

A new source of maize hybrid vigor

June 28 2012

Steve Moose, an associate professor of maize functional genomics at the University of Illinois and his graduate student Wes Barber think they may have discovered a new source of heterosis, or hybrid vigor, in maize. They have been looking at small RNAs (sRNAs), a class of double-stranded RNA molecules that are 20 to 25 nucleotides in length.

"Hybrid vigor" refers to the increased vigor or [general health](#), resistance to disease, and other superior qualities arising from the [crossbreeding](#) of genetically different plants. "We've always known that there's a [genetic basis](#) for this [heterosis](#)," said Moose. "[Charles Darwin](#) noticed it and commented that corn was particularly dramatic."

Scientists have been debating the sources of hybrid vigor since the early 1900s when Mendel's laws were rediscovered. Many of them disagreed with the model that prevailed from the 1920s to the 1950s, which linked heterosis to a single gene or to the interaction of several genes. "It seemed that the whole genome was involved," said Moose.

The discovery of DNA in 1953 eventually caused a paradigm shift in the way people looked at hybrid vigor but, Moose said, there was no unifying theory. Even as new genetic technologies were developed, the genes did not seem to explain everything.

"We thought that maybe it's the rest of the genome, the remaining 85 percent of the corn genome, that's important," said Moose.

sRNAs were originally found in 1998 in roundworms. Researchers

studying [virus resistance](#) in plants then began to notice them and observed that the way that they function is very different from the functioning of protein-coding genes.

"Every time we have a breakthrough in our knowledge of genetics, people have looked to see if that breakthrough brings any insight into the mystery of the hybrid vigor," said Moose. "That's what we've done with the small RNAs."

"When you think about what small RNAs do, they participate in regulating growth and they tell other genes what to do," he continued. "So they have the two properties that we know fit what has been described (about heterosis) even though we do not have an explanation. We would argue that, while they are part of the explanation, they may not be the whole explanation."

Moose and Barber sampled small RNAs from the seedling shoot and the developing ear of maize hybrids, two tissues that grow rapidly and program growth, to investigate how the small [RNA](#) profiles of these hybrids differed from those of their parents. In collaboration with associate professor of crop sciences Matt Hudson, they analyzed what they described as a "deluge" of data.

"There were 50 million data points, but we whittled it down to the most important ones," said Barber.

They found that differences are due mainly to hybrids inheriting distinct small interfering RNAs (siRNAs), a subset of sRNAs, from each parent. The siRNAs interfere with gene expression. They also found that hybridization does not create new siRNAs, but hybrids have a more complex siRNA population than their parents because they inherit distinct siRNAs from both parents.

Moreover, the differences in parental siRNAs originated primarily from repeats, which are the result of retrotransposon activity.

Retrotransposons are elements that move around and amplify themselves within a genome.

"This is a new source of genetic diversity that people had overlooked," said Barber.

"We are not saying that genes are not important," said Moose. ""But probably the way corn properties are altered in the hybrid situation is mediated by the small RNAs in addition to the genes."

Moose and Barber hope that their work might provide more insight into how to decide which inbred maize lines to cross. "We don't want to alter how the plant grows, but if we can tweak it to do whatever it already does either faster or more, that could be an advantage," said [Moose](#).

More information: The article describing this work, "Repeat Associated Small RNAs Vary Among Parents and Following Hybridization in Maize" by Wesley T. Barber, WeiZhang, Hlaing Win, Kranthi K. Varala, Jane E. Dorweiler, Matthew E. Hudson, and Stephen P. Moose was published in the June 26, 2012, issue of *Proceedings of the National Academy of Sciences*.

Provided by University of Illinois at Urbana-Champaign

Citation: A new source of maize hybrid vigor (2012, June 28) retrieved 24 April 2024 from <https://phys.org/news/2012-06-source-maize-hybrid-vigor.html>

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