



Genetic Stocks-Oryza (GSOR) Collection



Rice Genetic Stocks Collection

The USDA Genetic Stocks – *Oryza* (GSOR) Collection at DBNRRRC serves as distribution center for genetic mutants and molecularly characterized genetic resources that are important to the rice research community. These genetic stocks have been created using specialized techniques such as induced mutation and cross-breeding. The GSOR program is responsible for storing, maintaining, documenting, and distributing (free of charge) these materials to the scientific community for use in genetic and genomic research. Ultimately these materials will aid in the understanding of the genetic control of traits that can be used to enhance the development of new cultivars that meet the needs of the U.S. rice industry.

Growth of GSOR Collection

YEAR RECEIVED	TYPE OF ENTRY	NUMBER OF LINES
2003	Individual Mutants	19
2004	Individual Mutant	1
2005	Katy/Zhe 733 Mapping Population	355
	Nipponbare	1
2006	Cocodrie/MCR01-0277 Mapping Population	327
	Individual Mutants	8
	Kinoshita Mutant Collection	193
2007	Jodon Mutant Collection	38
	California Mutant Collection	12
	Early/Katy Mapping Population	240
	USDA Core Collection	1794
2008	Katy Deletion Mutants	20103
	Nipponbare TILLING Mutants	6156
	Teqing/Lemont Mapping Population	125
Grand Total Lines		29372

Types of Entries Within the GSOR Collection

Collections within the GSOR are unique sets of material that have been described/donated by an individual researcher.

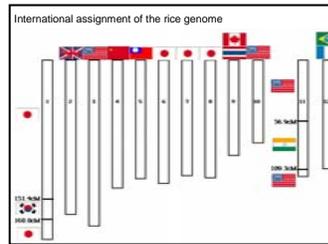
A deletion is defined as a fragment of DNA that was deleted from the rice genome. A **deletion mutant** is a rice line that carries this altered genome. These are useful to study the function of DNA sequences by evaluating how traits are impacted when a gene is “knocked-out” or deleted.

Individual mutants are lines that have been purposely mutated using chemicals and have novel characteristics such as male sterile (used to make hybrids), lesion mimic (used to study disease response), early flowering, double dwarf, colored hulls, and giant embryo.

Types of Entries Within the GSOR Collection (cont'd)

Mapping populations are used to study the genetic variation which occurs as a result of recombination of genes from two differing parental lines. The mapping populations in the collection are segregating for agronomic traits, disease resistance, maturity, yield, milling quality, and cooking quality.

TILLING (Targeting Induced Local Lesions In Genomes) is a reverse genetics technique that uses traditional chemical mutagenesis to create libraries of individual rice plants can be evaluated using high throughput screens for the discovery of mutations. (Source: http://tilling.ucdavis.edu/index.php/Main_Page)



This shows the assignment of the 12 chromosomes of rice to 10 different nations that participated in the International Rice Genome Sequencing Project. In 2005, this international consortium produced the complete genetic sequence of the Japanese cultivar, **Nipponbare**. This sequence information will serve as the baseline for comparison with other rice varieties to identify genes that control economically important traits. GSOR serves as an international distributor of the exact source of Nipponbare that was sequenced for use in genomic research.

Distribution Activity

Since the establishment of the GSOR, 6,455 genetic stocks have been distributed to U.S. and international researchers. A collection catalog is available on the GSOR web site: <http://ars.usda.gov/Main/Docx.htm?docid=8318>.

Data Collection

Barcoding software and handheld data collection devices have been implemented to streamline inventory, data collection and distribution activities.



For further information contact Anna McClung (anna.mcclung@ars.usda.gov) or Lorie Bernhardt (lorie.bernhardt@ars.usda.gov).