

FOREWORD

Plant Cell Signal Transduction: The Emerging Phenotype

It is remarkable how 20 years have changed concepts of plant signaling—from a situation in which even the words “signal” and “transduction” received no mention to Special Issues devoted to this critical topic. In fact, signaling in its broadest sense is now a major preoccupation of plant research. To place this in perspective, we can ask how many genes are likely to be involved with the specification of signal transduction components. It is thought that a minimum of 300 genes are required to produce a bacterial cell. That estimate is based in part on deduction and in part on the number of genes contained in organisms such as *Mycoplasma*. Attempts are under way to construct such minimal bacteria. However, bacteria such as *Escherichia coli* contain 3000 genes. The apparently inessential 2700 (90%) are thought necessary to provide bacteria with the ability to tolerate randomly fluctuating environmental variation, thereby endowing the organism with a more sophisticated capacity for response.

If those figures are extrapolated to higher plants, which develop and reproduce in an equally daunting and variable environment, then most of the genome may be involved with signal transduction of one sort or another. Growing experimental plants for signal transduction research in a growth room may have its disadvantages: much could be missed! In addition to the physical and chemical signals of the continually fluctuating environment and internal signals, an uncountable number of putative pathogens, pests, and herbivores increase the requirements for complex transduction processes to resist damage and disease. A substantive number of genes will be involved with the signaling necessary to specify cell position and fate in developing

leaves or roots. A plethora of signaling molecules for cell development must be present with their transduction machinery, because cells continually change position during growth and must continually update their spatial and temporal conditions. Although sugars and auxins may be simple molecules, they have long been seen as signals in vascular tissue differentiation. Furthermore, other complex signal transduction circuitry must be present to ensure the stability of morphogenesis, the overall form of leaves, roots, and flowers, in chaotic environmental conditions. Although some plant characteristics are resistant to environmental variation, many others respond plastically, adding an extra layer of morphogenetic and biochemical complexity that is largely unique to plants. Cytokinins, abscisins, ethylene, and gibberellins, as well as the more recently discovered brassinosteroids, jasmonates, and peptide hormones, are agents that help to strengthen plasticity.

What do we know about the **control circuitry** that underlies such signaling complexity? Requirements can be easily suggested. It is obvious that control circuits are **networks**. Network behavior needs to be **robust**, and robustness can be gained using complex mixtures of **negative feedback** and **feed-forward** control. The control of many genes provides excellent examples of simple feedback control, and we can expect such control to operate frequently elsewhere. **Redundancy** is necessary for reliability; we can expect protein isoforms to be present in abundance and overlapping control circuits to provide **fail-safe** solutions. Good examples are to be found in the families of 14-3-3 proteins and calcium-dependent protein kinases. Control circuits are likely to be **modular**, with some el-

ements specific for each signal but other elements shared. **Structural stability** also must be present. Otherwise, changes in signaling parameters that result from cell and tissue variability (i.e., individuality) (Gilroy and Trewavas, 2001) or substantive constituent protein change in evolution would destroy the basic programs that support morphology. The investigation of **network dynamics** is in its infancy, but only limited kinds of network structures exhibit both **stability** and **resilience** in the face of perturbation. The strength of **connectance** between the elements of the network will be variable: some weak, some strong. As the environmental context changes, so will the strength of connections vary between the proteins and other molecules that make up the network. This difficulty can be approached using a **sensitivity analysis** (Trewavas, 1987). Modifying the constituents in a controlled manner, as in the release of caged molecules or inducible promoters, should receive greater use.

Animals perceive their local environments by complex signal transduction processes. Intelligent responses are computed, and fitness is increased by behavioral changes that commonly involve movement. Movement is a fundamental part of the animal lifestyle that arose in evolution from the requirements to find food and to mate. However, the sessile plant also must change behavior to increase fitness as the local environment fluctuates. The ubiquitous distribution of light has never provided evolutionary pressure to develop movement; instead, behavioral changes are exemplified by phenotypic plasticity. But the need for detailed environmental information, accurate sensing, assessment, and intelligent computation are just as strong (Trewavas, 2002).

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A strong spatial dimension underlies signal transduction; for example, plants must be able to detect gradients in signals (such as light) and resources (such as nitrate and water). Plant development itself also is decidedly polar. The spatial dimension is satisfied in many ways. Cells place receptors, channels, G proteins, and kinases in specific membranes. Some signaling protein complexes are permanent, such as the relatively stable and perhaps hard-wired COP9 signalosome. Other signaling protein complexes are likely to be ephemeral and formed immediately as a result of signaling. There are at least 600 receptor kinases in Arabidopsis, and most of them are membrane bound. Incompatibility and disease defense signal transduction use receptor kinases. After ligand binding and autophosphorylation, such kinases may act as nucleation sites for the construction of ephemeral signaling complexes that contain many proteins. Many other GTPases, 14-3-3 proteins, kinases, and phosphatases may cluster around these nucleation sites, forming kinase cascades, and the regulation of specific transcription factors (e.g., by phosphorylation) will complete the pathway.

Calcium and cyclic nucleotide signaling both can act in local microdomains near the site of Ca^{2+} entry or the region of cyclic nucleotide synthesis. Again, ephemeral protein complexes attached to the relevant channels can be expected once signaling commences. The constituents of these “transducers” are likely to be Ca^{2+} receptors such as calmodulin, calmodulin binding proteins (e.g., kinesin, or microfilament-organizing proteins), and calcium-dependent protein kinases. The signaling complex can form around voltage-gated channels or the recently described cyclic nucleotide-gated ion channels. Particular

membrane lipids, scaffold proteins, and proton pumping ATPases also can act as nucleation sites and perhaps even as the attachment sites of microfilaments to membranes.

Temporal controls, little investigated at present, will become prominent as details arise from microarray analysis and improved understanding emerges regarding how cells change, once signaled, and how they respond to further signaling. Our understanding of the control circuitry that underlies flowering time likely will act as a paradigm in studies of other timing processes in development signaling.

This view of signaling places a heavy premium on protein–protein interaction, whether the proteins are attached to membranes or sitting on promoter regions. Pleckstrin homology domains and 14-3-3 proteins may represent just two of many types of proteins that regulate protein–protein interactions in plant cells. The two-hybrid method using interactive peptide domains is a primary technique, and its use should burgeon in this area of research. Protein affinity chromatography and other specific immunoprecipitation of protein complexes will rapidly enhance our knowledge of protein–protein interactions.

In trying to answer questions of signaling in single cells, the response of the whole plant must not be neglected. Coordination between the different cells and tissues of individual plants requires complex mechanisms of signal communication. Proteins, peptides, and RNAs, as well as a plethora of growth regulators, nodulation factors, sugars, mechanical signals (such as those that arise from turgor changes), and other yet to be discovered signals, are involved in tissue and cell communication (Gilroy and Trewavas, 2001; Trewavas, 2002). Recent breakthroughs in plasmodesmatal research

and the signaling mechanisms involved in successful nodulation present paradigms for understanding cell-to-cell communication. But even within a cell, communication and coordination—such as between chloroplast and nucleus—is equally crucial. Such communication and subsequent transduction is remarkably well tuned and highly successful. After all, plants dominate every landscape of the planet.

In this introduction, I have placed the 24 individual chapters of this Special Issue in the perspective of overall signal transduction. The flowering of one of the newest and most challenging of plant research areas is to be found in the subsequent pages. We will truly be in the decade of plant molecular cell biology as transduction studies come to fruition.

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