

**PLANT GENOME RESEARCH****\$89,470,000**

The FY 2005 Budget Request for the Plant Genome Research (PGR) Subactivity is \$89.47 million, equal to the FY 2004 Estimate.

**Plant Genome Research Funding**  
(Dollars in Millions)

	FY 2003 Actual	FY 2004 Estimate	FY 2005 Request	Change over FY 2004	
				Amount	Percent
Plant Genome Research Projects	84.45	89.47	89.47	0.00	0.0%
<b>Total, Plant Genome Research</b>	<b>\$84.45</b>	<b>\$89.47</b>	<b>\$89.47</b>	<b>\$0.00</b>	<b>0.0%</b>

The Plant Genome Research Subactivity was initiated in FY 1998, building upon an existing base of genome research supported throughout the BIO Activity. PGR supports projects that make significant contributions to our understanding of plant genome structure and function. Emphasis is placed on plants of economic importance, as well as plant processes of potential economic value. Long-term benefits of this research include fundamental breakthroughs in our understanding of plant biology and practical applications to crop improvement, and the development of novel, plant-based products.

The program was established as part of the National Plant Genome Initiative (NPGI). NSF plays a major role in the NPGI. Other participating agencies are USDA, DOE, USAID, and NIH. The NSF program is managed according to the guidelines and objectives of the NPGI, and it works closely with the other agencies in coordinating funding activities.

The National Plant Genome Initiative has issued its new five-year plan for 2003-2008. The FY 2005 Budget Request for PGR will support activities to meet the goals of the new NPGI plan, including:

- **Functional Genomics including Rice Functional Genomics:** Taking advantage of the recently completed sequence of the rice genome by an international consortium, PGR will support efforts to identify the function of all the rice genes and to develop functional genomics tools for rice. These efforts will be coordinated across agencies as well as internationally. Functional genomics research in other plant systems will continue to be supported.
- **Large-scale Sequencing of Genomes of Economically Important Plants:** The recent success in using new methods to concentrate gene-rich regions of large genome species, like maize, for sequencing will likely lead to increased efforts to sequence gene-rich regions of several other economically important plant species.
- **Informatics Tools Development:** Enormous amounts of data on many different aspects of plant genomics are rapidly accumulating. It is critical that seamless ways to access and make use of them by biologists be developed. Training that integrates informatics technologies and plant genomics research is also needed.
- **Interagency Activity on Research Collaboration with Scientists in Developing Countries:** As an important outreach activity for the NPGI, PGR plans to participate in the interagency program to support research collaboration between U.S. scientists and scientists in developing countries with a focus on plant genomics and plant biotechnology. Research will focus on crops important to developing countries such as banana and cassava, and traits critical to developing countries such as drought tolerance and disease resistance.

Highlights of areas supported:

**An integrated physical and genetic map of the maize genome.**

Research resources and research tools have been developed that now make it possible for scientists located anywhere in the U.S. to participate in plant genome research. For example, a five-year project to develop a detailed integrated physical and genetic map for maize has been completed and the map is allowing basic researchers to rapidly locate and clone genes of interest.



Variants of Maize

**Sequencing the maize gene space.**

Maize is the most economically important crop in the US and knowledge of its genome sequence can help improve crop yield and nutritional quality, and expand its uses. The maize genome is large (about the same size as the human genome at almost 3 billion base pairs) and complex, containing islands of genes among the sea of repetitive DNA sequences. Genes account for 1/4 to 1/3 of the genome.

Two Virtual Center projects funded in 2002 are trying several methods to isolate and sequence regions of the maize genome containing genes. Those projects have already released over a million sequences. Many new genes have been discovered in this collection, including genes involved in economically important processes such as flowering and disease resistance. The maize sequencing effort is also pioneering a novel method to sequence large genomes more efficiently.

**Studying gene expression in individual cells.**



A new method, laser capture microdissection, is being used by two projects to select individual cells from specific plant tissues. This method allows for more precise analysis of gene expression than had previously been possible. The data from these studies will be used to develop a gene-expression atlas for rice plants, and to dissect the expression patterns of genes regulating the development of maize shoot meristems, the part of

the plant that gives rise to the leaves.

**International collaboration in legume genomics.**

PGR has supported large-scale genome projects that will enable scientists to address major biological questions in plants, such as plant responses to environmental and biological stresses. Many of the projects are conducted by Virtual Centers each of which involves scientists from multiple institutions and disciplines. NSF's investment in plant genome research has stimulated international collaboration, including the international wheat genome research group, the international rice functional genomics consortium, the international tomato sequencing consortium, and the international *Medicago truncatula* (a model legume) research consortium. An international project to sequence the gene-rich portions of the *Medicago* genome was initiated in FY 2003 with support from PGR and the European Union (EU).

**Bringing the excitement of genomics to the classroom.**

High school teachers are being trained in genomics as part of a project studying the rice pathogen Magnaporthe. Teachers gain hands-on experience in cutting edge genomics research and develop new classroom materials to take back to their schools. The curricular materials are developed in line with state standards.

