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Microarray analysis of plant defenses

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Abstract

Three major defense signaling molecules have been shown to trigger partly overlapping gene expression profiles in *Arabidopsis*.

Significance and context

In addition to numerous regulatory proteins, three hormone-like small molecules have been implicated in the regulation of pathogen resistance in plants. Salicylic acid (SA), ethylene (ET) and jasmonates (JA), including the volatile derivative methyl jasmonate (MJ), are synthesized in response to infection by certain pathogens and trigger defense reactions. Whereas SA and JA are known to act antagonistically, JA and ET appear to act together in the control of at least some defense responses. The effects of these three molecules on the expression of plant genes involved in defense have so far been examined using only a limited set of marker genes. Schenk *et al.* have used cDNA microarray analysis to provide the first comprehensive comparison of transcriptional responses triggered by SA, ET and MJ.

Key results

Gene expression changes were monitored using a cDNA microarray with 2,375 *Arabidopsis thaliana* ESTs predominantly representing putative defense-associated and regulatory genes. *Arabidopsis* plants were either treated with SA, ET or MJ or infected with the fungal pathogen *Alternaria brassicicola*, which is recognized by the plant and triggers defense reactions. Significant changes in expression were detected for 705 genes in response to one or more of the treatments. Some genes responding to the treatments encode potential defense regulators such as transcription factors or protein kinases. Other functional classes of responsive genes comprise previously described antimicrobial genes or genes potentially involved in the oxidative burst and hypersensitive programmed cell death - two early defense reactions. Many genes affected have unknown functions.

Whereas a substantial fraction of the gene expression changes were specific for individual treatments, many genes were up- or downregulated in response to more than one defense condition. Strikingly, 55 genes were co-induced by SA and MJ, which were previously shown to act antagonistically. Expression of 28 genes was co-repressed by both treatments. Similar overlaps were observed between the responses

to all four treatments. These results suggest a high degree of cross-talk between the signaling pathways specified by the individual treatments.

Links

[Arabidopsis defense gene regulation](#) cluster analysis data for this study can be downloaded and [Supplementary data to PNAS 2000, 97:11655-11660](#) is available.

Reporter's comments

The data presented appear reliable, as only genes that showed consistent expression behavior between two independent replicate array experiments for each treatment were included in the final data set. The identification of genes that are co-induced or co-repressed by more than one treatment is significant and may serve as a starting point to study interactions between different defense signaling pathways. Given the strong emphasis in the paper on signal cross-talk, however, combinations of SA, ET and MJ could have been applied to test for synergistic or neutralizing effects of different, simultaneously operating pathways.

Table of links

[Proceedings of the National Academy of Sciences of the United States of America](#)

[Arabidopsis defense gene regulation](#)

[Supplementary data to PNAS 2000, 97:11655-11660](#)

References

1. Schenk PM, Kazan K, Wilson I, Anderson JP, Richmond T, Somerville SC, Manners JM:
Coordinated plant defense responses in *Arabidopsis* revealed by microarray analysis. Proc Natl Acad Sci
U S A. 2000, 97: 11655-11660. 0027-8424