

# Exploring the Genetic Basis of Transgressive Variation in Rice

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#### Summary of Scientific Objectives

Evidence to date suggests that the natural subpopulations in rice (Oryza sativa) and its progenitor, O. rufipogon are indicative of general combining ability. similar to the heterotic groups of maize. If true, this hypothesis has immediate implications for applied rice improvement and also offers insight into a fundamental problem in basic biology. We propose to test the hypothesis that sub-population structure in rice is predictive of transgressive variation (the occurrence of progeny displaying phenotypes more extreme than either parent) and to begin to characterize the underlying genetic basis of this phenomenon. To do this, we

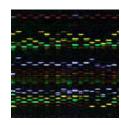
- 1. Develop a 10,000
  SNP chip for rice and create a haplotype map (ricehapmap) to document the differences in allelic variation within and between the different subpopulations of 0. sativa and 0. rufipogon
- Evaluate 26 core agronomic and grain quality traits in replicated field trials to provide the basis for association mapping
- 3. Develop libraries of chromosome segment substitution lines (CSSLs) along with high-resolution near isogenic lines (NILs) to explore the relationship between

- diversity and transgressive variation that occurs when subpopulations are crossed
- 4. Augment the collection of genetic resources for rice and make them available through the Genetic Stocks-Oryza (GSOR) at the Dale Bumpers National Rice Research Center (DBNRRC) in Stuttgart, Arkansas
- 5. Establish a dataset on rice diversity to help identify and characterize the genes and gene networks underlying a wide range of agriculturally valuable phenotypes in the cereals.

## What is meant by "transgressive variation"?

Transgressive variation refers to the production of offspring with phenotypic traits or characteristics (such as flowering time, number of seeds per plant) that exceed the phenotypic traits of the better parent.

This may result from positive cooperation between the genes present in the parental types. For example, genes from one parent could be activators or master switches at the top of the biological network leading to a phenotype.



What are molecular markers?

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#### Broader Impact

A better understanding of the genetic basis of transgressive variation in inbred crop species will have an immediate impact on the global research agenda for crop improvement. Presently, there is a great deal of interest in breeding hybrid rice as a mechanism for delivering superior varieties to farmers. But without a sound scientific understanding of the genetic mechanisms that underlie superior performance in naturally inbreeding species, we may overlook some of the most promising opportunities to capture superior performance in the world's inbred crop varieties. The knowledge we gain from this project will help inform our thinking about how to best characterize and manage *Oryza* gene pools and about the relative investments that we, as a society, choose to make in developing inbred and/or hybrid varieties of our most important food staples.

We work closely with the U.S. rice germplasm (GRIN) and Gramene databases to ensure public availability of

data and to enhance its comparative potential for the cereals community. As part of a targeted educational outreach effort, we will conduct hands-on genomics exercises in local high schools, host high school and undergraduate students as summer interns with an emphasis on broadening participation of under-represented groups, and will develop a multi-media video presentation exploring the culture of rice in America and in Africa to be shared with K-8th graders.

#### What is Phenotyping?

The phenotype of a plant is of great agricultural and economic importance, as it represents the coordinated set of traits and performance characteristics that are manifested by an individual variety over a range of environments.

Phenotypes that are important to crop production include yield, disease resistance, abiotic stress tolerance, flowering time, plant stature, grain quality and many other userelated traits. To begin

clarifying the relationship between phenotype and genotype, we collected data on 10 yield-related characteristics and 37 additional traits in the panel of 400 diverse cultivated rice varieties and over 100 wild rice species (0. rufipogon).

The phenotyping team at the Dale Bumpers National Rice Research Center (DBNRRC) in Stuttgart, Arkansas in cooperation with the University of Arkansas, collect information from field-grown plants. We recorded measurements on six plants for each of the 400 rice varieties in two locations over two years, evaluating a total of more than 4,800 plants during 2006 and 2007. Phenotypic data on greenhouse-grown O. rufipogon plants was collected at both Cornell University and at the DBNRRC. To keep track of the data, we created a bar-coding system that allows us to enter measurements for each plant directly into a database.



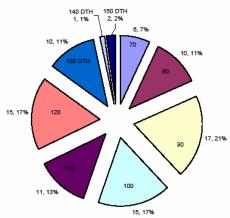
Phenotyping — the observable properties of an organism that are produced by the interaction between the genotype and the environment.

O. rufipogon being grown in

the greenhouse at the DB NRRC.



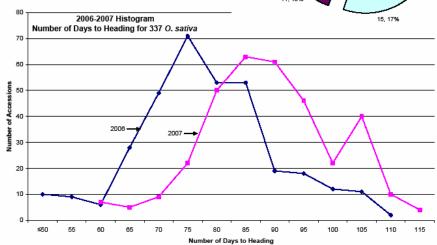
2007 DB NRRC NSF-TV Days to Heading for 87 O. rufipogon



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or http:// www.ars.usda.gov/ news/events

#### Interactions with other groups

- ·Bar-coding system implemented at DB NRRC
- •RiceCAP
  - Inclusion of an association mapping panel representing 470 historical and recent U.S. varieties
- Inclusion of the RiceCAP mapping population parents in the phenotyping and genotyping effort
- Include at least one *O. rufipogon* accession with sheath blight resistance
- Inclusion of the 20 O. sativa accessions selected for the Oryza SNP project using the SNP technology developed by Perlegen
- Inclusion of advanced rice breeding lines in SNP chip genotyping
- Gramene Coordination of the terminology and acronyms used for the phenotypic traits
- International Rice Research Institute (IRRI), Philippines

   Coordinating the terminology used for phenotyping the accessions