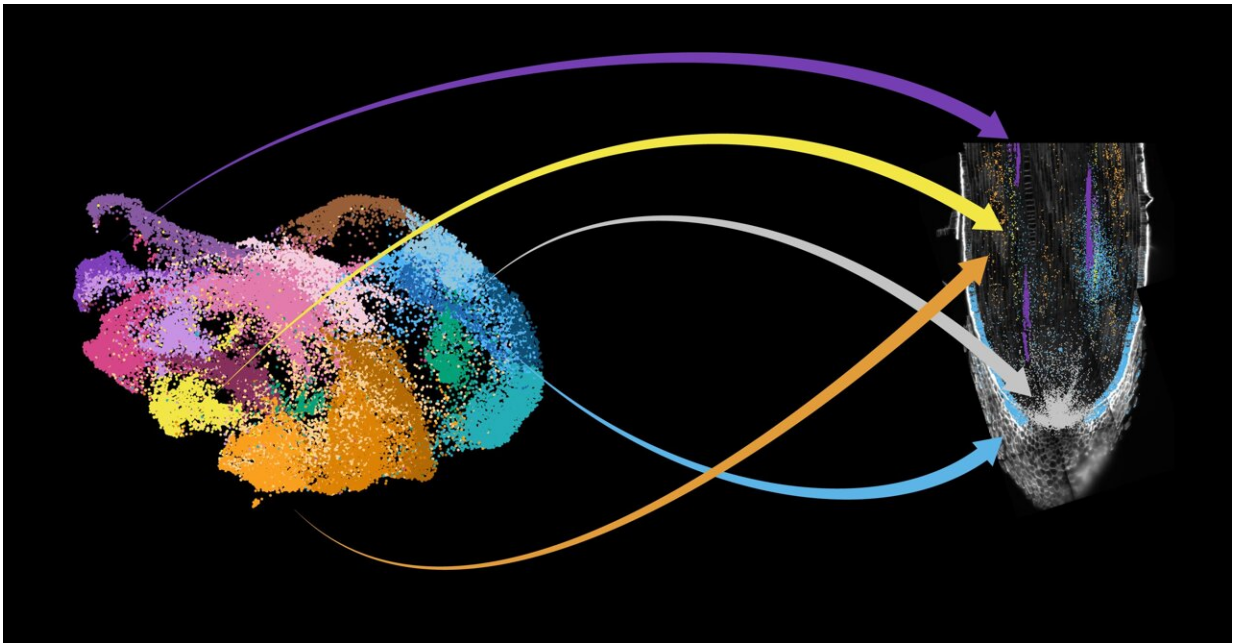


# Crops evolved by swapping genetic modules between cells: Study

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The researchers used a technology called Molecular Cartography, a spatial transcriptomics method, in collaboration with Resolve Biosciences to map the cellular location of about a hundred genes at once. This allowed them to validate the cell-by-cell cross-species map of gene expression. Credit: Bruno Guillotin/Ramin Rahni

Comparing individual cells across corn, sorghum and millet reveals evolutionary differences among these important cereal crops, according to a new study led by New York University researchers.

The findings, published in *Nature*, bring researchers closer to pinpointing which [genes](#) control important agricultural traits such as drought tolerance, which will help scientists faced with a changing climate adapt crops to drier environments.

Corn, sorghum, and millet provide food for humans and animals around the world. Corn and sorghum are ancient relatives that evolved into two different species roughly 12 million years ago, and millet is a more distant relative.

Despite their shared ancestry, the crops have substantial differences in key traits—for instance, sorghum is far more tolerant to drought than is corn, and the plants release unique gooey substances from their roots to shape how they interact with their surrounding soil. These differences may be traced back to corn undergoing a whole genome duplication after its split from sorghum.

"The importance of these crops, their evolutionary proximity, and their functional differences present an exciting opportunity for comparing patterns of gene expression at the cell level," said

Bruno Guillotin, a postdoctoral associate in NYU's Department of Biology and the study's first author. "While these three crops are similar, how they differ from each other is important because they have traits that we may want to transfer from one to the other, such as drought tolerance."

The researchers conducted single-cell mRNA profiling of the roots of corn, sorghum, and millet, dissecting the roots to look at the cells individually and observing precisely where genes are expressed in a particular cell. They then compared the same specialized cells across the three crops.

"Roots are the first line of defense against drought and heat. You can think of the [root](#) as a machine with many working parts—in this case, cell types—so knowing how the machine works to collect water and to deal with drought and heat is really important," said Kenneth Birnbaum, a professor in NYU's Department of Biology and Center for Genomics and Systems Biology and the study's senior author. "Comparing the different species helps us tease apart which genes lead to key agricultural traits."

In examining how cells have evolved and diverged in the different species, the researchers identified several trends that point to "tinkering"—or the rearrangement of existing elements—of cells over time. First, they observed that cells often trade gene expression modules, or groups of 10 or 50 genes with coordinated functions, between cell types over evolution.

"This gene module swapping has been shown in animal systems, but the data we generated is the first time it's been illustrated on a large level in plants," added Birnbaum.

This swapping of modules was demonstrated in a discovery about root slime—the gooey substance filled with nutrients that roots emit into the soil. Slime is useful for lubricating the soil so roots can pass through and can attract beneficial bacteria that protect the plant or provide hard-to-get nutrients.

The researchers found that the genes that help produce root slime were located in different parts of the corn, sorghum, and millet root. In sorghum, the slime genes were found in the root's outer tissue, while in corn these were swapped into a new cell type in the root cap, an [evolutionary change](#) that may enable corn to attract bacteria that helps the plant to gain nitrogen.

They also identified other gene regulators that were switched around in different [cell types](#) depending on the crop, providing researchers with prime candidates for testing genes that convey specific traits.

In addition, the researchers found that the [whole genome duplication](#) in corn after its split from [sorghum](#) 12 million years ago affected specific types of cells, allowing [corn](#) cells to rapidly specialize. They also observed that certain kinds of cells acted as the donors of new genes while others seemed to collect new gene duplicates, which may suggest that gene duplication sped up the evolution of certain cells.

Recent advances in single-cell sequencing techniques made this research possible and open up new methods to explore the connection between genes and cellular traits in crops.

"A decade ago, we were only able to analyze a dozen or a few dozen cells with the early single-cell sequencing techniques. Now we can profile tens of thousands of cells in a pretty routine experiment," said Birnbaum.

Future studies will compare how single cells of these three crops respond to stress, such as drought.

"It's that response that may be the key to finding that set of genes that are really important for drought tolerance," said Birnbaum.

**More information:** Kenneth Birnbaum, A pan-grass transcriptome reveals patterns of cellular divergence in crops, *Nature* (2023). [DOI: 10.1038/s41586-023-06053-0](https://doi.org/10.1038/s41586-023-06053-0).  
[www.nature.com/articles/s41586-023-06053-0](https://www.nature.com/articles/s41586-023-06053-0)

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