# Plant steroids offer new paradigm for how hormones work

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Steroids bulk up plants just as they do human athletes, but the playbook of molecular signals that tell the genes to boost growth and development in plant cells is far more complicated than in human and animal cells. A new study by plant biologists at the Carnegie Institution used an emerging molecular approach called proteomics to identify key links in the steroid signaling chain. Understanding how these plant hormones activate genes could lead not only to enhanced harvests but also to new insights into how steroids regulate growth in both plant and animal cells.

The study by Zhi-Yong Wang and Wenqinag Tang of the Carnegie Institution's Department of Plant Biology with seven co-authors* is published in the July 25 issue of *Science* magazine.

Plant steroids, called brassinosteroids, are key hormones throughout the plant kingdom. They regulate many aspects of growth and development, and mutants deficient in brassinosteroids are often extremely stunted and infertile. Brassinosteroids are similar in many respects to animal steroids, but appear to function very differently at the cellular level. Animal cells respond to steroids using internal receptor molecules within the cells nucleus, whereas in plants the receptors are anchored to the outside surface of the cell membranes.

A challenge for researchers has been to piece together the steps by which the hormonal signal is transmitted from the cell surface receptor to its action in the nucleus, where genes are the targets of regulation. Traditionally, genetic methods have been used to identify several

components of the BR signaling pathway. However, genetic approach cannot identify all the components of a signaling pathway largely because of genetic redundancy (many genes play the same role in the cell).

To identify the links in the signal transduction chain, the researchers used the techniques of proteomics. "Proteomics is analogous to genomics," says Wang. "In genomics, we aim for a comprehensive survey of all the genes in genome. In proteomics, we're mapping the proteins." Because there can be hundreds of thousands of different proteins in a single organism, proteomics requires techniques, such as 2-dimensional gel electrophoresis, which can process and segregate thousands of proteins at a time based on differences in their size and charge.

But even with these methods, isolating the low-abundance signaling proteins was a daunting task. "Earlier attempts to identify these molecules failed, because the analyses were swamped by the more abundant proteins," says Wang. "But because we knew the proteins would be associated with the cell membrane, we tried separating the membranes from the rest of the cell material and just analyzed that fraction. And that worked."

The study targeted a class of proteins called kinases, which transmit signals by exchanging phosphate ions. The electrophoresis analyses identified a group of kinases that responded to the presence of brassinosteroids. The researchers called these proteins BSKs (brassinosteroid signaling kinases). Follow-up analyses confirmed their crucial function in brassinosteroid signaling.

"BRKs are the first major signaling component to be identified by a quantitative proteomics approach in plants." says Wang. "Finding them fills a major gap in the brassinosteroid signal pathway and may have

major implications for our understanding of other signaling processes in plants as well. The plant genome codes for many hundreds of receptors at the cell surface, but a major missing link is their connection to the intracellular signaling cascades. Plant cells also contain quite a number of proteins that are similar to BSK, so it is tempting to speculate that they represent these missing connections". Wang's findings have not only helped establish the connections of the steroid signaling pathway, but possibly offers a paradigm for both kinase signaling in plants and for steroid signaling by cell-surface receptors in general. More importantly, the success of the proteomic methods demonstrated by Wang's study will have a major impact on studies of other signal transduction pathways.

Source: Carnegie Institution

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