

Study shows how plants sort and eliminate genes over millennia

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Hybrid plants with multiple genome copies show evidence of preferential treatment of the genes from one ancient parent over the genes of the other parent, even to the point where some of the unfavored genes eventually are deleted.

Brian Dilkes, an assistant professor of genetics at Purdue University, worked with a team of scientists at the University of California Davis and University of Southern California to study the [genome](#) of *Arabidopsis suecica*, a [hybrid species](#) with four chromosome sets formed tens of thousands of years ago from a cross between *Arabidopsis arenosa* and *Arabidopsis thaliana*, a plant commonly used in laboratories for genetic research. Dilkes said the findings, published in the journal *Genome Biology* and featured as an editor's choice article in the journal *Science*, give a glimpse into the evolutionary forces and ultimate fates of genes contributed by the two parents to a hybrid

"There often is no visible signature of these genes when we look at the plants with a microscope, but we can still observe those genes in the [genome sequence](#)," Dilkes said. "Moreover, the ability to make crosses between *Arabidopsis thaliana* and *Arabidopsis arenosa* gives us the opportunity to compare laboratory-derived plants that were generated yesterday with naturally occurring species from the wild and compare the two kinds of species hybrids. This is essentially allowing us an opportunity to 'replay the evolutionary tape,' in the words of Stephen J. Gould."

The researchers compared the genomes and [gene expression](#) among *Arabidopsis suecica* plants that have evolved over tens of thousands of years to similar species of hybrids made in the lab from fresh crosses.

When the contribution of genes from each parent was compared, they were not equal. One parent's genes were preferentially expressed at higher levels. In the cases where that happened, it was three times more likely that the preferentially expressed genes came from *Arabidopsis arenosa*.

The team also found that gene pairs that are co-expressed in similar tissues are preferentially expressed from the same parent. Even in the rare cases when an *Arabidopsis thaliana* gene was more abundantly expressed in the hybrid, co-expressed genes would also be preferentially expressed from the [Arabidopsis thaliana](#) copy.

"Our findings suggest an additional network dependence, where genes fine-tuned to work together within either parental species prior to hybridization are more likely to be expressed together in the hybrid. This, in turn, ensures that these genes acquired from one parental species are kept together and are not lost in the genome over time," said Peter Chang, a graduate student at USC and lead author on the paper. "Plants have had a remarkable ability to adapt to different conditions throughout Earth's history, and we are just beginning to understand some of ways this is done."

Previous work has shown that plant genomes with historical duplications from tens of millions of years ago have lost one of the two copies in large blocks along the chromosome, consistent with the preferential loss of one parent's contribution.

Dilkes said the retained genes may have a role in the plants' fitness but genes that weren't expressed would be deleted from the genome.

"The genome is moving toward a two-copy organization, a diploid, by preferentially deleting one parent. When others have looked at genomes that have ancient duplications they see large blocks of duplications in which one block has a large number of [genes](#) and the other has a sparse gene content," Dilkes said. "Perhaps a cause of this pattern in the organization of genomes is preferential expression, and, all other things being equal, the gene that is more abundantly expressed will carry a greater proportion of the fitness load for any essential function."

More information: Homoeolog-specific Retention and Use in Allotetraploid *Arabidopsis Suecica* Depends on Parent of Origin and Network Partners, Peter L. Chang, Brian P. Dilkes, Michelle McMahon, Luca Comai, Sergey V. Nuzhdin, *Genome Biology*.

Provided by Purdue University

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