



# American Society of Plant Biologists

*Cultivating a better future through plant biology research.*

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## **ASPB Members Lead New Plant Genome Research Program Awards**

*NSF makes 28 new awards worth \$101.9 million for plant genomics*

ROCKVILLE, Md. -- Members of the American Society of Plant Biologists (ASPB) are helping advance our understanding of plants and their genes, efforts that in addition to furthering our fundamental knowledge of plant biology, will improve our ability to enhance agricultural productivity, grow nutritious foods, and diminish the effects of devastating plant parasites. ASPB members are leading the majority of the 28 new research awards recently announced by the National Science Foundation (NSF) under its Plant Genome Research Program (PGRP). In fact, two former ASPB presidents are playing leadership roles in the newly funded projects.

The projects supported under the PGRP awards use the techniques of modern genomics—sequencing and analyzing genetic material—to advance our understanding of how plant genes function and govern plants' interactions with the environment in economically important crop species including barley, corn, cotton, rice, soybean, tomato, and wheat. Each project will also incorporate outreach and educational activities, engaging K–12, community college, and undergraduate students and teachers—as well as the public—in plant-related activities. (A complete list of funded projects and their principal investigators is attached.)

The PGRP, which was established in 1998 as part of the National Plant Genome Initiative, is coordinated by an Interagency Working Group on Plant Genomes of the National Science and Technology Council. A total of \$101.9 million was awarded under this new announcement.

NSF has also recently released the 2011 PGRP solicitation with a target date for proposals of January 28, 2011. Additional information about the program is available at [http://www.nsf.gov/funding/pgm\\_summ.jsp?pims\\_id=5338&org=BIO](http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5338&org=BIO).

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*ASPB is a professional scientific society, headquartered in Rockville, Maryland, devoted to the advancement of the plant sciences worldwide. With a membership of nearly 5,000 plant scientists from throughout the United States and more than 50 other nations, the Society publishes two of the most widely cited plant science journals: The Plant Cell and Plant Physiology. For more information about ASPB, please visit <http://www.aspb.org/>. Also follow ASPB on Twitter [@ASPB](https://twitter.com/ASPB).*

**National Science Foundation  
Plant Genome Research Program**

**2010 Awards<sup>1</sup>**

Principal investigator (PI) and co-PIs are listed  
(\* indicates member of American Society of Plant Biologists)

- **Henry W. Bass** with co-PIs **Jonathan H. Dennis**, **Karen M. McGinnis** (all at Florida State University), and **Oghenekome U. Onokpise** (Florida A&M University) will characterize the genetic structure of the maize genome using novel biochemical and computational techniques to map the location of DNA structural elements and their impact on gene expression. The project will engage the public through a living map of the maize chromosomes made up of corn plants, the *Maize-10-Maze*.
- **Thomas P. Brutnell\*** (Boyce Thompson Institute for Plant Research), co-PI **Erik W. Vollbrecht\*** (Iowa State University), and collaborators will develop a resource to define gene function in maize using transposable elements, which will facilitate the efforts of scientists to connect gene sequence with function. The project will also engage educators in developing and implementing inquiry-based plant science activities for high school and college biology courses.
- **Ana L. Caicedo** (University of Massachusetts Amherst), co-PIs **Kenneth M. Olsen** (Washington University) and **Yulin Jia** (University of Arkansas/USDA Agricultural Research Service Dale Bumpers National Rice Research Center), and collaborators will examine the evolution of red rice, a weedy relative of domesticated rice. Identification of genes that are important for weediness and assessment of the impact of herbicide resistant cultivars on weed emergence will help in the development of effective weed control strategies. The project leaders will also train a teaching summer intern to develop a red rice classroom activity and mentor teachers in biotechnology research.
- **Z. Jeffrey Chen\*** (University of Texas at Austin) with co-PIs **Foo Cheung** (J. Craig Venter Institute), **Candace H. Haigler\*** (North Carolina State University), **Brian E. Scheffler** (Alcorn State University), and **David M. Stelly** (Texas A&M University) will identify cotton genes and regulatory elements that are important to the development of cotton fibers and the synthesis of the cellulose that makes up these fibers. Improving the yield of cotton fibers would provide a sustainable alternative to petroleum-based synthetic fibers. The project team will also develop resources for sequencing the genomes of the two major cultivated species, Upland and Pima cotton, and expand a scalable outreach program in the Mississippi Delta in the area of plant genomics and bioinformatics for middle and high school teachers and for graduate students in bioinformatics and biotechnology at two Historically Black institutions.
- **Gloria M. Coruzzi\*** (New York University) with co-PIs **Robert DeSalle** (American Museum of Natural History), **W. Richard McCombie** (Cold Spring Harbor Laboratory), **Dennis E. Shasha** (New York

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<sup>1</sup> Award abstracts for 2010 and all other years are available at <<http://www.nsf.gov/news/longurl.cfm?id=209>>.

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University), and **Dennis W. Stevenson** (New York Botanical Garden) and other personnel will use diversity of plant genomes to discover new genes involved in the development of seeds. It is expected that the data and software resources generated under this project, such as a phylogenomic tree of 150 plant species, will enable others to identify genes associated with any traits of interest or economic value.

- **R. Kelly Dawe\*** (University of Georgia) with co-PIs **James A. Birchler** (University of Missouri), **Jiming Jiang\*** (University of Wisconsin–Madison), **Gernot Presting\*** (University of Hawaii at Manoa), and **Jeffrey Ross-Ibarra** (University of California, Davis) will complete the sequence and assembly of the central region of chromosomes, known as centromeres, which will help in understanding these regions critical to chromosome activity and the production of artificial chromosomes in maize and related species. The project team also provides hands-on training through an annual workshop and facilitate international exchange with the National Autonomous University of Mexico.
- **Dean DellaPenna\*** with co-PIs **C. Robin Buell\*** (both at Michigan State University), **Edward S. Buckler\*** (Cornell University/USDA Agricultural Research Service), and **Torbert R. Rocheford** (Purdue University) and other collaborators will identify the genes and their most useful variants that determine the levels and compositions of vitamin E and carotenoids such as beta-carotene in maize seeds, building on work in the model plant *Arabidopsis*. This work will lead to breeding strategies to increase the levels of these compounds to enhance the quality of food and feed derived from maize. The project is tied to international breeding programs in developing countries and will engage a diverse group of students in education and outreach activities.
- **Claude W. dePamphilis\*** (Pennsylvania State University) with co-PIs **Victor A. Albert** (University at Buffalo, State University of New York), **W. Brad Barbazuk** (University of Florida), **James Leebens-Mack** (University of Georgia), **Hong Ma\*** (Penn State and Fudan University, China), **Douglas A. Soltis**, and **Pamela S. Soltis** (both at the University of Florida) will sequence the *Amborella trichopoda* genome to aid in the understanding of the origin and early diversification of flowering plants, which include most crops and economically important plants. The team will also hold educational workshops for teachers and mentor minority students in plant sciences.
- **Robert B. Goldberg\*** (University of California, Los Angeles) with co-PIs **John J. Harada\*** (University of California, Davis) and **Matteo Pellegrini** (University of California, Los Angeles) will characterize all aspects of soybean seed development, including the interaction of different genetic components that lead to mature soybean seeds, which are a major source of protein feed and vegetable oil. The project will engage undergraduates in science and humanities from three institutions, including a Historically Black university.
- **Michael G. Hahn\*** with co-PIs **William S. York**, **Geert-Jan Boons**, **Malcolm A. O'Neill**, **Harry Gilbert**, and **Christopher S. King** (all at the University of Georgia) will generate a set of molecular probes directed against plant cell wall carbohydrate structures that will enable researchers to expand their studies of plant cell wall polysaccharides in living plants. They will also hold a week-long course on microscopic methods for cell wall research each summer and engage students in summer research.
- **Adrian D. Hegeman\*** with co-PI **Jerry D. Cohen\*** (both at the University of Minnesota) and collaborators will seek to develop techniques to measure the dynamics of the metabolome, the set

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of small molecules that result from metabolism. Although the work will focus on rice and tomato, the methods and procedures are expected to be applicable to many plant species. The project will also organize a summer workshop in metabolomics and engage primarily undergraduate institutions as well as research-intensive universities.

- **David Jackson\*** (Cold Spring Harbor Laboratory) with co-PIs **Anne Sylvester** (University of Wyoming) and **Agnes Chan** (J. Craig Venter Institute) will aim to generate genetic tools in maize that can be used to enable expression of any gene in a number of specific chosen tissues or cell types, providing a means to understand gene function during development. The project will also organize an annual genetics workshop for Native American students and generate three-dimensional interactive animations of a maize cell and the growing plant.
- **Robert K. Jansen** (University of Texas at Austin) with co-PIs **Jeffrey P. Mower** (University of Nebraska) and **Jeffrey D. Palmer\*** (Indiana University) will examine the basis for the rapid evolution of the mitochondrial and plastid genomes in the plant family containing Geranium to understand how the multiple genomes within a single plant cell influence one another and co-evolve over time. The project will engage high school students as summer research interns and develop teacher training modules.
- **Harry J. Klee\*** (University of Florida) with co-PIs **James J. Giovannoni\*** (Boyce Thompson Institute for Plant Research/USDA Agricultural Research Service Robert W. Holley Research Center for Agriculture and Health), **Denise Tieman** (University of Florida), and **Zhangjun Fei\*** (Boyce Thompson/USDA-ARS) and collaborators will seek to identify networks regulating the synthesis of flavor and nutrition compounds in the Solanaceae, which includes tomato. The team will focus on the pathways for the synthesis of folic acid, carotenoids, and a set of flavor and fragrance compounds.
- **June M. Kwak\*** (University of Maryland College Park) with co-PIs **Sarah M. Assmann\*** (Pennsylvania State University), **Joel S. Bader** (Johns Hopkins University), **John K. McKay** (Colorado State University), **Scott C. Peck\*** (University of Missouri), and **Julian I. Schroeder\*** (University of California, San Diego) will seek to develop varieties of canola, an important oilseed crop, that are more drought tolerant by understanding genes associated with drought response in the guard cell that controls microscopic pores on plant leaves. The project will also engage undergraduate students in a program that will educate them about communicating research findings to the general public.
- **W. Richard McCombie** (Cold Spring Harbor Laboratory) and co-PI **Doreen Ware\*** (Cold Spring Harbor Laboratory/USDA Agricultural Research Service Robert W. Holley Research Center for Agriculture and Health) will use next generation sequencing technologies to identify the vast majority of genes in wheat and in three closely related progenitor genomes of wheat. Providing access to these raw data is expected to accelerate functional genomics in wheat.
- **Susan R. McCouch** with co-PIs **Jason Mezey** (both at Cornell University), **Georgia C. Eizenga**, and **Anna M. McClung** (both at University of Arkansas/USDA Agricultural Research Service Dale Bumpers National Rice Research Center) and collaborators aim to gain a deeper understanding of the breadth and depth of genotypic and phenotypic variation in the rice gene pool and empower the rice community to efficiently translate their knowledge into practical applications in plant improvement.

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Specifically, they will explore transgressive variation where crosses between genetically different parents produce offspring that outperform the parents.

- **Dahlia Nielsen** (North Carolina State University) with co-PIs **Valerie Williamson** (University of California, Davis), **David Bird\*** (North Carolina State University), **Mark Melton** (Saint Augustine's College), and **Jennifer Schaff** (North Carolina State University) and collaborators will examine the relationship between plants and their nematode parasites. Nematodes cause yield losses of greater than 10% across all crops, reflecting an estimated \$125 billion annual cost worldwide. In particular, the researchers will seek to answer the question of how the genetic makeup of the nematode influences the expression of genes in the host plant.
- **Seung Yon Rhee\*** (Carnegie Institution for Science) will develop an automated pipeline to reconstruct plant metabolic pathways from genomic data. This pipeline will be used to create pathway databases for 18 agriculturally and industrially important plants. The project will also engage community college interns and collaborate with a high school teacher to produce a teaching module on plant metabolism tied to national and state biology education standards.
- **Edgar P. Spalding\*** with co-PIs **Nicola J. Ferrier** (both at the University of Wisconsin–Madison), **A. Mark Settles\*** (University of Florida), **Tessa L. Durham Brooks\*** (Doane College), and **Nathan D. Miller\*** (University of Wisconsin) and collaborators will integrate engineering and computer science methodologies into biology to improve the ability to detect and quantify plant phenotypes. This will help identify examples when one phenotype can predict another. The project will emphasize both hardware and software development and will utilize cyber-enabled virtual organization to span geographic distances.
- **Nathan M. Springer\*** (University of Minnesota) and co-PI **Matthew W. Vaughn\*** (University of Texas at Austin) will study the prevalence, heritability, and potential consequences of epigenetic variation—heritable genetic differences that are not due to changes in DNA sequences—in maize. This phenomenon is not well understood but can lead to large changes in phenotype, which is important for plant breeding and crop improvement.
- **Gary Stacey\*** with co-PIs **Dong Xu** and **Jianlin Cheng** (all at the University of Missouri) and collaborators will study the response of a single plant cell type, the soybean root hair, to infection by a beneficial nitrogen fixing bacterium as a model for exploring systems biology. The project will seek to understand the regulatory networks that control the infection process leading to a successful symbiotic relationship. The study will also contribute to understanding of plant cellular function; root development; and nitrogen fixation, which has great agronomic and ecological importance.
- **C. Eduardo Vallejos\*** with co-PIs **James W. Jones**, **Kenneth J. Boote\***, **Melanie J. Correll** (all at the University of Florida), **Arthur Berg** (Penn State Hershey College of Medicine), **Rongling Wu** (Pennsylvania State University), and **Juan Osorno** (North Dakota State University) and collaborators will generate a crop model capable of using the genetic makeup of a plant to predict the phenotype under a range of environments. The resultant model will have a wide range of applications in plant biology, including genetics, functional genomics, ecology, and plant breeding. The project will engage undergraduate students and high school teachers as summer interns and organize hands-on workshops in these technologies.

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- **Doris Wagner\*** (University of Pennsylvania) with co-PIs **Craig S. Pikaard\*** (Indiana University) and **Robert Martienssen** (Cold Spring Harbor Laboratory) will establish a Research Collaborative Network (RCN) to organize the U.S. and international plant epigenomics communities to prioritize goals and research needs. The RCN will identify the challenges that limit progress in the field; promote data sharing; and develop community standards for data collection, deposition, and dissemination. Results will include the formation of an Epigenomics of Plants International Consortium and a document outlining recommendations for future funding priorities.
- **Cynthia Weinig** (University of Wyoming) with co-PIs **C. Robertson McClung\*** (Dartmouth College), **Stephen M. Welch**, **Sanjoy Das** (both at Kansas State University), and **Julin N. Maloof\*** (University of California, Davis) will examine plant responses to vegetation density, commonly referred to as “shade avoidance,” which greatly affects yield in crop species. The team will use both genetic and environmental data with model plants to develop computational approaches for reconstructing gene networks that regulate density responses and for predicting traits such as height and flowering time from complex genotypes. They will also develop modules to educate teachers on evolutionary theory and molecular genetics, provide seed kits for inquiry-based student exercises, and hold an annual teacher workshop that will ultimately reach the majority of biology teachers in Wyoming.
- **Rod A. Wing\*** with co-PIs **Michael J. Sanderson** (both at University of Arizona), **Manyuan Long** (University of Chicago), **Carlos A. Machado** (University of Maryland College Park), **Jianxin Ma,\*** and **Scott A. Jackson\*** (both at Purdue University) and colleagues will generate a set of genomics resources for the genus *Oryza*, which contains the world’s most important food crop: rice. These resources will allow cross-species analyses with other related genomic sequences and both help improve cultivated rice and address fundamental questions in evolutionary and comparative genomics. The project will also foster science education, including a “Plant Science Family Night” program to engage elementary students and families in thinking about plants and role of plant science in ensuring a safe, sustainable, and secure food supply.
- **Roger P. Wise\*** with co-PIs **Julie A. Dickerson,\*** **Adam J. Bogdanove**, **Daniel S. Nettleton**, and **Adah Leshem-Ackerman** (all at Iowa State University) and collaborator **Pietro Spanu** (Imperial College, London) will address fundamental questions about the susceptibility and resistance of host plants to infection focusing on the barley–powdery mildew system and comparisons in maize and rice. They will seek to identify new genes in the regulation of plant innate immunity and plant targets that promote or suppress defenses. The project will also incorporate classroom educational materials, international research exchanges, and training and mentoring of students.
- **Daniel Zilberman**, co-PI **Robert Fischer\*** (both at the University of California, Berkeley), and collaborators will explore the role of genomic imprinting on the development of endosperm, which serves as the major source of food for humans and livestock, using rice as a model system. This research on epigenetic changes to DNA sequences, such as the addition of methyl groups, modifications to DNA-associated proteins, and small RNA molecules, may lead to new technologies that will increase crop yield to feed a growing population. The project will also engage undergraduates from groups underrepresented in the biological sciences as part of the research team.