# Study a step toward disease-resistant crops, sustainability

November 12 2008

A five-year study that could help increase disease resistance, stress tolerance and plant yields is under way at Purdue University.

The $4 million project uses a new technique called "mutant-assisted gene identification and characterization," or MAGIC, to identify potentially useful gene combinations in crop species.

"If we can understand these genes better, we could engineer plants to be immune to most diseases," said principal investigator Guri Johal, an associate professor of botany and plant pathology.

First using the corn genome, the method will add to the collection of useful alleles, or pairs of genes, that create certain traits. This will improve crop gene diversity, a quality that dwindles as crops are bred. Since natural selection has preserved such alleles, they likely confer a selective advantage that increases the ability of plants to survive, Johal said.

The MAGIC technique is described in a review article published this month in the journal *Crop Science*.

Maize contains more genetic diversity than any other model organism, making it an ideal plant for gene exploration, Johal said. In fact, two lines of corn are more different from one another than humans are from chimpanzees, said study co-author Cliff Weil, a professor of agronomy.

"Maize grows in places as different as northern Quebec, where it is cold and growing seasons are short, and the Mexican highlands, where it is very hot and dry," he said. "Natural adaptation to different environments has come by combining just the right sets of alleles in each variation."

MAGIC is a new tool needed to find genes, Johal said. Many recent research methods used to this end involve mutagenesis, with scientists deliberately causing a specific gene or genes to malfunction in order to determine the gene's impact on the plant.

"Mutagenesis has worked well, but we are reaching a period of diminishing returns," Johal said. "We've identified most of the genes that have effects on their own, but now we need to understand how combinations of genes interact. We suggest going back to nature to find additional genes involved in a wide range of different processes."

Any genes discovered also could benefit other plants; all use the same pathway to fight infection, Johal said.

"The same approach could be used in other organisms, such as in animals," he said. "And insights could also apply to human disease."

To map genes, scientists often cross mutant plants with crop lines that have well-described genetics. In doing so, they usually try to reduce or eliminate the impact of unknown natural variants so the information they're looking for - typically regarding the mutant gene - is not altered.

"To date most of us were taught in genetics class that when you find a mutation, for example in corn, you cross it with corn from different backgrounds, pick the background where the mutant's appearance, or its phenotype, is the most dramatically altered, and then find the genetic changes that cause the phenotype," Weil said.

But Weil and Johal are instead looking for natural genes that either enhance or diminish certain traits.

"We are basically 'mining' natural variation for genes of interest," Weil said.

The research started when Johal crossed a mutant gene that affects lesions to a couple of different inbred lines of corn. In one cross it disappeared; in another it became toxic.

"We figured the natural variations in these two inbreds were having a huge effect and decided to take advantage of a large, existing set of mapping data for the two inbreds to find out why," Weil said.

Another example is sweet corn, Johal said. The varieties most people are familiar with derive from a specific mutation that originally rendered sweet-tasting kernels small and shrunken. But researchers bred it with various lines - effectively using natural variation to their advantage - to increase kernel size.

Funding from the National Science Foundation began last month for the study, which will also include educational components. North Carolina State University researcher Peter Balint-Kurti is a review co-author and study collaborator.

"The nice thing is knowing this idea is going to work," Weil said. ""The alleles, the variation in expression and the data to map them are already there. We will find a lot of things we expected and a whole lot of things we never even imagined."

Source: Purdue University