



Genetic Stocks-Oryza (GSOR) Collection 2009 Update



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 Mutants	1
2005	Katy/Zhe733 Mapping Population	355
	Nipponbare	1
2006	Cocodrie/MCR01-0277 Mapping Population	327
	Individual Mutants	8
	Kinoshita Mutant Collection	193
	Jodon Mutant Collection	38
2007	California Mutant Collection	12
	Early/Katy Mapping Population	240
	USDA Core Collection	1794
	Katy Deletion Mutants	22842
2008	Nipponbare TILLING Mutants	6156
	Cybonnet x C101A51 Mapping Population	183
2009	RiceCAP Association Mapping Population	462
	RiceCAP MY1 Mapping Population	210
	RiceCAP MY2 Mapping Population	300
Grand Total Lines		33141

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.

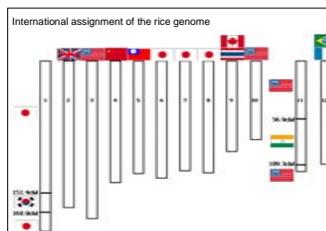
A deletion is defined as a fragment of DNA that was deleted from the rice genome. A **deletion mutant** is a rice line that carries this altered genome. These are useful to study the function of DNA sequences by evaluating how traits are impacted when a gene is “knocked-out” or deleted.

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, 6,741 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.



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