/631/449/2169 Plant immunity
/631/449/2169/2673 Effectors in plant pathology
/631/449/2169/2107 Pattern recognition receptors in plants
/631/61/212/2019 Transcriptomics

Strapline: Plant immunity

Title: Different threats, same response

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Standfirst (37w, 250c): Plants can experience a range of challenges, from osmotic stress to pathogen attack, requiring different types of responses. Despite this variety, two recent studies of plant transcriptomes reveal a surprising commonality in the genes induced by stress.

Main text (873 words): Plants cannot run away from their enemies. Nor can they relocate when conditions change for the worse. Therefore plants have evolved an elaborate system of defences to identify, respond, and adapt to stresses ranging from limited nutrient availability to pathogen attack, and to distinguish them from harmless stimuli like commensal microbes. In this issue of Nature Plants, two groups from Switzerland explore these stress responses in greater molecular detail[1,2], systematically characterizing changes in gene expression triggered by a wide variety of challenges in the model plant *Arabidopsis thaliana*. As a result they unveiled features shared across diverse stress responses, and identified genes not previously implicated in defence.

In the first study from Bjornson et al[1], a diverse set of molecules (Pathogen-, Microbe-, or Damage-Associated Molecular Patterns, or P/M/DAMPs) that elicit a strong, broad-range immune response (PTI for pattern-triggered immunity) were applied to *Arabidopsis* plants. These molecules are derived from bacteria, fungi, insects, or even plant tissue, and their perception by plant membrane receptors (Pattern Recognition Receptors, or PRRs) signals an imminent danger: a foreign organism is present or plant cellular damage has occured[3]. After application, the authors measured global transcriptomic responses in short time scales (within 3 hours). Remarkably, they observed that the two largest clusters of differential expression were the genes modified by the most active elicitor only (flg22), and genes modified by any of the 7 tested elicitors. It points to a large overlap and a core of coordinated gene expression in response to pathogen perception.

Even more intriguing, when these gene expression phenotypes were compared to those induced by other environmental stresses (e.g. light, heat, salt), a large overlap was observed, suggesting that a General Stress Response (GSR) is central to P/M/DAMP-induced immunity, especially in the very early stages of exposure

(figure 1). Notably, impairment of the GSR also interfered with PTI, indicating a tight coupling between these responses. Lastly, the study focused on genes that are strongly impacted by P/M/DAMP elicitors, but not affected by abiotic stress, termed “Core Immunity Response”, or CIR genes. Among these, they identified a set of calcium channels (Glutamate Receptors, or GLRs) that, when mutated, dampen the plant immune response to a bacterial pathogen.

Moving beyond elicitors, independent work by Maier and colleagues[2] brought a diverse panel of live bacterial strains to bear on plants. The goal was to explore commonalities and differences among members of the plant microbiome, including pathogenic and commensal species, in how they impact plant gene expression. This study focused on longer time scales - days instead of minutes or hours - and also identified a surprisingly small set of just 24 genes, termed General Non-Self Response, or GNSR (figure 1). These genes are induced by all bacterial strains, regardless of the nature of each strain’s relationship with the plant. The study also identified a core set of metabolites (especially those derived from the amino acid, tryptophan) that change in abundance when the plant is colonized by bacteria, and found that some of those metabolites are regulated by GNSR genes.

This pair of studies highlights the utility of a systematic approach to characterizing plant stress responses, particularly when using global transcriptome profiling technology. While previous work had examined transcriptional responses to bacterial and fungal species[4], none had done systematic, controlled comparisons across different stresses and elicitors, clarifying which differences are due to true differential stress response as opposed to experimental features like plant growth setup, timing or mechanism of stress exposure. The data not only reveal commonalities among diverse biotic stimuli, but will enable the identification of differential responses to specific elicitors and bacteria, opening the door to understanding, amongst other things, how plants differentiate between friend and foe.

While the new gene expression resources produced by these studies shed new light on the nature of plant stress responses, they also raise questions about how immune responses are elicited within the spatial context of the leaf or root. Do these core sets of genes behave the same way in all cell types of the plant? Are there distinct features of cells directly impacted by microorganisms that are not shared with those that are distal to the site of invasion? Do genes that respond strongly to a biotic stimulus have a more broad expression profile across cell types, or does the increased expression result from specialized action of a subset of cells? These studies investigated gene expression changes across all tissues in the phyllosphere (Maier, et al) or in whole seedlings (Bjornson et al.). However, tissue type or spatial features could play a significant role in determining the magnitude and quality of the immune response[5]. Indeed, Bjornson et al. note differences in

expression patterns of glutamate receptor genes of interest with regard to their bias toward stomatal guard cells.

New single-cell approaches, increasingly applied to plants, offer the ability to identify distinct responses of individual cell types and thereby address these important questions. Droplet-based single cell RNA-seq[6] and spatial transcriptomics[7] methods could reveal the temporal and spatial evolution of transcriptional responses[8,9], either reinforcing the “core” nature of the identified gene sets or breaking them into differentially regulated modules. Such a finer-scale dissection of potentially heterogeneous responses to biotic stimuli could identify cells or tissues that house these “core” responses, further enabling their study and manipulation.

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Figure 1: Global transcriptome analysis reveals partially overlapping core gene sets induced in response to diverse stimuli.

Microbes and purified immunity-triggering elicitors trigger an acute reprogramming in the plant transcriptome, as do many abiotic stresses. Successful host/microbe interactions result from microbes suppressing some plant immune responses, however a common core set of genes (GNSR) are still influenced by microbial presence. A General Stress Response (GSR) is commonly activated by biotic and abiotic stimuli alike, while a Core Immune Response (CIR) is triggered by microorganisms or other immune elicitors. These gene sets are not mutually exclusive, supporting the idea that core stress pathways are rapidly activated regardless of the nature of the threat.