

Computational Analysis Shows That Plant Hormones Often Go It Alone

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Unlike the Three Musketeers who lived by the motto “All for one, one for all,” plant hormones prefer to do their own thing. For years, debate swirled around whether pathways activated by growth-regulating plant hormones converge on a central growth regulatory module. Now, the cooperation model is challenged by researchers at the Salk Institute for Biological Studies. They show that each hormone acts largely independently in the Aug. 11 issue of *Cell*.

The Salk team found that specific plant hormones often activate different factors rather than a common target. “This result was completely unexpected because hormones with similar effects on plant growth seem to act on different gene sets,” says the study’s lead author Joanne Chory, Ph.D., a professor in the Plant Biology Laboratory and investigator with the Howard Hughes Medical Institute.

Plants rely on hormones, which act as chemical messengers to regulate every aspect of their biology. Growth, for example, is stimulated by multiple hormones -- brassinosteroids, auxins and gibberellins among them. The fact that these and several other hormones stimulate plant growth suggested to some investigators that eventually they all switch on the same growth-promoting genes.

To test that idea, the Chory team poured over data derived from the new gene-chip technology, in which samples of almost every gene expressed in a cell are spotted onto a tiny glass slide known as a microarray and analyzed under different physiological conditions. Although the analysis

sounds complex, it answers a simple question: After stimulation with seven different growth hormones, are the same genes activated or not?

The teamwork model would predict yes, but Chory's team found otherwise. Co-lead authors Jennifer L. Nemhauser, Ph.D., a former postdoctoral fellow in Chory's lab and now assistant professor at the University of Washington in Seattle, and Fangxin Hong, Ph.D., a biostatistician in Chory's lab, found that each of the seven hormones activated largely its own repertoire of target genes. "We found shockingly little overlap," Nemhauser reports.

The microarray data used by Chory's team were collected as part of a multinational effort known as the AtGenExpress project cataloguing gene expression in the model plant *Arabidopsis thaliana*, which has become the lab mouse of the plant world. The laboratory of Detlef Weigel, Ph.D., an adjunct professor in the Laboratory for Plant Biology at the Salk and a professor at the Max Plank Institute for Developmental Biology in Tübingen, Germany, is one of the most prolific providers of micro-array data for *Arabidopsis*.

Participants in the project send results from their lab's microarray analysis of *Arabidopsis* genes to a publicly available database, where data is shared by colleagues investigating diverse biological questions. "The data was there but nobody had compared the effects of different growth hormones on gene expression side by side," says Nemhauser.

The amount of data analyzed by the Chory group was enormous. The activity of about 22,000 genes, each detected by on average 15 detectors after treatment with the seven hormones, was crunched—not once—but twice, resulting in roughly 14 million data points. "Since we didn't generate any of the data ourselves, we had to perform extensive quality controls to extract meaningful information," explains Hong.

The Salk researchers' analysis revealed that surprisingly few genes were switched on by multiple hormones. And when more than one hormone did initiate a similar program, such as activating genes encoding proteins called "expansins" that loosen plant cell walls to allow for growth, the investigators found that they mobilized different members of the expansin gene family.

"The data analysis showed that there is likely a complex set of interactions between the levels of hormones," explains Chory, "which suggests that long-term effects of all hormone treatments represent a 'domino effect' that resets many systems within the plant."

Combining traditional biological approaches with computational analysis will move plant biologists closer to answering the age-old question of how plants grow, the Salk researchers predict. "Microarrays are very useful for those of us studying physiology and development. They can reveal new interactions, or lack thereof, between biological processes and identify candidates for direct targets of transcription factors controlling development," says Chory.

Source: Salk Institute for Biological Studies

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