

# Breakthroughs Will Boost Research Into Corn's Genetic Makeup

ST. LOUIS, Mo. — Recent announcements regarding significant breakthroughs in human and rice genomics provide a major boost for corn genome research, the National Corn Growers Association (NCGA) noted.

Since 1996, funding plant genomic research — a process that determines the genetic makeup of the plant, in this case corn — has been the number one appropriations priority for the NCGA. It is hoped that this checkoff-funded program will open the doors for the development of improved corn hybrids that are more nutritious, provide greater yields, and are more adaptable to seasons, climates, and soils.

Monsanto announced a major scientific breakthrough in decoding the genetic makeup of rice that according to Monsanto "will provide a new level of understanding of almost all the

genes in rice." Similarly, Celera Genomics of Rockville, Md., announced that it has completed the sequencing phase of a human's genome. Both of these breakthroughs involve a "shotgun" or shortcut sequencing technique that identifies nearly all of the genes in rice and human organisms.

"The human genome breakthrough will prove validity of the shotgun approach to sequencing, particularly the validity as it applies to very complex organisms such as humans. Corn is estimated to be as complex," said Floyd Schultz, a grower from Plainfield, Ill. and chairman of the NCGA Customer and Business Development Action Team. "Things that we can learn from humans will help us advance significantly in corn."

Schultz noted that every advancement that has oc-

curred to date in human genome research has been applied to the plant level with some success, through the Plant Genome Initiative.

"The human effort has significantly driven the plant effort, and plant research has helped to drive the human effort," he noted.

The rice breakthrough is also significant in boosting corn genomic research, Schultz said.

"Similar to corn, rice is a grass, so we're much closer to applicability to corn," he said. "Rice is certainly not as complicated as corn, but with the working draft now available, it's going to jumpstart a major project under the Plant Genome Initiative that involves locating significant genes in rice and using them to locate key corn genes. This comparative genomics will be quite significant."

All of these advances will allow researchers to continue

to make strides in genomic research involving all economical crops, such as corn.

In recent testimony to the U.S. House Subcommittee on VA, HUD and Independent Agencies on Appropriations, Boyd Smith of York, Neb., outlined the importance of plant genomics.

"We strongly urge you to provide not less than \$80 million for the National Science Foundation (NSF) Plant Genome Initiative (PGI) and \$25.5 million for the '2010 Project,' the functional genomics project for *Arabidopsis thaliana*," Smith said.

Smith noted that a vigorous plant genomics program will allow researchers to create new hybrids and varieties that will:

- Improve human and animal health.
- Reduce medical costs because of more nutritious, healthier food for individuals.
- Reduce worldwide malnutrition through higher yielding and more nutritious crops.

• Reduce environmental problems for crop and livestock producers.

• Expand plant-based renewable resources for raw materials, industrial feedstocks, chemicals and energy.

• Enable growers to get more income from the market, thereby reducing reliance on federal farm programs.

Referencing the breakthroughs in genomic research, Smith noted that another key factor in the recent announcements is ensured accessibility to fundamental genetic information.

"Our interest from the beginning has been to try to ensure accessibility to the basic genetic information. We were concerned early on that interests in other countries would lock up genetic information and preclude work in corn because of the similarity between plants," he said. "The great thing about the rice announcement is that it puts all of the fundamental knowledge about rice

in the public domain."

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