National Program 302 Plant Biological and Molecular Processes Annual Report

FY 2006

National Program 302, Plant Biological and Molecular Processes, includes much of the Agricultural Research Service's fundamental research with plants that is necessary to understand the biological principles for plant growth and development. The research focuses on mechanistic understanding of specific plant processes and properties. The knowledge and tools developed can be used in an integrated research approach to achieve practical improvements in the functions and properties of crops that address consumer concerns. The Action Plan for this National Program was rewritten in 2004 with stakeholder input to ensure that the components of the program were relevant to current needs of U.S. agriculture. The first component is Functional Utilization of Plant Genomes: Translating Plant Genomics into Crop Improvement, with research aimed at bridging the gap between fundamental DNA-based science and the applications of that science for crop improvement. The second component, Biological Processes that Determine Plant Productivity and Quality, encompasses mechanisms of plant growth and development, disease resistance, photosynthesis, productivity, and environmental responses that relate molecular events and processes to attributes of the whole organism. It also includes research to identify and enhance nutritional quality of foods. The third component, Plant Biotechnology Risk Assessment, houses research of two types: identification and evaluation of possible unwanted environmental or genetic consequences of genetic engineering, and development of new technology to mitigate or eliminate unwanted consequences.

The year 2006 marked the first term of the second 5-year cycle of research performance for the National Program 302. The Action Plan provided guidance for the implementation of many new peer-reviewed projects that led to many important scientific discoveries and advances, some of which are described below. By no means do these selected accomplishments capture the important achievements of the entire research program. Rather, they highlight the type of activities carried out under this program and the type of benefits that result. In that regard, significant emphasis was demonstrated on program accomplishments in the areas of plant protection against diseases such as Asian Soybean Rust, and the improvement of nutritional quality and functionality of seed proteins, carbohydrates and oil.

Component I: Functional Utilization of Plant Genomes: Translating Plant Genomics into Crop Improvement

Problem Statement 1A: Advancing From Model Plants to Crop Plants

Problem Statement 1B: Applying Genomics to Crop Improvement

Genes identified to improve bioenergy crops. Leaves from grass species, such as corn or switchgrass, are likely to be a significant feedstock resource for a bio-based economy. Researchers at ARS, Albany, California, have cloned the Corngrass mutation of maize. Corngrass mutants make many more tillers that are vegetative and have reduced lignin. The researchers have also cloned a maize gene ("milkweed pod") in collaboration with researchers at HortResearch, New Zealand, that regulates tissue and vascular development of the maize leaf. Cloning these genes that affect cell wall content and plant architecture will provide new genetic targets in the development of plant materials with increased energy availability for biofuels.

New knowledge about nutritional compounds (carotenoids) in fruits and vegetables. Tomatoes are a rich source of carotenoids, which are compounds necessary for human health (precursors to vitamin A) in addition to being strong anti-oxidants. Understanding the nutritional value of carotenoids requires better knowledge of the complex biochemical pathways that affect the availability and nutritional value of different carotenoids as constituents of the human diet. ARS researchers at Ithaca, New York, have identified a new molecular mechanism involving feedback regulation that governs the carotenoid biosynthetic pathway. This discovery will benefit other researchers and plant breeders who are attempting to modify carotenoid accumulation in crop plants and could provide a more effective means for enhancing the nutritional value of carotenoids in fruits and vegetables.

Component II: Biological Processes that Determine Plant Productivity and Quality

Problem Statement 2A: Understanding Growth and Development

Better to fertilizer rhododendron nursery plants in summer than in spring. Rhododendron nursery plants are more reliant on fertilizer in summer than spring. Fertilizers are commonly applied throughout the spring and summer during nursery production of Rhododendron, even though timing of plant demand for nutrients was unknown. ARS scientists at Corvallis, OR, in collaboration with Oregon State University scientists, determined that nitrogen uptake and uptake efficiency of container grown Rhododendron plants were low until July, indicating that fertilizer application prior to this time may not be effectively taken up by plants. Nitrogen fertilizer management in the production of Rhododendron from liner stock should therefore ensure nitrogen availability is high during the period of rapid growth in July and August. This information will aid in the development of fertilizer management strategies for nursery container production to decrease fertilizer use and production costs, improve plant quality, and minimize nitrogen losses to the environment.

Problem Statement 2B: Understanding Plant Interactions with Their Environment

New heat tolerant cotton germplasm with excellent fiber quality. ARS released three improved germplasm lines of upland cotton to the public (jointly with Cotton Incorporated) that possess superior fiber length and strength characteristics and improved yield performance under heat stress environments. Future profitability for US cotton growers requires improvements in fiber quality and plant productivity under abiotic stress, including high heat conditions. The lines provide public and private breeders with resources for concurrent improvement of fiber quality and heat tolerance in upland cottons for the mid-south and southeastern United States. The lines also serve as genetic resources for improving heat tolerance in Acala cottons of the southwestern and western United States. Thus the new germplasm has the potential to provide superior germplasm that will impact cotton production over a larger portion of the cotton belt in the US.

Heat tolerance genes identified. ARS scientists at Lubbock, Texas, have identified two genes (digalactysyldiacylglycerol synthase and AtFtsH11 protease) that contribute to basal heat tolerance in plants. This discovery advances understanding of the cellular components impacting heat tolerance and in combination with additional gene discoveries, will allow scientists to develop more heat-tolerant crops.

Problem Statement 2C: Developing High-Value Products

Manipulating antinutritional and nutritional factors in soybean seed. ARS scientists at Columbia MO and W. Lafayette IN have replaced the Bowman-Birk Inhibitor (BBI), an anti-nutritional protein in seeds, with an inactive form of BBI. BBI accounts for more than 50% of the sulfur content in the seed. Accordingly, inactive, mutant BBI cDNA was put under the control of a strong seed promoter and introduced into soybean using a modified cot/node transformation protocol. A number of independent transformants were identified that bear the mutant gene, which is expressed at a high level. Despite the continued presence of the Kunitz trypsin inhibitor (KTI) and wild type BBI in the transformed lines, data collected reveals that protease inhibitory activity is reduced 50-80% compared to the untransformed control. The levels of expression of wild-type BBI mRNA remain constant. Protein analysis of seeds from transformants revealed the large accumulation of a protein which was identified as the mutant BBI. These results indicate that protease inhibition can be down-regulated without removing BBI and losing critical levels of sulfur in seeds.

<u>Soybean seeds with improved vitamin E antioxidant content</u>. ARS scientists at Columbia MO in collaboration with DuPont Inc. transformed soybeans with a gene for the barley homogentisate geranylgeranyl transferase (HGGT), which catalyzes the first step in the synthesis of the tocotrienol form of vitamin E. Expression of the gene for the barley HGGT under control of a strong seed-specific promoter was accompanied by increases in the total vitamin E antioxidant content of soybean seeds by four- to six-fold. The vitamin E produced in the engineered seeds was principally delta- and gamma-tocotrienol, which have been shown to have the greatest efficacy for stabilizing vegetable oils in frying applications. In addition, the increase in total vitamin E antioxidant achieved in these studies greatly exceeds that obtained to date by conventional breeding or by biotechnological approaches that have targeted only one gene. It is anticipated that vegetable oils from these genetically enhanced seeds will have improved oxidative stability for food processing and high temperature lubricant applications. In addition, the use of these antioxidant-enriched seeds in livestock feed may result in meats with improved appearance and shelf-life. It is expected that the end users of these genetically enhanced seeds will be soybean oil processors and bio-based lubricant manufacturers.

<u>Component III: Plant Biotechnology Risk Assessment</u>

Problem Statement 3A: Improving and Assessing Genetic Engineering Technology

<u>Determination of genes that affect wheat dough and baking properties</u>. Millers and bakers need high-quality wheat, but the basis of good quality wheat is not well understood. ARS researchers at Albany, California, have used wheat biotechnology to determine the role of two wheat glutenin proteins in affecting dough quality and strength. The dough mixing properties of transgenic wheat flours that contained increased levels of either glutenin protein or both were determined. Results can be used to develop wheat lines with a range of dough strengths that could be valuable to many different end-users in the food industry.

Problem Statement 3B: Interaction of Transgenic Plants with Their Environment

<u>Identification of proteins associated with Asian soybean rust resistance</u>. ARS scientists at Beltsville MD identified numerous proteins that may be important to the interactions of soybean with Asian soybean rust (ASR). Mass spectrometry was used to identify proteins from rust spores. A majority of the proteins were heat-shock proteins, translation elongation factors and other proteins. Novel proteins were also discovered and these proteins may be unique targets for chemical inhibition. The results suggest that an abundance of heat-shock proteins, translation elongation factors and other protein making machinery enable spores to jump-start protein production upon germination and withstand environmental extremes. These abilities likely help

improve a spore’s ability to survive and infect plants. This data will aid scientists in identifying soybean proteins and genes involved in susceptibility and resistance to ASR, so soybean can be engineered with broader resistance to ASR. The protein data will also be of use to scientists at universities, government agencies and companies who are designing new fungicides to fight rust diseases.