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Different threats, same response

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1 /631/449/2169 Plant immunity
2 /631/449/2169/2673 Effectors in plant pathology
3 /631/449/2169/2107 Pattern recognition receptors in plants
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6 **Strapline:** Plant immunity

7

8 **Title:** Different threats, same response

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10 **Authors:** Benjamin J. Cole and Susannah G. Tringe

11

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

16

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

27

28 In the first study from Bjornson et al¹, a diverse set of molecules (Pathogen-,
29 Microbe-, or Damage-Associated Molecular Patterns, or P/M/DAMPs) that elicit a
30 strong, broad-range immune response (PTI for pattern-triggered immunity) were
31 applied to *Arabidopsis* plants. These molecules are derived from bacteria, fungi,
32 insects, or even plant tissue, and their perception by plant membrane receptors
33 (Pattern Recognition Receptors, or PRRs) signals an imminent danger: a foreign
34 organism is present or plant cellular damage has occurred³. After application, the
35 authors measured global transcriptomic responses in short time scales (within 3
36 hours). Remarkably, they observed that the two largest clusters of differential
37 expression were the genes modified by the most active elicitor only (flg22), and
38 genes modified by any of the 7 tested elicitors. It points to a large overlap and a
39 core of coordinated gene expression in response to pathogen perception.

40

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

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

51

52 Moving beyond elicitors, independent work by Maier and colleagues² brought a
53 diverse panel of live bacterial strains to bear on plants. The goal was to explore
54 commonalities and differences among members of the plant microbiome, including
55 pathogenic and commensal species, in how they impact plant gene expression. This
56 study focused on longer time scales - days instead of minutes or hours - and also
57 identified a surprisingly small set of just 24 genes, termed General Non-Self
58 Response, or GNSR (figure 1). These genes are induced by all bacterial strains,
59 regardless of the nature of each strain’s relationship with the plant. The study also
60 identified a core set of metabolites (especially those derived from the amino acid,
61 tryptophan) that change in abundance when the plant is colonized by bacteria, and
62 found that some of those metabolites are regulated by GNSR genes.

63

64 This pair of studies highlights the utility of a systematic approach to characterizing
65 plant stress responses, particularly when using global transcriptome profiling
66 technology. While previous work had examined transcriptional responses to
67 bacterial and fungal species⁴, none had done systematic, controlled comparisons
68 across different stresses and elicitors, clarifying which differences are due to true
69 differential stress response as opposed to experimental features like plant growth
70 setup, timing or mechanism of stress exposure. The data not only reveal
71 commonalities among diverse biotic stimuli, but will enable the identification of
72 differential responses to specific elicitors and bacteria, opening the door to
73 understanding, amongst other things, how plants differentiate between friend and
74 foe.

75

76 While the new gene expression resources produced by these studies shed new light
77 on the nature of plant stress responses, they also raise questions about how
78 immune responses are elicited within the spatial context of the leaf or root. Do
79 these core sets of genes behave the same way in all cell types of the plant? Are
80 there distinct features of cells directly impacted by microorganisms that are not
81 shared with those that are distal to the site of invasion? Do genes that respond
82 strongly to a biotic stimulus have a more broad expression profile across cell types,
83 or does the increased expression result from specialized action of a subset of cells?
84 These studies investigated gene expression changes across all tissues in the
85 phyllosphere (Maier, et al) or in whole seedlings (Bjornson et al.). However, tissue
86 type or spatial features could play a significant role in determining the magnitude
87 and quality of the immune response⁵. Indeed, Bjornson et al. note differences in

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

90

91 New single-cell approaches, increasingly applied to plants, offer the ability to
92 identify distinct responses of individual cell types and thereby address these
93 important questions. Droplet-based single cell RNA-seq⁶ and spatial transcriptomics⁷
94 methods could reveal the temporal and spatial evolution of transcriptional
95 responses^{8,9}, either reinforcing the “core” nature of the identified gene sets or
96 breaking them into differentially regulated modules. Such a finer-scale dissection of
97 potentially heterogeneous responses to biotic stimuli could identify cells or tissues
98 that house these “core” responses, further enabling their study and manipulation.

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

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