Genetic-Diversification Program Is a "GEM" of a Resource for Corn Growers

Since 1994, the ARS-led Germplasm Enhancement of Maize (GEM) project has sought to help broaden the genetic base of America's corn crop by identifying promising exotic germplasm and crossing it with domestic lines.

New hybrids derived from such crosses have provided corn researchers and the producers they serve with access to many valuable traits that might not otherwise have been readily available to them. These may include improved or alternative native sources of resistance to insect pests such as corn rootworms and diseases like northern leaf blight, better stress tolerance, superior silage, increased oil content, and enhanced bioenergy potential.

GEM's aim is to provide sources of useful genetic maize diversity to help producers reduce risks from new or evolving insect and disease threats or changes in the environment or respond to new marketing opportunities and demands, says Mike Blanco, a plant geneticist who oversees GEM at the North Central Regional Plant Introduction Station, Ames, Iowa.

Blanco coordinates the evaluation and development of germplasm geared to midwestern corn production systems. Plant geneticist Matt Krakowsky, with ARS's Plant Science Research Unit in Raleigh, North Carolina, coordinates breeding and evaluation activities for the southeastern United States. Collaborating with them are more than 60 GEM cooperators from other ARS labs, state and foreign universities, private industry, international organizations, and nongovernmental organizations.

During the 2009 growing season, the Ames and Raleigh locations managed or coordinated evaluations on 17,200 nursery plots as well as 14,000 yield trial plots in Ames and 12,000 in Raleigh. A new "allelic diversity" study is devoted to exploring and capturing the genetic variation represented by over 300 exotic corn races. In 2010, 420 nursery rows at Raleigh and 369 rows in Ames are devoted to the objective of the allelic diversity project, which is to develop and release adapted germplasm lines representing this diversity.

GEM researchers use newer technologies to achieve their objectives and, when necessary, devise new ones. For example, using the "doubled haploid" method reduces the time it takes to produce homozygous plants derived from tropical or semitropical corn from the 8-10 growing seasons required by conventional breeding to just 2 growing seasons. Use of photoperiod-control "shade houses" created in Ames enables tropical corn lines to flower in midwestern long day-length periods.

"This allows us to make crosses we'd normally have to go to a short day-length nursery in the Tropics to make," says Blanco. More crosses can be made, affording greater quality control over research.

Since 2001, GEM has released 221 new corn lines to cooperators for further development into elite commercial hybrids.—By **Jan Suszkiw,** ARS.

Mike Blanco is with the USDA-ARS Plant Introduction Research Unit, Iowa State University, G212 Agronomy Hall, Ames, IA 50011; (515) 294-3758, michael.blanco@ars.usda.gov. ✳

Corn Genomics: At the Touch of a Keystroke

The Maize Genetics and Genomics Database (MaizeGDB) is a web-accessible resource (www.maizegdb.org) that furnishes geneticists, breeders, and others with all things corn—from molecular markers and sequence data to genetic maps and bioinformatics tools for mining them.

"MaizeGDB puts data together in a way that would have taken researchers a long time to chase down and compile on their own," says Carolyn Lawrence, a plant geneticist and MaizeGDB director at ARS's Corn Insects and Crop Genetics Research Unit (CICGRU) in Ames, Iowa.

Launched in 1991 as "MaizeDB," MaizeGDB is the product of many collaborators from CICGRU, ARS's Plant Genetics Research Unit in Columbia, Missouri, ARS's Plant Gene Expression Center in Albany, California, and cooperators worldwide. In addition to its support from ARS, MaizeGDB is also funded by the National Science Foundation and other organizations.

For all the powerful science behind it, MaizeGDB is surprisingly easy to use and offers straightforward explanations of key terminology—including how database information can be used.

For example, under a subhead titled "data centers," clicking on the term *QTL* links the user to the following explanation: "A QTL (or quantitative trait locus) refers to a particular region of the genome that is associated with a particular trait. This association is made through statistical methods based on the counting and measurement of easily observed traits, such as the weight of 1,000 kernels, the height of the second leaf at a particular stage of development, and so forth."

Conduct a QTL search for *plant height* and you get a list of experiments that evaluated plant height as well as links to the trait itself and 60 references describing it.

"At an early stage, the MaizeGDB team partnered with potential users to develop the database," says CICGRU research leader Craig Abel. "The resulting feedback and the creativity of the MaizeGDB team to develop solutions have produced an exceptional genomic database."

A recent noteworthy addition is a new genome browser that graphically displays sequence data for the inbred line B73. Another is the "Locus Lookup Tool." According to Lawrence, this tool can help researchers locate specific genes that will help them develop a better corn plant. Ultimately, growers will benefit from this technology as healthier and higher yielding corn plants are developed.—By **Jan Suszkiw,** ARS.

Carolyn Lawrence is in the USDA-ARS Corn Insects and Crop Genetics Research Unit, 1034 Crop Genome Informatics Laboratory, Iowa State University, Ames, IA 50011; (515) 294-4294, carolyn.lawrence@ars.usda.gov. ✳