

Researchers re-sequence six corn varieties, find some genes missing

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Patrick Schnable, is a researcher in agronomy at Iowa State University. Credit: ISU photo by Bob Elbert

Most living plant and animal species have a certain, relatively small, amount of variation in their genetic make-up.

Differences in height, skin and eye color of humans, for example, are very noticeable, but are actually the consequences of very small variations in [genetic makeup](#).

Researchers at Iowa State University, China Agricultural University and the Beijing Genomics Institute in China recently re-sequenced and compared six elite inbred corn (maize) lines, including the parents of the most productive commercial hybrids in China.

When comparing the different inbred [corn lines](#), researchers expected to see more variations in the genes than in humans.

Surprisingly, researchers found entire genes that were missing from one line to another.

"That was a real eye opener," said Patrick Schnable, director of the Center for Plant Genomics and professor of [agronomy](#) at ISU.

The research uncovered more than 100 genes that are present in some corn lines but missing in others.

This variation is called the presence/absence variation, and Schnable thinks it could be very important.

Schnable's research is the cover article for the current edition of the journal *Nature Genetics*, and has been highlighted by the association Faculty 1000, which identifies the top 2 percent of important research from peer-reviewed journals worldwide.

"One of the goals of the research is to try to identify how heterosis (hybrid vigor) works," said Schnable.

Heterosis is the phenomenon in which the offspring of two different lines of corn grow better than either of the two parents. This is the attribute that has enabled corn breeders to produce better and better hybrids of corn.

For instance, two lines of corn can be bred to produce a hybrid that increases yield or resists drought or pests better than either of the parents.

With the current discovery that certain genes are missing from inbred

corn lines, Schnable thinks science is a step closer to identifying which genes are responsible for which traits.

Knowing which genes are important would provide a shortcut for breeders to produce hybrids with specific traits.

For example, if one inbred line is missing a gene and is drought susceptible, crossing that line with a line that includes the missing gene and is drought tolerant, might lead to a better hybrid, according to Schnable.

"If we can understand how heterosis works, we might be able to make predictions about which inbreds to cross together," said Schnable. "I don't think we'll be able to tell plant breeders which hybrids will be the absolute winners. But we might be able to say 'These combinations are probably not worth testing.'"

Schnable sees combining genes from two lines as a chance to introduce the best from both plants.

"These are complementing somehow," he said. "It's like a really good marriage. She's good at this, and he's good at that, and together, they form a good team."

The potential for improvement is great, but Schnable cautions that much work needs to be done.

"We are at the point where we think this is going to be important, but we don't know which [genes](#) specifically are going to be important," he said. "Now we need to figure out which genetic combinations will be predictive of hybrid success."

More information: www.nature.com/ng/journal/v42/n11/index.html

Provided by Iowa State University

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