



## **USDA scientists, cooperators sequence soy genome, leading the way to better beans**

**By Agri-Pulse Staff**

© Copyright Agri-Pulse Communications, Inc.

Washington, Jan. 13 – U.S. Department of Agriculture (USDA) scientists are part of a team which has sequenced the majority of the soybean genome, providing an unprecedented look into how this important legume crop converts four critical ingredients – sunlight, water, carbon dioxide and nitrogen – into protein and oil, the basic building blocks for many consumer products. The research team from 18 federal, state, public and private organizations published their research Wednesday in the journal *Nature*.

“Soybean and other legumes play a critical role in global food security and human health and are used in a wide range of products, from tofu, soy flour, meat substitutes and soy milk to soy oil-based printing ink and biodiesel,” said Molly Jahn, USDA Deputy Under Secretary for Research, Education and Economics. “This new information about soybean’s genetic makeup could lead to plants that produce more beans that contain more protein and oil, better adapt to adverse environmental conditions, or are more resistant to diseases.”

This sequencing of the soy genome is the culmination of more than 15 years of collaborative research. The team used a so-called “whole-genome shotgun” (WGS) approach to sequence 85 percent of the 1.1 billion nucleotide base pairs that spell out soy’s entire DNA code. The sequence also provides researchers with a critical reference to use in deciphering the genetics of some 20,000 other legume species.

Geneticists Randy Shoemaker, Perry Cregan, David Hyten, Steven Cannon and David Grant with USDA’s Agricultural Research Service (ARS) contributed to the *Nature* paper. Their work involved the creation of genetic markers and the development of the soybean (*Glycine max*) genetic map that facilitated “anchoring” of the genome sequence to the 20 sets of soybean chromosomes. ARS is USDA’s principal intramural scientific research agency.

The Department of Energy’s Joint Genome Institute; Purdue University at West Lafayette, Ind.; the University of Missouri at Columbia, and the University of Arizona at Tucson also participated in the soybean sequencing project, which was supported by the National Science Foundation and USDA’s National Institute of Food and Agriculture

(NIFA). Through federal funding, NIFA invests in science to solve critical issues impacting people's daily lives and the nation's future.

According to USDA's Shoemaker, who is with the ARS Corn Insects and Crop Genetics Research Unit in Ames, Iowa, integrating the new sequence with existing physical and genetic maps of soy will move researchers closer to linking observable physical traits of soy to their associated genes and alleles – alternate versions of genes. Ultimately, this will speed the development of new soybean cultivars offering higher seed yields, increased protein and oil contents, better adaptability and improved disease resistance, particularly to Asian soybean rust (ASR) which threatens America's \$27 billion soy crop.

“Overlaying the sequence onto available maps will expedite identification and orientation of genetic markers such as single nucleotide polymorphisms which are often located near genes that control agronomically important traits,” Shoemaker said.

Using such markers, soy breeders can rapidly determine which offspring plants have inherited these traits without growing them to maturity, saving time, money and resources.

“We've mapped the locales for about 90 important traits affecting soybean growth and development, seed yield, seed protein and oil, and disease resistance, to name but a few,” Shoemaker added. “With this high-quality sequence, we now have access to candidate genes that we've never had before, which will enable us to look at their patterns of expression, develop molecular markers to track them in breeding programs, and work with them to determine their function or modify them to improve their function.”

Some key discoveries already gleaned from the whole-genome sequence include the first soybean gene conferring resistance to ASR, which can cause soy losses of 10 to 80 percent; a mutation that could make soybeans easier to digest by producing lower levels of a carbohydrate called stachyose; a mutation for higher levels of production of the enzyme phytase that could enable livestock to absorb more phosphorus from soybean feed so less gets excreted as a potential water contaminant; and 52 genes that orchestrate development of soy plant root nodules, where symbiotic bacteria transform atmospheric nitrogen into a form soy and other crops can use for their growth and development.

For other *Agri-Pulse* news stories, go to: [www.agri-pulse.com](http://www.agri-pulse.com).

#30