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Researchers use

# MAGIC

to identify useful  
gene combinations  
in crops

You wouldn't think scientists would have much in common with magicians, but researchers at Purdue University have found that they do since they've started practicing MAGIC. But for them, MAGIC is an acronym for "mutant-assisted gene identification and characterization." It's a new technique for identifying potentially useful gene combinations in crop species that could help increase disease resistance, stress tolerance, and plant yields. The tool is described in the November–December 2008 issue of *Crop Science*.

"If we can understand these genes better, we could engineer plants to be immune to most diseases," says principal investigator Guri

Johal, an associate professor of botany and plant pathology at Purdue.

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 explains.

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

"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 says. "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 says. 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.

## Understanding How Gene Combinations Interact

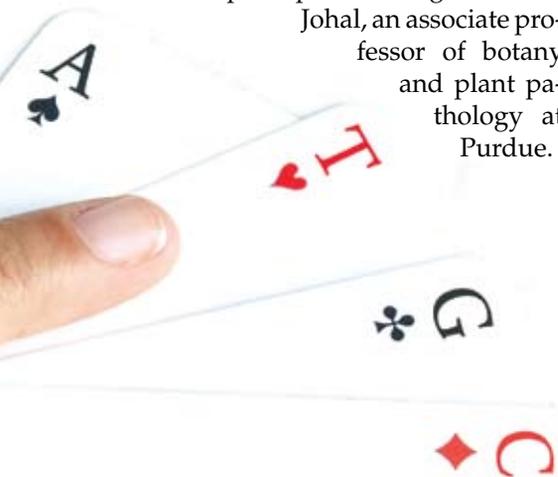
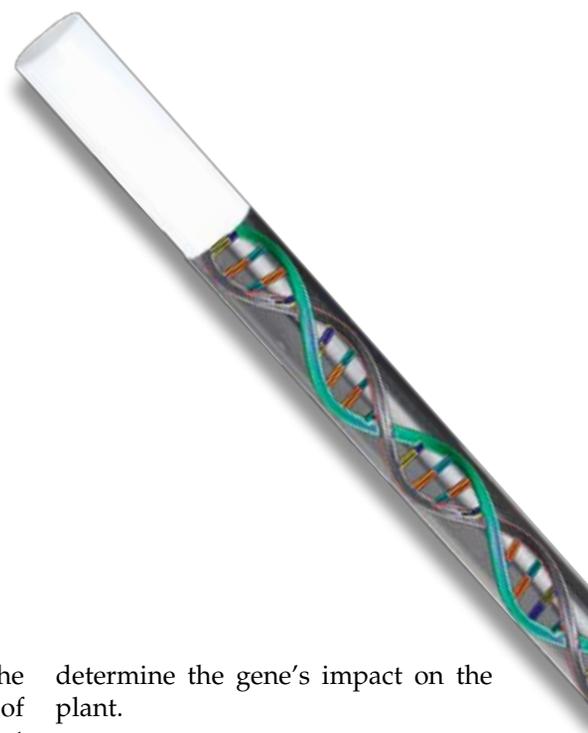
"Mutagenesis has worked well, but we are reaching a period of diminishing returns," Johal says. "We've identified most of the genes that have effects on their own, but now we need to understand how combinations of genes interact. We suggest going back to nature to find additional genes involved in a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

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

"The same approach could be used in other organisms, such as in animals," he says. "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 that 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



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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 says.

### Mining Natural Variation

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 explains.

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 says.

Another example is sweet corn, Johal says. 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.

"The nice thing is knowing this idea is going to work," Weil says. "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."

The five-year, \$4 million study is funded by the National Science Foundation. North Carolina State University researcher Peter Balint-Kurti is a review co-author and collaborator on the study.

—SOURCE: Purdue Agriculture Report. See [www.agriculture.purdue.edu/agcomm/news/agresearch/index.html](http://www.agriculture.purdue.edu/agcomm/news/agresearch/index.html). For the complete Crop Science paper, see Johal, G.S., P. Balint-Kurti, and

C.F. Weil. 2008. Mining and harnessing natural variation: A little MAGIC. *Crop Sci.* 48:2066–2073. Posted online at <http://crop.scijournals.org/content/vol48/issue6>

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