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Overall Project Objective

To understand how genes in rice (*O. sativa*) and its wild relatives evolved during domestication and how this affected plant and seed traits. Those traits selected by man and influencing the yield potential of modern-day rice varieties will be highlighted.

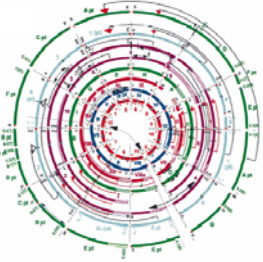
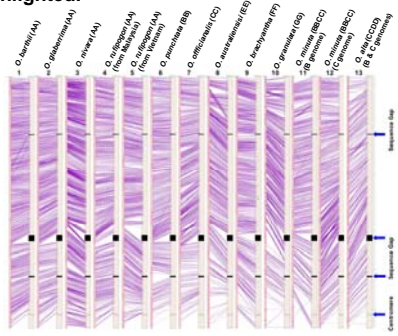


Diagram showing the relationship between the DNA found in cultivated rice, *O. sativa*, and the DNA found in six other rice wild *Oryza* species. (The relationships shown in this diagram are based on BAC-end sequence.)



Framework maps for 12 species, showing the short arm of chromosome 3 aligned against the Nipponbare (*O. sativa*) reference map. The Nipponbare map is on the right side of each alignment.

General Method: Mapping populations and other genetic stocks will be developed from crosses between these wild *Oryza* species and cultivated rice varieties described below. These populations will allow the desirable traits found in the *Oryza* species to be incorporated into the cultivated rice background and provide plant materials for research aimed at understanding the function of genes affecting yield, resistance to biotic and abiotic stresses. Ultimately, these studies will lead to improved modern rice cultivars.

Desirable traits found in *Oryza* species used for crossing

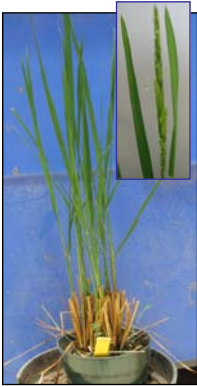
- O. nivara* – resistance to: blast, sheath blight, grassy stunt virus
- O. glaberrima* – weed competitiveness, more biomass, rice yellow mottled virus resistance
- O. rufipogon* - yield potential, blast and sheath blight resistance, tolerance to: aluminum, acid sulphate, iron toxicity
- O. barthii* - abiotic stress tolerance, green leathopper and bacterial blight resistance

Rice (*O. sativa*) parental varieties used for crossing

- LaGrue – Southern long-grain rice variety developed in Arkansas
- M-202 – Medium grain California rice variety
- Nipponbare – Medium grain Japanese rice variety that has been sequenced

Nipponbare x *O. nivara* Mapping Population

The objective is to discover where the phenotypic traits described below are located on the molecular "pseudo-molecule" for *O. nivara* and the sequence map for Nipponbare by creating a linkage map based on approximately 120 DNA (SSR) markers selected as polymorphic (different) between the two parents.



Nipponbare parent (cultivated rice)



Plants from the F2 mapping population



O. nivara parent

Research currently underway with this population:

Plant traits being evaluated

Heading date	Plant height	Basal leaf sheath color	Panicle length
Awn color	Culm type	Culm color	Leaf width
Panicle type	Lemma color	Seed shattering	Leaf length
Culm length	Palea color		

Seed traits being evaluated

Seed length	Curved seed length
Seed width	Curved seed width
Seed surface area	Seed volume

Development of the linkage map

Approximately 300 Nipponbare x *O. nivara* F2 progeny are being genotyped with 120 DNA (Simple Sequence Repeat) markers.

The genotypic (DNA) and phenotypic trait data will be used to construct a genetic linkage map for the phenotypic traits using JoinMap and MapQTL softwares.

This map will be compared to the previously developed Nipponbare DNA sequence map to see if the map positions for the traits are the same in the wild *O. nivara* as in cultivated rice (*O. sativa*).

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For more information visit:
<http://www.ars.usda.gov/news/events>
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