The GRiSP Global Rice Phenotyping Network:  
A multi-environment program to tap into  
useful genetic diversity

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The GRiSP Global Rice Phenotyping Network

• International community of rice scientists

• 3-yr phenomics program: kicked off in March 2011, phenotyping activities started in Oct. 2012

• Objective: Mining of genetic diversity to discover useful genes and alleles for rice molecular breeding
General strategy

• Conduct phenomics trials on the same diversity panel (two genetic groups – indica and tropical japonica, 300 acc. each)

• Full data sharing among partners with centralized data curation

• Genome Wide Association Studies (GWAS)

• Broad trait coverage with priority on yield potential, climatic adaptation and abiotic stresses
General strategy

• Traits are phenotyped in multilocation field hubs for GxE analysis

• Complementary HTP platforms for specific, crucial component traits

• Geographic, infrastructural linkages with major breeding programs and INGER*

• Compatibility with precursor projects such as GenPhen and ORYTAGE

• 700K SNP chip of Oryza SNP Consortium

*International Network for Genetic Evaluation of Rice
Highlights and Challenges

• Innovative approaches
  o Model assisted phenotyping (RIDEV, Ecomeristem)
  o Leaf antioxidant activity
  o Non-structural carbohydrate reserves
  o Lodging

• Need for high-throughput methodologies for field-based phenotyping (grain yield, yield components, biomass)
Outlook

• Completion of phenomics program for diversity panels by late 2014
• Published outputs on candidate genes, donor materials, and trait x trait and G x E interactions by 2015
• What’s next: in-depth studies on candidate genes discovered; moving into recombinant populations
• Need for HTP field phenomics for agronomic traits (grain yield, yield components, biomass)
Thank you.

See our poster and the Network’s website (http://ricephenonetwork.irri.org) for more details