Sweet corn genes related to crowding stress identified

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Plants grown in high-density or crowded populations often put more energy into growth and maintenance than reproduction. For example, flowering may be delayed as plants allocate resources to growing taller and escape competition for light. This sensitivity to crowding stress has been observed in some varieties of sweet corn, but other varieties show higher tolerance, producing high yields even in crowded conditions. A recent University of Illinois and USDA Agricultural Research Service study attempted to uncover the genetic mechanisms of crowding tolerance in sweet corn.

"We were trying to find genes that differentiate sweet corn hybrids that have potential to produce higher yields under crowding stress versus hybrids with lower yields under the same growing conditions," explains U of I crop science researcher Eunsoo Choe.

Choe and her team measured observable or phenotypic traits for high- and low-yielding hybrids under crowding stress; these included traits known to correlate with crowding stress, such as plant height, leaf area, and time to maturity. Other traits, such as yield, kernel mass, kernel moisture, and fill percentage were also measured. Lastly, the team extracted genetic material from the plants to explore correlations between gene expression patterns and measured traits.

"We found clusters of genes that were related to yield under crowding stress," says Choe.

Although gene expression patterns indicated each hybrid utilized unique mechanisms for tolerating crowding stress, the researchers did confirm a common genetic basis for the yield response in the six hybrids tested. Low-yielding hybrids had gene activities related to various stress responses while high-yielding hybrids utilized gene activities more directly related to carbohydrate accumulation.

Choe says that genes involved with cell growth were prevalent in low-yielding hybrids; these genes may be responsible for delayed flowering under crowding stress. Conversely, genes associated with carbohydrate metabolism were prevalent in high-yielding hybrids; these genes may relate to maintaining yield under crowding stress.

"The gene clusters we identified were very broad in their biological functions," notes Choe. "Our results will have to be tested further for agronomic improvement by breeders. But narrowing down the pool of genes to those most likely influencing yield is an important step."

The article, "Identification of crowding stress tolerance co-expression networks involved in sweet corn yield," is published in *PLoS ONE*. Martin Williams, an ecologist at USDA ARS and the University of Illinois, and Jenny Drnevich, a bioinformatics specialist at the University of Illinois, also contributed to the paper.

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