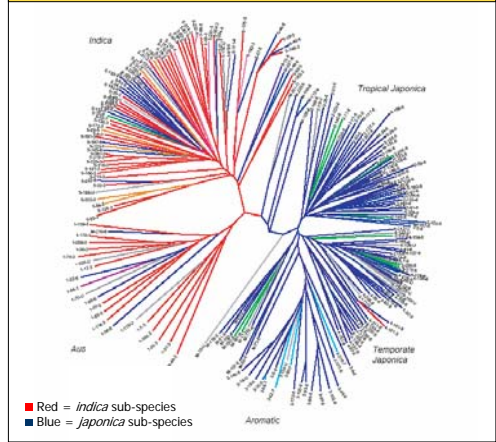




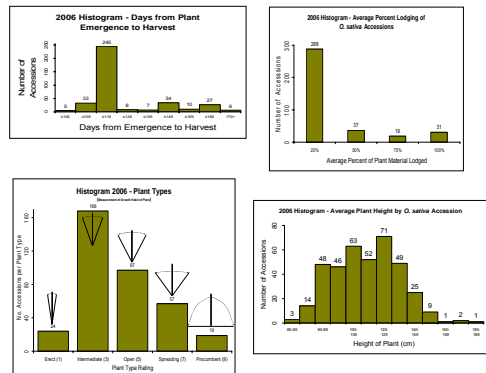
Abstract

Rice (*Oryza sativa* L.) has been divided into *indica* and *japonica* types (sub-species) since ancient times. Morphological, ecotypic and genetic differences distinguish these groups. Recently, five different sub-populations were identified using SSR markers. As part of this project, we aim to examine the genetics of quantitative trait variation for 32 agronomically important traits in the different sub-populations of *O. sativa* and to trace the sub-population origin of discrete molecular variants that are associated with the QTLs. During summer 2006 (and 2007), phenotypic data was collected on a diverse collection of 400 *O. sativa* accessions grown in the field at Stuttgart, AR using a RCB design with two replications. Data for heading date, plant height, plant type, tiller number, flag leaf length and width, panicle length, branches per panicle, and seed per panicle were collected. In addition, preliminary data on seed traits determined using the WinSeedle image analysis system including hull color, grain color, and seed length and width of paddy and brown rice are summarized. Variation for these traits will be compared to that of 100 accessions of the rice ancestral species, *O. rufipogon*. Once the second year of phenotypic data is collected on the *O. sativa* and *O. rufipogon* accessions, and all 500 accessions have been genotyped with SSR and SNP markers, we will use an association mapping approach to identify the genetic basis of quantitative variation in these materials.

Unrooted neighbor-joining tree based on C.S. Chord that identified the five rice sub-populations based on 234 *O. sativa* accessions genotyped with 169 SSR markers randomly distributed throughout the rice genome (Garris et al., 2005; Genetics 169: 1631–1638).

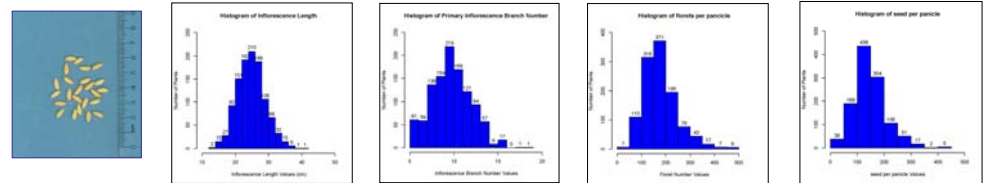
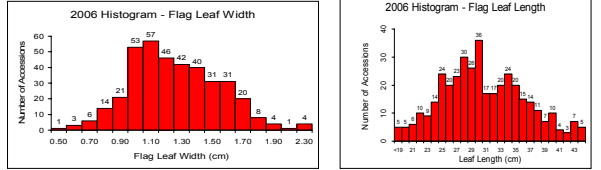


Field Traits



Flag Leaf Measurements

Single Panicle Traits



Variation in Plant and Seed Traits Found in a Diverse Collection of Rice Accessions

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Univ. of Arkansas Participants @ Stuttgart
Teresa Hancock, Program Technician
Daniel Wood, Greenhouse Technician
Grant Brock and Jason London, Student Interns

PROJECT MAIN OBJECTIVE

Determine if the sub-population structure in rice is predictive of transgressive variation (the occurrence of progeny displaying phenotypes more extreme than either parent) and begin to characterize the underlying genetic basis of this phenomenon in part by developing chromosome segment substitution lines (CSLs) between rice (*Oryza sativa*) and its progenitor, *O. rufipogon*.

Project Sub-objectives

Population Development and Phenotyping

- Purification and phenotypic analysis of 400 *O. sativa* for 32 traits in the field at Stuttgart, AR in 2006 and 2007
- Purification and phenotypic analysis of 200 *O. rufipogon* accessions at Cornell Univ. and Int. Rice Res. Inst. (IRRI), Philippines
- Field evaluation of 50 NILs with yield QTLs

Genotyping and Population Structure Analysis

- Population structure analysis of *O. rufipogon* using chloroplast and nuclear markers
- Selection of 3 wild *O. rufipogon* donors for chromosome segment substitution line development
- Choose a set of informative SNPs for association mapping

Database and project website

- Project web-site: www.ricehapmap.org
- Use of controlled vocabularies and standard descriptors for uploading into Gramene database (www.gramene.org)

Outreach

- Developing country collaboration including a 3-week course on rice production at IRRI, Philippines
- Summer internships – High School and undergraduate students
- Curriculum enhancement for middle schools in Harlem

Summary of the Association Mapping Study

Phenotyping *O. sativa* accessions

- Single plant purification of 400 *O. sativa* in the field at Stuttgart, AR in 2006 and 2007
- Phenotypic analysis of *O. sativa* for 32 traits (data summary to date shown on this poster)
- Bar-coding implemented for tracking plants and seeds
- Bar-code scanner used to collect data for several traits and identify the single plant from which data is uploaded into the project database

Phenotyping *O. rufipogon* accessions

- 100 *O. rufipogon* accessions were selected from 208 accessions based on plant type, seed set and crossability at Cornell Univ.
- Three plants of each *O. rufipogon* accession were genotyped with 36 nuclear SSR, chloroplast SSR and InDel markers
- Three plants from each of the 100 selected *O. rufipogon* accessions are growing in greenhouse to be phenotyped for the selected traits at Stuttgart, Arkansas

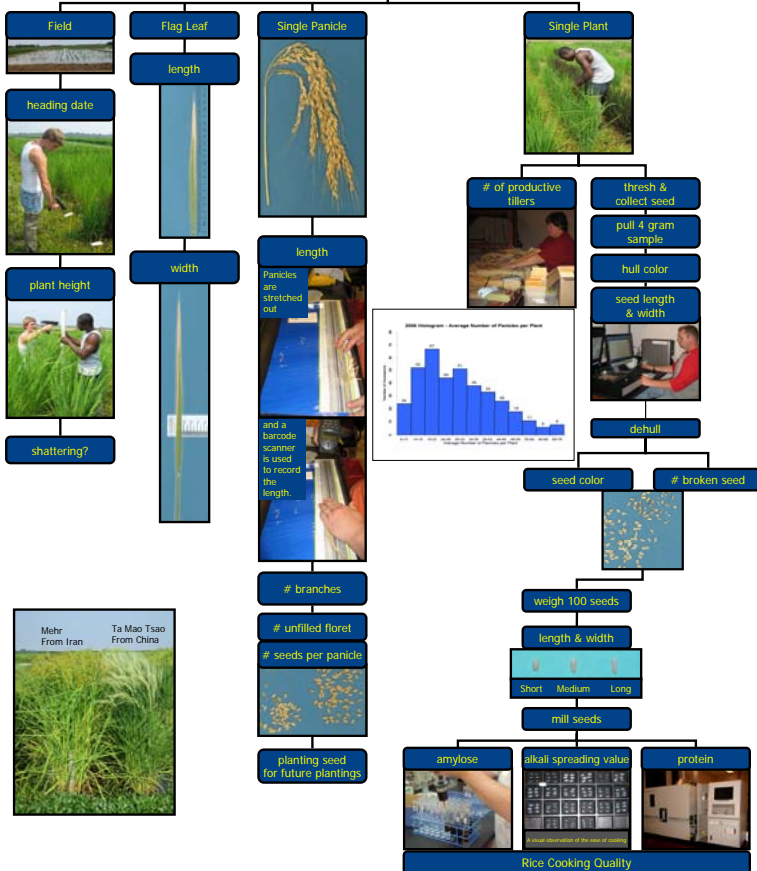
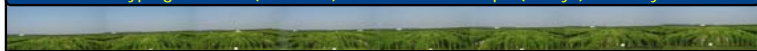
SNP chip development for association mapping

- In co-operation with co-PI: Carlos Bustamante (Dept. of Biological Statistics & Computational Biology, Cornell Univ.)
- Analysis of the *Oryza* SNP Project data which resequenced 20 diverse *O. sativa* genomes, suggested LD decayed at ~250 kb in *indica* sub-species and more slowly in *japonica* sub-species
- Based on these findings, tagging the entire *O. sativa* genome would require no more than ~16,000 SNPs
- It is expected that a 10,000 SNP chip will be sufficient for association mapping in rice

Association mapping

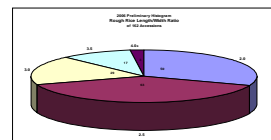
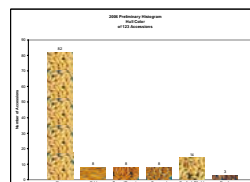
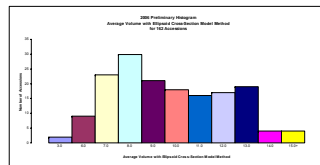
- The association mapping analysis will be conducted with the 10,000 SNPs on the 400 *O. sativa* and 100 *O. rufipogon* accessions for the 32 phenotypic traits

Phenotyping 400 rice (*O. sativa*) accessions in 2 reps (8 bays) over 2 years

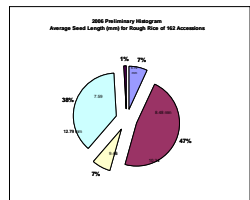
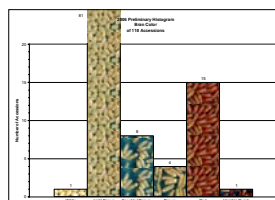


Seed Traits from WinSeedle Image Analysis System

Seed with the Hull



Dehulled Seed



Project Collaborators

Stefan Einarson (Translational Learning Center, Cornell Univ.)
Ken McNally (IRRI, Philippines)
David Galbraith (Univ. of Arizona)

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USDA-ARS, NSGC:
Dr. Harold Bockelman
USDA-ARS Beaumont, TX

Interactions with other groups

- Bar-coding system implemented at DB NRRC
- Include advanced rice breeding lines in SNP chip genotyping
- RiceCAP
 - Include parents of RiceCAP mapping populations in the phenotyping and genotyping effort
 - Include at least one *O. rufipogon* accession with sheath blight resistance
- Include the 20 *O. sativa* accessions selected by IRRI for *Oryza*SNP genotyping by Perlegen

Research supported by NSF Plant Genome Project grant "Exploring the Genetic Basis of Transgressive Variation in Rice" to Cornell Univ. with a sub-grant to the Univ. of Arkansas

For more information visit:

