

# Study finds prioritizing rather than canvassing entire plant genome may lead to improved crops

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A new study may help scientists produce better climate-resistant corn and other food production plants by putting a spin on the notion that we are what we eat.

Kansas State University geneticists and colleagues found that by applying a genetic-analysis method used to study and prioritize the [genes](#) in humans, it improved the likelihood of finding critical genes in food [production plants](#). These genes control quantitative traits in plants, such as how the plants grow and when they flower.

Additionally, this method can be used to study how food production plants respond to drought, heat and other factors—giving scientists a greater chance at improving crops' resistances to harsh weather and environments.

"Right now we know most of the genes that make up several of these food production plants, but finding the right genes to increase food yield or heat tolerance is like finding a needle in a haystack," said Jianming Yu, associate professor of agronomy at Kansas State University and the study's senior author.

Yu made the finding with Xianran Li and Chengsong Zhu, both agronomy research associates at Kansas State University; Patrick Schnable, Baker professor of agronomy at Iowa State University, and

colleagues at Cornell University; the Cold Spring Harbor Laboratory; the University of Minnesota; and the U.S. Department of Agriculture-Agricultural Research Service.

Their study, "Genic and non-genic contributions to natural variation of quantitative traits in maize," was recently published in the journal [Genome Research](#). The National Science Foundation funded the research.

For the study, researchers looked at the sequenced genome of corn. A genome is the [genetic blueprint](#) of an organism and contains all of the DNA and genes that give the organism its traits, like height and color. Staple food crops like corn, wheat, barley and oats have comparable and sometimes larger, more complex genomes than humans and mammals. That poses a challenge for scientists attempting to modify the plant and improve aspects like production and [heat tolerance](#).

"Like humans, plants have complex traits and complex diseases," said Li, the study's first author. "In plants, those are things like drought tolerance and grain yield. Sometimes one specific gene can make a big change. Frequently, though, it involves multiple genes. Each gene has a small, modest effect on the trait and many genes are involved. This makes it really difficult to study."

Historically, scientists have analyzed an isolated region of a plant genome—often taking a trial-and-error approach at finding what genes control what traits.

Instead, researchers approached the corn genome with a relatively new analysis method that is used to study the genome of humans. The method, called genome-wide associate studies—or GWAS—searches the entire genome for small, frequent variations that may influence the risk of a certain disease. This helps researchers pinpoint genes that are

potentially problematic and may be the key in abnormal traits and diseases.

"Conducting routine, full-scale, genome-wide studies in crop plants remains challenging due to cost and genome complexity," said Schnable, the other senior author. "What we tried to get out of this study is a broad view of which regions of crop genomes should be examined in detail."

Using the GWAS method for multiple analyses and complementary methods in identifying genetic variants, researchers were able to find that, on average, 79 percent of detectable genetic signals are concentrated at previously defined genes and their promoter regions.

According to Yu, the percentage is a significant increase compared to looking at the gene regions alone.

"We used to think that genes are the only search priority and there were just many other less important or useless DNA sequences," Yu said. "But now we are starting to see that these other regions harbor some important genetic codes in them. Canvassing without prioritizing can be cost prohibitive, however, and efficient GWAS in crops with complex genomes still need to be carried out by taking advantage of a combination of [genome](#) technologies available."

Provided by Kansas State University

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