

# Maize diversity discoveries may help ease world's hunger pangs

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Researchers at the University of California, Davis, report that ancient farmers had a stronger impact on the evolution of maize, or corn, than modern plant breeders have had on the grain — now one of the world's top production crops.

The findings, together with a companion study on maize diversity, will be published June 3 in the online edition of the journal *Nature Genetics*. The research was funded by the National Science Foundation and conducted by scientists from 17 international institutions, including BGI, the world's largest genomics organization. It will serve as the basis for future research in crop evolution.

"These two studies provide a new and more comprehensive understanding of genomic variation in maize, which will be critically important to plant breeders as they work to increase [corn](#) yield in the face of global population growth and climate change," said plant geneticist Jeffrey Ross-Ibarra, the lead researcher on the UC Davis-directed study.

The world's population is expected to climb from 7 billion people this year to an estimated 9 billion by 2050. The Food and Agriculture Organization of the United Nations predicts that food production will need to increase by 70 percent over the next four decades to meet anticipated demand. Globally, 90 percent of these production increases will need to come from increasing crop yield on existing farmland rather than by bringing new land into agricultural production.

The new UC Davis-led study analyzed the [evolution](#) of maize during the period when it was domesticated 10,000 years ago, as well as during subsequent breeding. The study was based on the resequencing of 75 genomes of maize and its relatives, including wild strains, traditional cultivated varieties and improved modern inbred lines. (The first sequencing of the reference [maize genome](#) was announced by a U.S.-based consortium of researchers in 2009.)

The new maize genome study showed that:

- Though a substantial amount of diversity was lost during domestication, new diversity has arisen since domestication in the form of novel mutations;
- Hundreds of identified genes appear to have played a role in domestication of maize from the wild, and many of these genes also appear to have been important for modern breeding;
- Selection applied during initial domestication appears to have been much stronger than selection applied more recently during maize breeding; and
- Modern strategies of breeding for hybrid vigor have been accompanied by marked changes in gene expression in maize.

The companion study was led by Doreen Ware, a U.S. Department of Agriculture-Agricultural Research Service computational biologist at Cold Spring Harbor Laboratory, New York. That study used a sophisticated population genetics-based scoring model to untangle the complexity of the maize genome. Through the study, the researchers:

- Identified more than 55 million genetic markers in the maize genome and demonstrated that the genome is continuously changing;

- Discovered that it is common for genes to be present or absent -- or to occur in varying numbers -- in both wild and domesticated maize, and these variations are associated with important agricultural traits; and
- Found that there is substantial continuity of gene content between maize relatives, suggesting that environmental adaptations such as perennialism, and frost and drought tolerance might be transferred from wild relatives into domesticated [maize](#).

Provided by UC Davis

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