Cell signalling and gene regulation

Editorial overview

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Cell signaling is central to our understanding of many aspects of plant biology, and molecular genetic analyses have provided much insight into the molecular nature of signal transduction in plants. It was not long ago that most signaling events in plants were represented as simple ‘black boxes’. Remarkable progress has been made in our understanding of many plant response pathways, including the identification of receptors for all five of the ‘classic’ plant hormones, as well as for other endogenous plant signals and environmental signals. The details of downstream signaling events have also begun to come into focus, and in some cases, the path from ligand binding to the regulation of gene expression has been found to be unexpectedly direct. In this issue of Current Opinion in Plant Biology, we focus on several areas of plant signaling in which noteworthy recent progress has been achieved.

The recent breakthroughs in our understanding of plant hormone signaling are highlighted by the identification of receptors for abscisic acid (ABA), gibberellic acid (GA) and auxin. Reviews from Quint and Gray and from Razem et al. discuss the latest findings regarding the discovery of the long-sought-after receptors for these hormones. Remarkably, the receptors for ABA, GA and auxin are localized within the cell rather than at the cell surface. Likewise, the ethylene receptors are also localized within the cell in the endoplasmic reticulum. Consistent with this, all four of these hormones are able to enter the cell, either freely by diffusion or, in the case of auxin, via transport proteins. In addition, auxin, ABA and GA all appear to act not via standard signaling intermediates but rather by novel and apparently very direct mechanisms.

In the 1980s, genetic analysis of auxin-response mutants identified various components of the machinery that regulates the turnover of proteins. In particular, components of the machinery that adds ubiquitin to proteins were identified. These components regulated the turnover of the Aux/IAA proteins, which are short-lived negative regulators of auxin-mediated gene expression. Quint and Gray discuss the role of the AUXIN RESPONSE FACTORS (ARFs) and Aux/IAAs in mediating auxin-regulated gene expression, and relate how the degradation of the latter proteins is regulated by auxin through direct binding to an SCF complex. This surprisingly simple and direct route from auxin perception to regulation of Aux/IAA turnover, involving the binding of a ligand directly to an F-box protein, is a novel mechanism for signaling. Additional examples of such pathways are beginning to emerge, suggesting that this might represent a novel cell signaling paradigm.

Razem et al. discuss the recent identification of receptors for GA and ABA, GIBBERELLIN INSENSITIVE DWARF 1 (GID1) and FLOWERING TIME CONTROL LOCUS A (FCA), respectively. Like the auxin and
ethylene receptors, both GID1 and FCA are present inside the cell, predominantly in the nucleus, though both might also be present at lower levels in the cytosol. Previous studies utilizing GA or ABA molecules that had been rendered cell-impermeable indicated a predominantly extracellular site of perception for these hormones. Razem et al. discuss these seemingly contradictory data, and go on to discuss how these newly identified receptors fit into a pathway incorporating other known signaling elements, including the possibility of other receptors for these hormones. GID1 is a homolog of animal hormone-sensitive lipases and FCA encodes a plant-specific RNA-binding protein, which suggests that the mechanism of action of these two hormones, like that for auxin, might be direct.

Lest one begins to think that all signals in plants are perceived at the cell surface, Morillo and Tax discuss the large family of plant genes that encode plasma-membrane-localized serine/threonine protein kinases (RLKs). They compare the RLK gene families in rice and Arabidopsis, and discuss how the relatively large number of RLK genes in the rice genome is due largely to an amplification of the clades that are involved in pathogen responses. These authors go on to highlight the various functions that have been ascribed to different RLKs. Several other reviews in this issue also discuss a role for RLKs in various processes, including stomatal development, meristem maintenance, and nodulation. This is surely the tip of the functional iceberg for this gene family, as only a fraction of the RLKs have been linked to a particular function. Determining the function of RLKs will be challenging, however, because of the widespread genetic redundancy in Arabidopsis. The RLK family offers no exception to this as functional redundancy has already been demonstrated for several RLK genes.

Phosphorylation is common signaling intermediate that plays a central role in multiple plant signaling pathways. A second review in this issue focuses not on kinases but on the role of protein phosphatases. Delong highlights recent work that has uncovered important roles for these signaling elements. She discusses the pleiotropic roles of the PP1 and PP2A serine/threonine phosphatases. She then goes on to describe the functions of other phosphatase families, including roles in determining flowering time, in hormone and defense signaling, and in the response to light. With the continuing refinement of methods for discerning gene function, the near future should see an increasingly long list of roles for this important class of signaling molecules.

Several reviews also discuss signaling from a developmental perspective. Bergmann reviews the signaling pathway that regulates the formation of stomata. Stomatal differentiation represents an excellent model system in which to study cell fate decisions in plants. Molecular genetic studies have identified several key players that regulate the specification and patterning of stomata, including the role of several functionally redundant leucine-rich repeat RLKs, ERECTA and ERECTA-LIKE1 (ERL1) and ERL2. Loss-of-function of these three leucine-rich repeat (LRR)-RLKs results in the overproliferation and altered spacing of stomata, indicating that these receptors play a role in stomatal differentiation. Intriguingly, mutations in the TOO MANY MOUTHS (TMM) gene, which encodes a LRR-receptor-like protein that lacks a kinase domain, also affect stomatal development. Elucidating how TMM and the ER and ERL RLKs interact to regulate stomatal development might provide a paradigm for RLK function. A mitogen-activated protein kinase (MAPK) kinase kinase called YODA also acts in stomatal development, and its relationship to ER ERL1 ERLS and TMM is also discussed in this review. Delong goes on to review the effect of environmental influences on stomatal number and spacing, and how the recent identification of ER as a major quantitative trait locus (QTL) that is linked to stomatal function might link these two areas of research.

Shani et al. review recent studies that shed light on the complex interplay of multiple plant hormones in the regulation of shoot apical meristem (SAM) function. The size of a SAM is generally remarkably constant over the life of a plant, which requires a balance between the numbers of cells that are removed from the meristem by differentiation (i.e. that become incorporated into lateral organs) and the number of cells added by division within the meristem. Elegant molecular genetic studies have defined the roles of several groups of transcription factors that are involved in SAM maintenance. More recent studies have begun to define the roles of several phytohormones, including cytokinin, auxin and gibberellin, in this process. Shani et al. further discuss how these hormone signaling pathways interact with each other and with the transcription factors that are involved in meristem maintenance.

One central aspect of meristem function is its role as a primary site of cell division, and Maughan et al. describe recent results that have improved our understanding of the regulation of the cell cycle. They discuss the integration of the regulation of cell division with various signals that control growth and differentiation in the meristems, and the influence of environmental signals on these processes. The various players in these regulatory circuits are described, including the cyclinD-RBR-E2F pathway and its integration into the root apical meristem regulatory circuit.

The noduleation of legumes is another developmental pathway reviewed in this issue, with the twist that an
interaction with another organism is involved. The number of nodules that form on a root is a highly regulated, as nodule function carries a high metabolic cost to the host plant. Oka-Kira and Kawaguchi discuss the long-distance signaling involved in the autoregulation of nodule number. Once again, we find that an RLK plays a major role, as the genes corresponding to several hypernodulating mutants (hypernodulation aberrant root1 [har1], nitrogen-tolerant symbiosis1 [nts1] and so on) turn out to encode orthologous LRR-RLKs. Intriguingly, these RLKs are most similar to CLAVATA1 (CLV1), which is involved in the regulation of the SAM (reviewed in this issue by Shani et al.). Consistent with this, HARI acts in the shoot. Other mutants described in Oka-Kira and Kawaguchi’s review act in the root in the autoregulation pathway, though the genes that are affected in these mutants have not yet been cloned. As the authors note, the molecular identification of these genes, as well as the ligand for HARI and its downstream signaling components, and the identification of the nature of the signals that are transported from the root to shoot and vice versa remain important goals for the future.

Light signaling is one of the most intensely studied signaling pathways in plants. Two reviews in this issue discuss recent advances in different aspects of light responsivenes. Kimura and Kagawa review recent developments in the area of blue-light mediated phototropism. They discuss the regulation and output of the photoreceptor phototropin, a protein kinase that is regulated by an amino-terminal light-responsive LOV domain. The role of auxin in phototropism was first suggested over a century ago, and hence Kimura and Kagawa also discuss the role of the ARF family of auxin-responsive transcription factors in this response. A major response of plant cells to light is a rapid change in gene expression. Lorrain et al. review various transcriptomic analyses of wildtype and mutant seedlings treated with different wavelengths of light, and discuss the mechanisms that underlie this regulation of gene expression. These mechanisms vary from the light-induced re-localization of the phytochromes into the nucleus to the regulation of the stability of various transcription factors in response to light.

Bargmann and Munnik review an important aspect of the emerging field of lipid signaling, namely the role of phospholipase D (PLD) in plants, focusing on the role of these enzymes in stress signaling. The PLD family in plants is much larger than those in animal or yeast, and Bargmann and Munnik describe the features of this plant gene family and the activities of the different classes of proteins that it encodes. They describe the potential generic function of PLDs in membrane degradation, vesicular transport, membrane tethering, and signaling via the phosphatidic acid product of the PLD reaction. They then survey the role of PLD in various stress responses, including ABA responses, wounding and pathogen interaction. These links have been made primarily from hypomorphic PLD mutants, and disruption of multiple PLD genes simultaneously might enhance these phenotypes and reveal novel roles for this gene family.

A novel group of plant signaling molecules, N-acylthetanolamines (NAEs) and the related alkamides, are probably derived from PLDs, and López-Bucio et al. review these and other novel signaling molecules. These authors describe the occurrence and biosynthesis of NAEs and alkamides, and the evidence that these molecules might play a role in regulating plant development. The recent exciting finding that the amino acid glutamate, a well-characterized mammalian signaling molecule, might also play a role in plants is discussed, as is its relationship to NAEs and alkamides.

Gene silencing has emerged as an important regulator of gene expression in plants and animals, and Calonje and Sung review one aspect of this phenomenon, Polycomb group (PeG)-mediated silencing. A tremendous amount has been learned about PeG complexes in Drosophila and humans, and Calonje and Sung draw from this literature to compare and contrast with the plant orthologs. As is often the case, two of the four components of this complex are represented by three paralogs in Arabidopsis, resulting in multiple PRC2-type PeG complexes, each with potentially unique functions. Molecular genetic and biochemical analyses have defined functions for several of these complexes. Calonje and Sung present a model for PeG action, drawn primarily from Drosophila studies, and extrapolate this to plants. Although great strides have been made, the authors nicely frame the many important questions that remain regarding the function of these interesting proteins.

One area that holds great promise for future discoveries in the field of plant signaling is proteomics analysis. It has been estimated that approximately one third of the proteins in a cell are phosphorylated, and a major challenge is to identify these sites of phosphorylation. Rossignol reviews recent advances in the large-scale analysis of phosphorylation sites in the proteome. Several promising high-throughput techniques have been developed but have not as yet been routinely applied to plant cells. This is clearly an area ripe for discovery, and these advances will help inform a myriad of questions in plant signaling research.

As these excellent reviews make clear, tremendous strides have been made in our understanding of plant signaling and gene regulation. It truly is an exciting time in these areas, and the near future should continue to yield fresh insights. We thank all the authors for their contributions to this issue.