varieties adapted to growing in the adverse growing conditions in the low-lying rice deltas. These regions are particularly vulnerable to the effects of climate change, meaning that there is an urgent need to understand the local diversity and use this knowledge to accelerate the breeding of new climate-resilient rice varieties. We have sequenced 616 rice (<i>Oryza sativa</i>) varieties from Vietnam using low-pass coverage whole genome sequencing (WGS) and obtained SNP variants, these represent 233 Japonica and 445 Indica subtypes with the remaining 35 being classified as admixed. We have added 107 accessions from the 3k Rice Genomes Project (3K) which represent all nine subpopulations, 56 from Vietnam and 51 from nearby East Asian countries. We have classified the Vietnamese Indica subtypes into six subpopulations, three of these subpopulations correspond to the modern bred varieties (XI-1B) and landraces native of Southeast Asia (XI-3) described by the 3K project. The subpopulation from South Asia (XI-2) is not represented in Vietnam as expected, and the admixture subpopulation (XI-adm) splits into two well defined subpopulations in Vietnam. There are four geographically defined Japonica subpopulations in Vietnam, two temperate (GJ-tmp) subpopulations centered around the red river delta, one subtropical (GJ-sbtrp) subpopulation in the northern highlands and one subpopulation in the south

which is related to GJ-trp. We are carrying out genome-wide phenotype-genotype association analysis (GWAS) on a variety of morphological traits, including grain characteristics, heading date, and inflorescence and leaf characteristics. Preliminary results show a strong association of grain length with markers on chromosome 3 for the whole population and for grain width with a different region on chromosome 3 for the Japonica subtypes. In addition we are characterizing the diversity and allele composition within the various subpopulation in relation to key breeding characteristics, such as resistance to pests, salinity, drought and geographical region of origin.

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