

# Novel way plants pass traits to next generation found: Inheritance behavior in corn breaks accepted rules of genetics

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New research explains how certain traits can pass down from one generation to the next – at least in plants – without following the accepted rules of genetics.

Scientists have shown that an enzyme in corn responsible for reading information from DNA can prompt unexpected changes in gene activity – an example of epigenetics.

Epigenetics refers to modifications in the [genome](#) that don't directly affect [DNA sequences](#). Though some evidence has suggested that [epigenetic changes](#) can bypass DNA's influence to carry on from one generation to the next, this is the first study to show that this epigenetic heritability can be subject to selective breeding.

Researchers bred 10 generations of corn and found that one particular gene's activity persisted from one generation to the next whether the enzyme was functioning or not – meaning typical genetic behavior was not required for the gene's trait to come through.

And that, the scientists determined, was because the enzyme targets a tiny piece of DNA – previously thought of as "[junk DNA](#)" – that had jumped from one area of the genome to another, giving that little fragment power to unexpectedly turn on the gene.

The gene in question affects pigmentation in the [corn plant](#). As a result of these experiments, the researchers were able to change yellow kernel corn to a blue kernel variety by compromising the activity of the enzyme in each male parent.

"This is the first example where somebody has been able to take an epigenetic source of variation and, through [selective breeding](#), move it from an inactive state to an [active state](#)," said Jay Hollick, associate professor of [molecular genetics](#) at The Ohio State University and lead author of the study. "The gene changes its expression in an epigenetic fashion and it doesn't follow standard inheritance behaviors. Those two factors alone have pretty [profound implications](#) not only for breeding but also for evolution."

The study appears online in the journal *The Plant Cell*.

Plant breeders tend to expect to generate desired traits according to what is known as Mendelian principles of inheritance: Offspring receive one copy of genes from each parental plant, and the characteristics of the alleles, or alternative forms of genes, help predict which traits will show up in the next plant generation.

However, epigenetic variations that change the predictability of gene behavior have complicated those expectations.

"The breeding community searches for novel traits that will have commercial interest and they really don't care what the basis is as long as they can capture it and breed it. Epigenetic [heritability](#) throws a kink in the expectations, but our findings also provide an opportunity – if they recognize the variation they're looking for is the result of [epigenetics](#), they could use that to their advantage," said Hollick, also an investigator in Ohio State's centers for RNA Biology and Applied Plant Sciences.

"Just by knowing that this allele behaves in this epigenetic fashion, I can breed plants that either have full coloration or no coloration or anything in between, because I am manipulating epigenetic variation and not genetic variation. And color, of course, is only one trait that could be affected."

With a longtime specialization in the molecular basis for unexpected [gene activity](#) in plants, Hollick had zeroed in on an enzyme called RNA polymerase IV ([Pol IV](#)). Multiple types of RNA polymerases are responsible for setting gene expression in motion in all cells, and Pol IV is an enigmatic RNA polymerase that is known in plants to produce small RNA molecules.

Pol IV has puzzled scientists because despite its strong conservation in all plants, it appears to have no discernible impact on the development of *Arabidopsis*, a common model organism in plant biology. For example, when it is deleted from these plants, they show no signs of distress.

In corn, however, Hollick's lab had discovered previously that the absence of Pol IV creates clear problems in the plants, such as growing seeds in the tassel.

Hollick and colleagues observed that plants deficient in Pol IV also showed pigmentation in kernels of ears expected not to make any color at all – meaning they were expected to be yellow.

"Since we knew the misplaced tassel-seed trait was due to misexpression of a gene, we hypothesized that this pigment trait might be due to a pigment regulator being expressed in a tissue where it normally is never expressed. Molecular analysis showed that that was in fact the case," Hollick said.

The researchers selected dark kernels and light kernels from multiple

generations of plants and crossed the plants derived from these different kernel classes to create additional new generations of corn.

"We found that the ears developed from those [plants](#) had even more darkly colored kernels and fewer lightly colored kernels. We could segregate the extreme types and cross them together and get this continued intensification of the pigmentation over many generations," he said. "We generated more progeny that had increasing amounts of pigment. This is taking a gene that is genetically null, that doesn't have any function in this part of the plant, and turning it from a complete null to a completely dominant form that produces full coloration.

"Essentially we were breeding a novel trait, but not by selecting for any particular gene. We were just continually altering the epigenetic status of one of the two parental genomes every time."

This led the scientists to question why the affected alleles of the pigmentation gene would behave in this way. An investigation of the affected alleles revealed the nearby presence of a transposon, or transposable element: a tiny piece of DNA that has leapt from one area of the genome to another.

Because the sequence of some small RNA fragments that come from Pol IV's activity are identical to the sequence of these transposons, the finding made sense to the scientists.

"Now that we know that Pol IV is involved in regulating transposons, it's not surprising that genes that are near transposons are now regulated by Pol IV," Hollick said.

Provided by The Ohio State University

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