2016 COTTON RESEARCH ACCOMPLISHMENTS

USDA AGRICULTURAL RESEARCH SERVICE
PLAINS AREA
Scientists of the Plains Area, Agricultural Research Service are committed to providing answers to key issues facing the nation’s cotton industry. We strive to partner with national and international collaborators, producers, ginners, manufacturers and commodity groups to conduct high quality research related to cotton.

- Improved control methodologies for pathogens and nematodes attacking cotton
- Improved aerial application of agricultural chemicals
- Germplasm enhancement of cotton
- Enhancing plant resistance to water-deficit
- Effective and environmentally sound approaches for management of the boll weevil
- Identifying disease resistance
- Use of cotton as a fiber source
- Use of cotton seed as a high-quality feed for cows
- Molecular characterization of nematode and fusarium wilt resistance in the cotton genome
- Development of new technologies and methods of cotton production and manufacturing

Below is an overview of accomplishments and progress made by USDA-ARS Scientists in the Plains Area.

ARS scientists and their partners have sequenced the genome of Texas Marker-1, the genetic standard for upland cotton, the world's most widely cultivated and genetically complex species of *Gossypium*. Photo courtesy of Russell Kohel, ARS (retired).

Jim Frelichowski, ARS Genetics working on the germplasm collection in the greenhouse.
**NEW MEXICO**

Enhancing the Quality, Utility, Sustainability and Environmental Impact of Western and Long-Staple Cotton through Improvements in Harvesting, Processing and Utilization

Cotton Ginning Research Unit, Las Cruces, NM  
**Project Number:** 3050-41000-009-00  
**Lead Scientist:** Derek Whitelock  
**Team Members:** Paul Funk, Ed Hughes, Carlos Armijo

**Burning Issue Resolved.** In 2009, the US Occupational Safety and Health Administration (OSHA) began developing a comprehensive mandatory combustible dust standard for general industry. The National Fire Protection Association defines combustible dust as “a finely divided combustible particulate solid that presents a flash fire or explosion hazard when suspended in air or the process-specific oxidizing medium over a range of concentrations”. While some agricultural industries like sugar and grain handling facilities could constitute combustible dust hazards and have been subject to rules on dusts for many years, other Ag processors like cotton gins or almond huller plants have had no issues with dust fires or explosions. At the request of the National Cotton Council (NCC), ARS researchers in Mesilla Park, NM collaborated on a study to determine the combustibility of cotton gin dust. Later, the Western Ag Processors Association (WAPA) requested that the ARS researchers again conduct tests to determine the combustibility of almond huller dust. These tests showed that cotton gin dust and almond huller dust collected in facility interiors were not combustible and therefore not an explosion hazard. These results were submitted to a peer-reviewed journal and should enable the NCC and WAPA to keep cotton gin and almond huller dusts from being classed as combustible. In turn, allowing cotton gins to keep their normal housekeeping practices, clearing the way for construction of new almond huller plants to serve this growing sector of agriculture, and all the while saving many thousands of dollars for explosion suppression hardware and practices.
Molecular diversity of the U.S. National Cotton Germplasm Collection. To be effective sources of variability for genetic improvement, germplasm collections must be genetically well-characterized. Knowledge of the structure of diversity within a collection is also necessary for its efficient and effective conservation and maintenance. ARS researchers at College Station, Texas; New Orleans, Louisiana; Stoneville, Mississippi; and Maricopa, Arizona, systematically characterized genetic resources within the National Cotton Germplasm Collection and were able to identify genetic variation between and within commercial cotton species. Molecular diversity that could partially differentiate among wild and improved lines within cultivated species was also identified, and molecular markers were used to identify varying levels of introgression among lines within these species. The use of molecular markers to characterize the Collection will allow the curator to efficiently and effectively increase and preserve the diversity of the Collection while maintaining the purity of its individual lines. Characterization of the Collection with molecular markers also allows breeders and geneticists to make more informed choices in their improvement efforts which will facilitate development of superior cotton varieties and products for the consumer.

National Cotton Germplasm Collection (NCGC) descriptor data and digital images posted online to the CottonGen database. The online depiction of a germplasm collection is critical to maximize the utility to plant breeders and researchers of cotton. Otherwise it is just a random collection of seed. ARS researchers at College Station, Texas, in cooperation with database managers of CottonGen (www.cottongen.org) at Washington State University, standardized morphological descriptors for the Germplasm Collection, created a visual descriptor key, and downloaded all descriptor data obtained since FY 2006. Descriptors data obtained prior to FY 2006 were transformed to the new standardized descriptor categories. The dataset covers more than half of the NCGC and has evolved to the extent that users have more accurately created subsets of the NCGC for their research or breeding purposes and
greatly reduced the size of seed orders. Gaps in this dataset more clearly prioritize future seed increases and characterizations of the NCGC.

Collecting and GPS tracking of a wild cotton in Arizona. Genetic diversity for desirable traits such as disease or insect resistance often resides in wild relatives of cultivated species. With genetic advances, this diversity has become increasingly accessible for use in the improvement of cultivated species. Therefore, it is important to collect and preserve the diversity of these wild relatives. A collection trip to Arizona in FY 2016 resulted in thirty seven populations of Gossypium thurberi, a wild relative of cotton, being identified, their locations being recorded with GPS coordinates, and seed harvested from 27 of them. The representation of the genetic diversity of this species in the National Cotton Germplasm Collection is now greatly improved, and the GPS locations will enable monitoring of native populations for in situ conservation. This information will also update the Crop Wild Relative Database collaborative research by USDA-ARS scientists in the National Plant Germplasm System.
Developing Genomic and Genetic Tools for Exploiting Cotton Genetic Variation

Crop Germplasm Research Unit, College Station, TX
Project Number: 3091-21000-038-00
Lead Scientist: Richard Percy
Team Members: James Frelichowski, Lori Hinze, John Yu

**Fine mapping of a dominant glandless gene in cotton.** Cottonseed is an excellent nutritional source of oil and protein, but its utilization is greatly limited by the presence of pigment glands containing toxic gossypol. ARS researchers at College Station, Texas, working in collaboration with international cooperators, mapped a dominant glandless gene Gl2^e to a 15-kb chromosome 12 fragment. One candidate gene was identified in this fragment encoding an MYC transcription factor that likely serves as a vital positive regulator in the production of pigment glands. Sequence and expression analysis of the gene showed a protein product of 475 amino acids present in glanded plants while almost absent in glandless plants. This accomplishment indicates that manipulation of the Gl2^e gene with a tissue-specific promoter could effectively inhibit the formation of the pigment glands in cottonseed. As the most important pigment gland-related gene identified in cotton, it would facilitate research on the glandless trait, cotton MYC proteins, and low-gossypol cotton breeding.

**Sequencing of the Upland cotton genome.** Developing a genetic coding sequence of cotton opens many avenues of research into how cotton develops, how it responds to its environment, and how its genetics can be manipulated for crop improvement. ARS researchers at College Station, Texas, working with international cooperators, published a cover article in Nature Biotechnology of the complete genome sequence of the world’s most widely grown cotton species, Gossypium hirsutum. This ground-breaking report sheds light into the comparative, evolutionary, and functional genomics among cotton species and as related to other plant species. As the first cultivated tetraploid cotton to be sequenced, this deciphering of the complex G. hirsutum genome will greatly facilitate biological studies of cotton including fiber evolution and development. This Nature Biotechnology publication and immediate data release of the cotton genome sequences are highly appreciated by cotton researchers to develop better cottons with enhanced yield and quality traits under various production environments.

Cotton Disease Management Strategies for Sustainable Cotton Production

Insect Control and Cotton Disease Research Unit, College Station, TX
Project Number: 3091-22000-031-00
Lead Scientist: Robert Stipanovic
Team Members: Enrique Medrano, Jesus Esquivel, Jinggao Liu, Alois Bell

**Release of nematode-resistant cotton lines.** Among pests, root-knot and reniform nematodes cause the greatest yield losses in cotton (ca. 4% of potential yield). The nematodes also act synergistically to increase the severity of seedling diseases and Fusarium wilt. ARS researchers at College Station, Texas, jointly with workers at Texas A&M AgriLife Research and Cotton Incorporated released eight new nematode-resistant germplasm lines. All eight lines are resistant to the reniform nematode, and five are also resistant to the root-knot
nematode. The lines also have elite agronomic performance; they will be valuable to plant breeders in their work to reduce pest losses and cost of pest control in cotton.

**Deficiencies of a Fusarium oxysporum f. sp. vasinfectum race 4 (Fov-4) detection kit.**
Fov-4, first identified in California in 2001, has spread to new fields planted to cotton in the San Joaquin Valley. Fov-4 is a serious seed borne pathogen that can cause disease without the root knot nematode, and is thus a potential threat to all U.S. cotton production. ARS researchers at College Station, Texas, evaluated an existing race 4 specific Polymerase Chain Reaction test kit for ability to discriminate between Fov races and genotypes. The test kit is currently the only available method to rapidly identify Fov-4 in the field. Inclusion of more representative races and genotypes in the evaluation revealed that these diagnostic tests are able to distinguish race 4 from races 1, 2, 6, and 8 but not from race 3 and race 7 isolates. Knowing the limitations of diagnostic tests is important in correctly identifying diseased fields and seed lots.

**Detection and Biologically Based Management of Row Crop Pests Concurrent with Boll Weevil Eradication**

Insect Control and Cotton Disease Research Unit, College Station, TX

Project Number: 3091-22000-029-00D

Lead Scientist: John Westbrook

Team Members: Charles Suh, Jesus Esquivel, Ron Nachman

**Modeling pest migration pathways.** The fall armyworm is a highly mobile insect pest of cotton and a wide range of crops, but must migrate northward from subtropical winter breeding regions each spring to re-infest cropping areas in temperate regions. Recent genetic analyses have characterized migratory pathways from winter-breeding regions, but knowledge is lacking about the atmospheric impact on the timing, distance, and direction of migratory flights. Project scientists working with collaborators in other states simulated migratory flight of fall armyworm moths from distinct winter-breeding source regions, and identified regions of dominant immigration from Florida and Texas source regions and overlapping immigrant populations in the Alabama–Georgia and Pennsylvania–Mid-Atlantic regions. The simulated migratory pattern corroborates previous migratory distributions of fall armyworms based on genetic profiles. This work facilitates risk assessment of source areas and migration pathways of fall armyworms and other migratory pests, and improvement of management strategies for migratory populations including those that may introduce insecticidal resistance traits.
Boll weevil eradication: Improved weevil detection. The Boll Weevil Eradication Program has eliminated the boll weevil from all cotton production areas in the United States, with the exception of the southernmost areas of Texas. The ability to detect and monitor boll weevil populations with pheromone traps is largely responsible for this extraordinary accomplishment. However, the inconsistent performance of pheromone traps during the past several years along with the subtropical climate and subsequent year-round presence of cotton has hindered eradication progress in South Texas. This project, the sole remaining ARS program that supports boll weevil eradication, developed a longer-lasting and more attractive pheromone lure through a Cooperative Research and Development Agreement with a commercial partner. The ARS scientists also demonstrated that the current replacement interval of kill strips, which are used in traps to reduce predation of captured weevils and incidence of weevil escape, was too long. Based on these findings, the eradication programs in Texas and Mexico have reduced the replacement interval of kill strips from four to two weeks. The scientists also developed analytical techniques, based on an aerial remote sensing platform, to identify cotton fields and volunteer plants that may harbor weevils during and beyond the production season. These techniques are currently being used by the Texas Boll Weevil Eradication Foundation to identify cotton fields and plants in the Texas Winter Garden production area, which has recently been re-infested with boll weevils.

Southern green stink bugs transmit pathogens causing boll rot. Southern green stink bugs and related species continue to plague cotton producers. In addition to traditional losses in yield quality and quantity caused by the southern green stink bug, our research has demonstrated that adults can ingest and introduce opportunistic disease pathogens into developing cotton bolls. Further, examination of specific sections of the alimentary system within these adults has shown that pathogens are selectively transmitted as evidenced by their presence in these specific sections. These pathogens cause rotting and necrosis of boll seed and lint which subsequently reduce yield and increase economic losses. Continued research towards understanding the feeding mechanism and environment within will improve our understanding of the southern green stink bug and pathogen relationship.
Applying droplet sizing calculators to optimize aerial applications. Successful aerial applications start with proper spray nozzle selection, setup and operation to ensure the resulting droplet size meets both pesticide product label requirements and meteorological and geographical conditions at the site of application. Recent computational droplet sizing models developed by ARS researchers at College Station, Texas, were adapted to a visual interface for use by applicators when making nozzle selections and operational decisions. Using the computational models, graphical representations of each nozzle's full operational spectrum were developed with droplet size classification data visually represented for quick and ready interpretation and selection. The new graphical interfaces greatly enhance the usability of the aerial nozzle droplet sizing models, thus allowing applicators to more quickly make operational decisions and document application parameters in order to meet pesticide product labels and ultimately optimize applications.

Consumer-grade cameras for aerial application. Consumer-grade cameras have been increasingly used in scientific research and remote sensing applications because of their low cost and ease of use. ARS researchers at College Station, Texas, assembled two imaging systems consisting of consumer-grade cameras for use on agricultural aircraft. They evaluated imagery acquired by the systems over a large cropping area for crop identification and assessment and compared different image mosaicking techniques for image stitching. Image classification and accuracy assessment showed that both normal color and near-infrared imagery acquired by the systems was useful for crop identification and crop growth assessment. The results from this study have provided useful information for aerial applicators and other remote sensing practitioners on the use of consumer-grade cameras. More than 20 aerial applicators have shown strong interest in assembling and using these cameras in their operations.
Sustainable acoustic absorber produced from agricultural waste fibers. In collaboration with cooperators, ARS researchers in Lubbock, TX developed a process that allows for a novel all-natural high-density composite to be produced solely based on a chitinous polymer. The polymer is grown by a unique variety of fungi during its natural production of the mycelium. The mycelium-bound natural fiber is pressed at select temperatures and pressures causing the mycelium to hold the natural fibers in a compressed state similar to pressboard, plywood, or particle board. This new bio-product is environmentally friendly, bio-degradable, and completely free of VOC's and petroleum based resins. The new process is being used in the manufacture of high density acoustic absorbers such as ceiling tiles. Ceiling products are forecasted to be a $2.5 billion industry in 2018 with specialty ceiling products, such as acoustic absorbers, to reach $540 million.
New accurate dust emissions data saves ginning industry millions. New regulations for dust smaller than 2.5 micrometers (PM2.5) posed a significant problem to the US cotton ginning industry because emissions data for this size of dust had never been measured from gins. In response to the new regulations and the lack of cotton gin PM2.5 emissions data, regulators in California attempted to make assumptions on the amount of PM2.5 emitted by gins during the air quality permitting process. ARS researchers from Lubbock, Texas; Las Cruces, New Mexico; and Stoneville, Mississippi, and researchers from Oklahoma State University conducted a four-year, nationwide cotton gin sampling campaign that yielded accurate emissions data for all regulated sizes of dust – including PM2.5. This newly published emissions data was adopted by regulators in California and several other states and has been used in the permitting process for hundreds of gins across the US cotton belt. If air regulators in California had used the erroneously assumed PM2.5 emissions data for gins and not the new accurate PM2.5 emissions data from this study, the recently permitted ginning facilities would have been required to install additional dust control measures at a cost of several hundred thousand dollars per facility.
New permitting process for Texas cotton gins. The air quality permitting process for cotton gins in Texas requires total annual emissions to be less than a specified value based on annual production, or gins must comply with major source permitting rules. The cost of major source classification for a cotton gin would be hundreds of thousands of dollars per year. ARS researchers from Lubbock, Texas; Las Cruces, New Mexico; and Stoneville, Mississippi, as well as research personnel from Oklahoma State University in Stillwater, conducted a four-year nationwide gin sampling campaign in which they quantified the level of dust emissions from each machinery process utilized during cotton ginning. Emissions data for each process from this study was used by ginning industry representatives and air regulators in Texas to develop a new permitting process for Texas gins. This new permitting process accurately inventories dust emissions from cotton gins and prevents them from being subject to major source permitting requirements and associated costs. Adoption of this new permitting process is being considered by other cotton-producing states.

Enhancing Plant Resistance to Water-Deficit and Thermal Stresses in Economically Important Crops

Plant Stress and Germplasm Development Research Unit
Project Number: 3096-21000-019-00
Lead Scientist: John Burke
Team Members: Junping Chen, James Mahan, Paxton Payton, Mauricio Ulloa, Zhanguo Xin

Cotton Nematode and Fungal Disease Resistance Traits Identified. Discovering nematode and disease resistance genes in the cotton genome is essential for speeding the development of cotton resistant varieties with improved yields. Using cotton chromosome substitution (CS) entries that carried chromosome segments from other cotton species (G. barbadense or G. tomentosum), ARS Researchers and University cooperators confirmed the location of root-knot nematode and fusarium wilt (FOV races 1 and 4) resistance genes. Analyses validated important regions on cotton chromosomes 11, 16, and 17 harboring nematode and fusarium wilt resistance genes. This study provides a foundation for effective plant breeding of nematode and disease resistance in cotton.

Genetic Diversity in Cotton Pollen Outcrossing. Pollen is the most heat and desiccation sensitive organ in higher plants. ARS Researchers at the USDA-ARS Cropping Systems Research Laboratory in Lubbock, Texas have identified genetic diversity for natural outcrossing associated with pollen stress sensitivities. Laboratory, greenhouse and field studies confirmed that more desiccation tolerant cotton pollen outcrosses more frequently than stress sensitive pollen. This research serves as a foundation to regulate genetic outcrossing through the basic characteristic of the pollen.
Visual indicators of genes controlling cotton fiber development. Environmental stresses, such as drought, high temperature and combination of both, not only reduce the overall growth of cotton plants, but also greatly decrease cotton lint yield and fiber quality. The impact of environmental stresses on fiber development is poorly understood due to technical difficulties associated with the study of developing fiber tissues and lack of genetic materials to study fiber development. ARS researchers at the USDA-ARS Cropping Systems Research Laboratory in Lubbock, TX have inserted reporter genes attached to fiber developmental gene switches to allow scientists to see when specific developmental genes are turned on. These newly developed materials provide new molecular tools for studying the effects of abiotic stresses on fiber development and may be used in study of cotton fiber development genes and eventually in the genetic manipulation of fiber quality.

New pima cotton germplasm resistance to fusarium wilt race 4. Over the past 12 years, the race 4 of the fungus causing Fusarium wilt (FOV) disease has impacted cotton production in California. Cotton varieties resistant to FOV race 4 have been effective in controlling yield losses, and an economical approach for dealing with this fungal disease. To continue providing germplasm with good levels of resistance to FOV race 4 to cotton researchers and breeders, ARS researchers in Texas developed and jointly released in collaboration with researchers at the University of California five Pima cotton germplasm lines (SJ-FR05, SJ-FR06, SJ-FR07, SJ-FR08, and SJ-FR09) with resistance to FOV race 4 combined with good yield and fiber quality properties. The SJ-FR05-FR09 lines provide needed alternative sources of FOV race 4 resistance to cotton breeders, and they should be helpful to speed efforts to broaden the genetic base, which is critical to maintaining a healthy Pima cotton industry in the San Joaquin Valley of California.