National Plant Genome Initiative

Progress Report
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National Science and Technology Council
Committee on Science
Interagency Working Group on Plant Genomes

EXECUTIVE OFFICE OF THE PRESIDENT
NATIONAL SCIENCE AND TECHNOLOGY COUNCIL
WASHINGTON, D.C. 20502

Dear Colleague,

This report is an annual update from the Interagency Working Group (IWG) on Plant Genomes on activities of the National Plant Genome Initiative (NPGI). This year, it includes highlights that illustrate activities supported and coordinated by the NPGI member agencies.

Plant genomics research in the United States continues to advance the frontiers of plant biology, addressing fundamental biological questions using the tools, resources and conceptual framework of genomics. Exciting new discoveries over the past year include the finding that genetic variants of tropical corn (maize) have novel sugar composition with potential uses for biofuel production. Outcomes from research supported under the NPGI are also providing important inputs for improved agricultural practices in peanut breeding, fruit tree cultivar development, as well as breeding of disease resistant and salt tolerant plants. Technological advances made in the past year include the development of innovative technology to enable automated, high-throughput analysis of plant growth and development and a novel X-ray system to analyze root development. Continued advances in both biological discovery as well as technology development will be important as reliance on plants increases for materials, energy and fuels. Plants will continue to serve as a key resource as we address the challenges of increasing population, decreasing agricultural land area, and the impacts of climate change.

U.S. scientists involved in plant genomics research continue to cooperate nationally and internationally. The newly funded iPlant Collaborative is the first national cyberinfrastructure center to tackle global grand challenge questions in plant biology that will impact larger issues in agriculture. Research collaborations continue to include developing country partnerships focused on issues of local importance such as flood tolerance.

The Interagency Working Group on Plant Genomes continues to provide strong leadership and stewardship for NPGI activities, ensuring continued world-class research and training to advance the application of genomics to the improvement of agriculturally important plants. This leadership remains essential as we address the major societal challenges of meeting the need for increased food and fiber production, the need for a cleaner environment and additional renewable resources.

Sincerely,

Sharon L. Hays Arden L. Bement Elias A. Zerhouni

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Committee on Science
National Science and Technology Council

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Introduction

The National Plant Genome Initiative (NPGI) was established in 1998 as the coordinated national plant genome research project. The completion of the tenth year marks the fourth year of the Initiative under the second NPGI Five-Year plan entitled, "National Plant Genome Initiative: 2003-2008" (http://www.ostp.gov/NSTC/html/npgi2003/index.htm). Coordination of activities, guidance and oversight is provided by the Interagency Working Group on Plant Genomes (IWG-PG) under the auspices of the Committee of Science of the National Science and Technology Council with the Office of Science and Technology Policy. Participating agencies include the National Science Foundation (NSF), Department of Agriculture (USDA), Department of Energy (DOE), National Institutes of Health (NIH), the U.S. Agency for International Development (USAID), the Office of Science and Technology Policy (OSTP), and the Office of Management and Budget (OMB). Each agency participates in the development of the NPGI plans and participates in its activities in a manner consistent with its specific mission and based on available resources.

Plants contribute to worldwide economic sustainability and security, as sources of food, fiber, feed, and fuel. Improvements in agronomic practices and production have led to record agricultural productivity, with the three major U.S. crops of corn, soybean, and wheat alone valued at over $60 billion and exports of these valued at over $24 billion.

The significant gains in crop productivity parallel the scientific achievements of plant genomic research. Work supported through the NPGI leverages expertise from basic plant biology through information sciences to breeding, with resources and in-kind contributions from multiple Federal agencies. These activities provide fundamental knowledge about the genetic makeup of plants, which has led, and will continue to lead to new discoveries about the biology of plants of economic importance and plant processes of economic significance.

This report includes brief highlights of activities in the past year, illustrating rapid advances across the spectrum of NPGI activities, rather than an exhaustive summary of ongoing projects being funded, supported and coordinated by the NPGI member agencies.

Plans for the next year

DOE will continue to support mission-relevant fundamental plant research in genomics and biotechnology at its national laboratories, academic institutions, and industrial partners. The DOE Joint Genome Institute will continue to provide fundamental information on complex genome structure of plants and microbes relevant to its missions in bioenergy production, carbon biosequestration, and environmental remediation. Recent plants selected for whole genome sequencing include eucalyptus and foxtail millet; additional EST sequencing will be conducted on pine and other conifers. The Genomics: GTL program will fully support the plant bioenergy research conducted at the three DOE Bioenergy Research Centers.

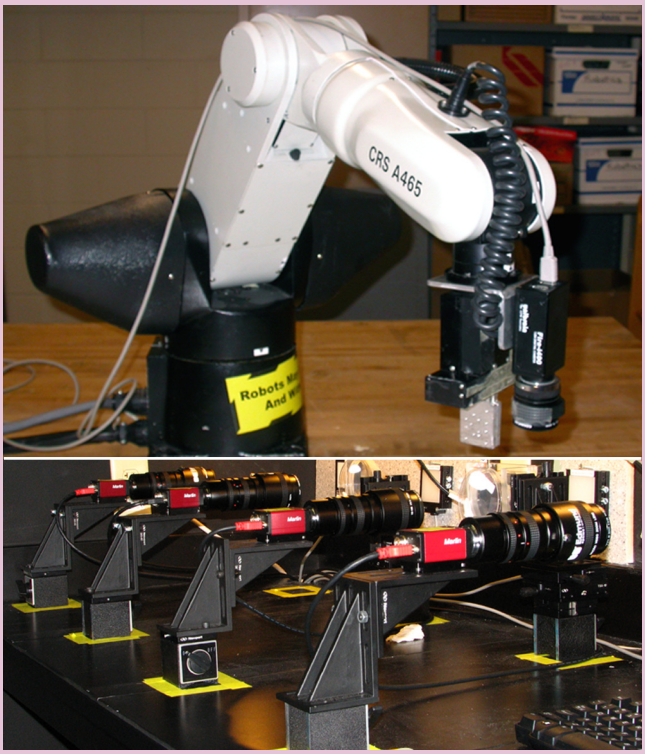
NSF will continue to support basic research in plant genomics to accelerate the acquisition and utilization of new knowledge and innovative approaches to elucidating fundamental biological processes in plants. The focus will be on plants of economic importance and plant processes of potential economic value.

USDA Agricultural Research Service (ARS) will continue to support intramural research for plant and microbial genetic resource management, crop informatics, genomics, functional utilization of plant genomes, crop genetic improvement, and biotechnology risk assessment. The ARS and Biodiversity International will partner with the Global Crop Diversity Trust to develop a powerful but easy-to-use, Internet-based, information management system for the world's plant genebanks. The USDA Cooperative State Research, Education and Extension Service (CSREES) National Research Initiative (NRI) will continue to support research to increase fundamental knowledge of plant genome structure, organization, and function, and to develop tools, genetic resources and bioinformatics capacity for genome-wide analysis and discovery. Important focus areas for 2008 will be the rosaceae and compositae species, and plant feedstock genomics relevant to bioenergy, through development of more efficient and effective methods for mining plant germplasm collections for valuable traits, and advancing translational genomics research to integrate education and extension opportunities with molecular breeding technologies and traditional breeding practices for crop improvement. US Forest Service Research and Development (FS R&D) will continue to support genomics-based research that will lead to improved use of biomass and plant feedstocks for producing ethanol, renewable chemical feedstocks, and fossil fuel substitutes; high-value wood products; restoration feedstocks; and for enhancing forest health and productivity. Genomics research will be coupled with plant breeding to optimize progress.

NIH's National Human Genome Research Institute (NHGRI) is beginning a new planning process through which it will develop a new vision for field of genomics and for the Institute. The future of genomic sequencing, technology development for even higher throughput sequencing and improvement of bioinformatics tools to meet the daunting challenge of handling the flood of data expected, as well as analyzing it to answer biological questions, will be important topics discussed as part of the planning process. NHGRI will continue to focus on understanding the human genome and how it can be applied to improving human health and disease, but much of the technology development, tools and methods developed will continue to be directly applicable to plant genomics.

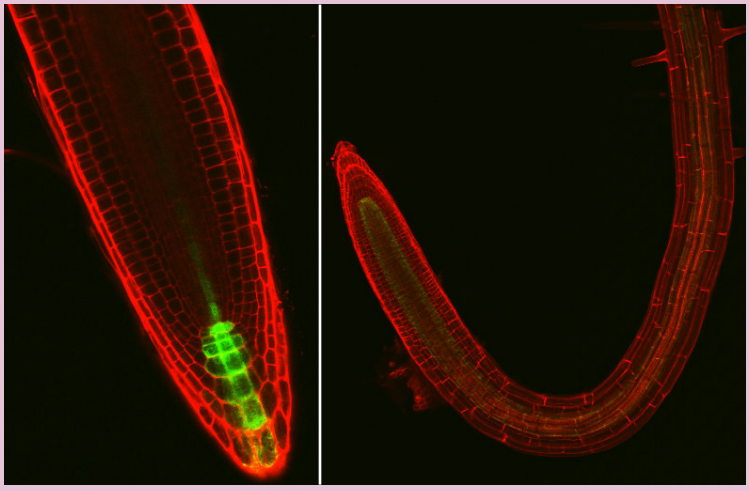
Major scientific developments in fundamental plant biology

Machine vision-based quantification of plant growth and development A multidisciplinary team of biologists, mathematicians, computer scientists, biophysicists and engineers at the University of Wisconsin have developed innovative technology to enable high-throughput image capture and automated visual analysis of traits within mutant and naturally-varying plant populations. By combining cameras, robotics, computational tools, and statistical analysis, these machine-vision tools are capable of generating data on plant developmental processes and gene function at much higher spatial and temporal resolutions than previously available.



New method for corn biofortification could improve nutrition in developing countries Vitamin A deficiency affects about 250 million people annually, and regular consumption of adequate quantities of corn high in vitamin A precursors, which are converted in the body to vitamin A, would reduce the chance of developing vitamin A deficiencies and associated health problems. A new method of increasing cultivation of high-vitamin corn designed to tap into its natural genetic diversity has been developed by scientists at Cornell University/ USDA-ARS and the University of Illinois. The identification of genetic markers associated with high levels of vitamin A precursors could significantly accelerate the vitamin biofortification of maize because it can be used by scientists in developing countries to quickly screen locally grown corn strains. International organizations, such as CIMMYT (the International Maize and Wheat Improvement Center) and the International Institute for Tropical Agriculture (IITA) are training plant breeders to use this new approach.

Using image analysis and genomics to understand plant root traits One of the major challenges facing plant breeders and geneticists within the 21st century is the ability to grow crops on degraded soils. By integrating experimental biology with mathematics and quantitative ecology, scientists at Duke University are using a novel X-ray imaging system coupled with mathematical descriptors to track how roots grow over time. By analyzing root growth and development under varying conditions, the team aims to identify genes involved in root system architecture traits. Since roots are the primary site of nutrient and water uptake, understanding the genetic basis of root system architecture has broader agricultural implications. Plant breeders will be able to use this information to develop crops optimized to grow in particular environments.



Providing baseline data for improved agricultural practices

Advancing knowledge of Breeding, Genetics and Genomics to Improve Fruit Tree Cultivar Development Researchers at Michigan State University have elucidated the genetic control of self-incompatibility in sour cherry that determines whether individuals can self-pollinate. Self-fertility is critical for any successful new sour cherry cultivar because self-fertile cultivars do not require neighboring pollinator trees and do not have an absolute requirement for bees for pollen transfer.

Research is underway to use marker assisted selection (MAS) for self-fertility in sour cherry breeding programs. Early selection of self-fertile seedlings through MAS will dramatically increase the efficiency of breeding efforts. Molecular markers for self-incompatibility are also used to examine pollen flow in grower orchards, enabling growers to identify the most effective pollinator for those cultivars currently in production that require cross-pollination.

Advancing Knowledge of Salt Tolerance New bioinformatic and microarray technologies are enabling researchers to analyze the expression of thousands of crop genes at a time in response to a wide range of developmental and environmental conditions. The benefits of the technology include reduced costs, more efficient experimental design leading to more robust and reproducible data sets. This advance has enabled researchers at the University of California, Riverside, to determine that a key feature of the response to salinity in barley is the induction of genes involved in making jasmonic acid, a key stress hormone in plants. A large number of heat, drought, and low temperature-related genes were also found to be responsive to salinity stress. Increased knowledge of salinity tolerance will overcome one of the major obstacles to increasing crop productivity worldwide.

Novel sugar accumulation profiles in tropical maize Scientists at the University of Illinois studying genes regulating maize growth and development in response to nitrogen have discovered that some lines of tropical origin, when grown in the Midwest, accumulate sugars in their stalks at levels comparable to those in sugarcane grown in Brazil. Tropical maize could have a dramatic impact on U.S. ethanol production for biofuel because it requires less nitrogen fertilizer than conventional corn and can be readily integrated into current crop rotations. Its high sugar content allows tropical maize to be processed without the additional treatments required by current biofuel crops such as switchgrass and corn stover to convert cellulose or starch into the sugars that are then fermented into ethanol.

Peanut Breeding and Variety Development Programs The narrow genetic diversity in cultivated peanuts has hindered progress in the development and application of genomics tools and resources to problems of biological and agricultural importance. The wild gene pool of peanut is thus an important source of genetic diversity for protecting the crop against environmental stresses and insect and disease pests and for enhancing nutritional quality. Researchers at the University of Georgia are developing DNA sequence and marker resources to accelerate gene discovery and marker-assisted selection in breeding programs. The genomes of two wild peanut species are being mapped genetically to create a resource for locating and manipulating genes underlying economically important traits. This research will have a long-term benefit to the peanut industry and society through the development of varieties with superior nutritional and agronomic qualities.

Classroom Activities in Plant Biotechnology Research educators at Colorado State University and Ohio State University have developed an outreach program that uses "Classroom Activities in Plant Biotechnology" to introduce children to the importance of food crops in their lives and the problems that will occur in food production if we are not able to overcome pathogens and climate changes. Presentations have been given to children in elementary and middle schools in Colorado and in areas with high Latino and/or American Indian populations. Two educational units introduce 1) the effects of plant disease on human and plant health and 2) the effects of global warming, to facilitate learning about how important agricultural science is in the solution to these issues.

Training the new generation of scientists

Secrets of Plant Genomes: Revealed! is a 20-minute video produced by Twin Cities Public Television that takes viewers on a lively, upbeat journey that explores how plants got to be the way they are and investigates how society can make better use of them in the future. The focus is the importance of plants in everyday life and the need to study plant genomes to understand basic plant biology and to develop crops with improved agronomic properties. Domestication of corn, disease resistance in potatoes and evolution of cotton fibers are used as examples. The video is available upon request at no cost to schools and museums and can be viewed over the web (http://www.nsf.gov/news/mmg/mmg_disp.cfm?med_id=61504&from=vid).

Understanding of Flood Tolerance For World Food Security Nearly all rice cultivars die within a week of complete water submergence, which can be caused by seasonal floods and poor irrigation practices. However, a few cultivars are highly tolerant of submergence stress and can survive up to two weeks of complete inundation. A collaboration between researchers at the University of California and the International Rice Research Institute in the Philippines has led to the discovery of a cluster of genes that control responses to flooding. These findings provide the opportunity to use classical breeding and genomics to effectively alter acclimation to flooding and submergence. Cultivation of submergence tolerant rice in Asia is expected to provide protection against damaging floods and increase world food security for resource limited farmers.

International collaboration

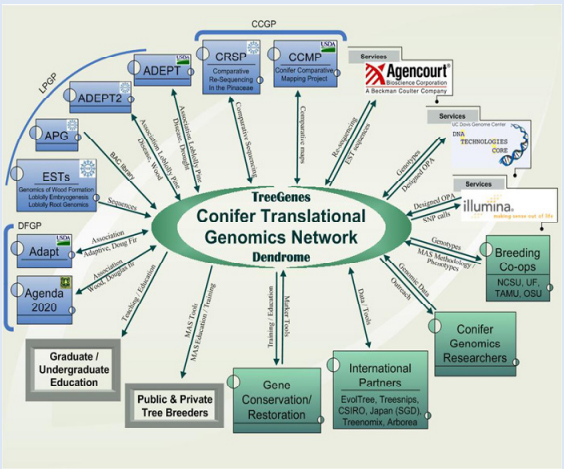
Developing Country Collaborations in Plant Genome Research (DCC-PGR) Pearl millet is a staple food and fodder crop for millions of people living in India and Africa, and drought stress is the most significant abiotic constraint to pearl millet production. Researchers at the University of Georgia have partnered with the Lake Chad Research Institute in Nigeria to identify the chromosomal regions involved in stay-green, a trait where green leaf area is retained under drought stress. Training Nigerian scientists and farmers in marker-assisted breeding techniques will facilitate the introgression of stay-green into locally adapted cultivars and may contribute to increased drought tolerance of a crop.

iPlant Collaborative: A Cyberinfrastructure-Centered Community for a New Plant Biology

The National Science Foundation has awarded $50 million to a University of Arizona-led team to create the first national cyberinfrastructure center to tackle global "grand challenge" plant biology questions that have great implications on larger questions regarding the environment, agriculture, energy and the very organisms that sustain our existence on earth.

Conifer Coordinated Agricultural Project (CAP)

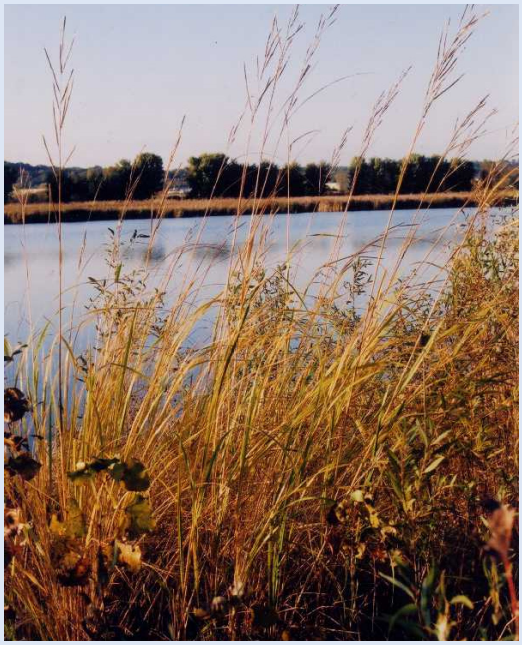
The Conifer CAP is a unique collaborative effort of USDA CSREES and Forest Service that brings together basic researchers and applied tree breeders in a combined agriculture and forestry research, education, and extension mission. The University of California – Davis is leading a consortium of researchers to provide tree breeders across the United States with new tools to enhance and accelerate traditional tree improvement activities. These "knowledge-based" tools derive value from experimentally demonstrated associations between traits of interest, such as wood density or disease resistance, and genetic markers. By adding genetic markers to their toolbox, breeders will be able to select superior trees more accurately, more rapidly, and at lower cost than using traditional approaches alone. It is anticipated that within five years cooperatives producing virtually all of the conifer seedlings in the United States (>1.3 billion annually) might benefit from this technology improvement.



New Centers

Joint Program In Plant Feedstock Genomics

DOE's Office of Biological and Environmental Research (OBER) and the USDA CSREES National Research Initiative implemented the second year of their competitive Plant Feedstock Genomics for Bioenergy program. The goal of the joint fundamental research program is to facilitate the use of plant tissues, specifically lignocellulosic materials, for bioenergy or biofuels. In August 2007, the agencies awarded eleven research grants for genomic research projects supporting an expanded set of plant feedstocks including poplar, corn, sorghum, switchgrass, cordgrass, rice, and the model bioenergy plant Brachypodium. All awards leveraged information and research tools developed and made available over the last 10 years by NPGI projects. For more information, see http://www.genomicsgtl.energy.gov/research/DOEUSDA/.



Bioenergy Research Centers

In June 2007, three new Bioenergy Research Centers were announced by DOE to accelerate basic research on the development of cellulosic ethanol and other biofuels (http://genomicsgtl.energy.gov/centers). The Centers are the BioEnergy Research Center (BESC) led by Oak Ridge National Laboratory, the Great Lakes Bioenergy Research Center (GLBRC) led by the University of Wisconsin in partnership with Michigan State University, and the Joint BioEnergy Institute (JBEI) led by Lawrence Berkeley National Laboratory. The purpose of the new Bioenergy Research Centers is to give greater impetus and focus to developing usable knowledge to advance biotechnology-based strategies for biofuel production and could ultimately lead to technologies deployable in the nation's energy economy. The Centers include interdisciplinary research in plant and microbial genomics, microbial and plant biology, biochemistry, structural and computational biology, bioinformatics, and engineering, each supported at a substantial annual investment of $25 million.

STATUS OF PLANT GENOME SEQUENCING PROJECTS

Plant Species	Genome Size	Products/ Public Access to Sequence	Project Status	Institution(s)
Barrel Medic (*Medicago truncatula*)	550 Mb	Gene-rich BAC sequence in GenBank http://www.medicago.org http://medicago.toulouse.inra.fr	In progress, anticipated completion in 2008	Medicago Genome Sequencing Project
Tomato (*Solanum lycopersicum*)	950 Mb	Gene-rich BAC sequence in GenBank http://www.sgn.cornell.edu/help/about/tomato_sequencing.pl	In progress	International Tomato Genome Sequencing Project
Sorghum bicolor	736 Mb	Whole genome shotgun sequence http://www.jgi.doe.gov/sequencing/why/CSP2006/sorghum.html	Completed	DOE Joint Genome Institute
Grape (*Vitis vinifera*)	500 Mb	Whole genome shotgun sequence http://www.vitaceae.org/molecular.html	Completed	INRA (France), IASMA (Italy)
Maize (*Zea mays*)	2600 Mb	BAC and whole genome shotgun sequences deposited in GenBank http://www.maizesequence.org	In progress, anticipated completion in 2008	Maize Genome Sequencing Project
Soybean (*Glycine max*)	1115 Mb	BAC and whole genome shotgun sequences deposited in GenBank	Completed	DOE Joint Genome Institute
Potato (*Solanum tuberosum*)	840 Mb	Gene-rich BAC sequence in GenBank http://www.potatogenome.net	In progress	The Potato Genome Sequencing Consortium
Brachypodium distachyon	355 Mb	Whole genome shotgun sequence http://www.jgi.doe.gov/sequencing/why/CSP2007/brachypodium.html	In progress	DOE Joint Genome Institute

About the National Science and Technology Council: The National Science and Technology Council (NSTC), a cabinet-level Council, is the principal means for the President to coordinate science, space, and technology to, in turn, coordinate the diverse parts of the Federal research and development enterprise. An important part of the NSTC is the establishment of clear national goals for Federal science and technology investments in areas ranging from information technologies and health research to improving transportation systems and strengthening fundamental research. The Council prepares research and development strategies that are coordinated across Federal agencies to form an investment package aimed at accomplishing multiple national goals. Additional information regarding the NSTC can be obtained from the NSTC website (http://www.ostp.gov/nstc/).

Image Credits The following individuals and organizations provided images used in this report: *Cover*: Wheat harvest on the Palouse, USDA-ARS. *Inside* (left to right): robotic imaging technology, Edgar Spalding, University of Wisconsin; white, yellow, and orange corn, Catherine Bermudez Kandianis, University if Illinois; confocal images of *Arabidopsis* roots, Philip Benfey, Duke University; sour cherry, Wikipedia; barley, *Hordeum vulgare* ssp. *vulgare*, Alain Bonjean, Beijing, P.R. of China; peanut, Wikipedia; roots of rice explants grown in tissue culture media, Janice Stephens, Colorado State University; transplanted rice, Ariel Javellana, IRRI; pearl millet, USDA-ARS; plants meet cyberinfrastructure, JupiterImages Corporation; prairie cordgrass, Jennifer Anderson, USDA-NRCS Plants Database.

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