

Corn genetics research exposes mechanism behind traits becoming silent

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Diverse maize cobs showing the varying genetic traits of kernel and cob colors.
Credit: Surinder Chopra, Penn State

For more than a century, plant geneticists have been studying maize as a model system to understand the rules governing the inheritance of traits, and a team of researchers recently unveiled a previously unknown mechanism that triggers gene silencing in corn. Gene silencing turns off genetic traits, an important consideration for plant breeders who depend on the faithful inheritance of traits from one generation to the next.

Historically, the maize *p1* gene has been used as a model by maize geneticists. Previous researchers did not know that two types of overlapping DNA methylation marks could modify, silence or activate this gene. The discovery adds to geneticists' knowledge of different mechanisms of non-Mendelian inheritance, according to lead researcher Surinder Chopra, professor of maize genetics, College of Agricultural Sciences, Penn State.

In findings reported in *PLOS One*, Chopra's team showed that silencing the corn pericarp color 1 gene—regulator of the kernels' outer layer color and the cob color—can have two "overlapping" epigenetic components—RNA dependent DNA methylation (RdDM) and non-RNA dependent DNA methylation (non-RdDM).

"DNA methylation, which is the addition of [methyl](#) groups to the DNA molecule, can change the activity of a DNA segment without changing the sequence," he said. "DNA methylation typically acts to repress [gene transcription](#), which is the first step of gene expression."

In plant cells, when and at what level a gene is expressed is under tight control between transcription activation and suppression, Chopra explained. Small RNAs—molecules essential in regulation and expression of genes—can mediate methylation of DNA strands and shut down transcription activity, therefore playing a role in silencing inherited genes or transgenes introduced to produce desirable crop traits.

In corn, the pericarp color 1 gene regulates the accumulation of brick-red flavonoid pigments called phlobaphenes. The pattern of pigmentation on the corn kernel pericarp and "glumes"—membrane covering the cob—depends upon the expression of the pericarp color 1 gene. Some examples of these patterns are: white kernels, red cob; red kernels, red cob; variegated kernels, variegated cob; red kernels, white cob; and white kernels, white cob.

"Our study on maize pericarp color 1 gene has demonstrated the involvement of both small RNA-dependent and small RNA-independent mechanisms for gene suppression," Chopra said. "This study reveals the additional layer of gene regulation by small RNAs, and improves our understanding of how [gene expression](#) is regulated specifically in one tissue but not in the other."

Typically, when plant breeders are creating new types of cultivars, several traits they are breeding for may disappear or their expression gets reduced in the progeny, he said. "And that, we now know, is because of gene silencing."

A better understanding of how gene-silencing mechanisms cause the disappearance of desired traits has long been needed, Chopra believes. It can be disastrous for a farmer to buy seeds that do not behave in the grow-out the way they were promised by the producer.

If one or more genes that are controlling a trait become silent due to overlapping DNA methylation, then that trait basically disappears from the population.

"That is a big setback for anyone trying to breed for traits such as high yield, which is regulated by several genes," said Chopra. "If one or two of those [genes](#) that are essential for high yield become silent, then a reduction in the overall yield may result."

Provided by Pennsylvania State University

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