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Stress and innate immune responses in plants

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Concepts in Plant Innate Immunity and stress signaling

Successful defense against abiotic stress and pathogens requires environmental perception followed by the execution of a preplanned defense posture. The plants reaction to stress and pathogens show commonalties. Innate immunity indicates that the ability to perceive pathogens is 'hard-wired' into the genome and draws its origins from a phylogenetically ancient form of immunity. In plants these elements are part of resistance genes and have been called 'sentinels' that duly scan the cellular environment for molecules of 'non-self' origin. Once recognition of pathogens or environmental insults occurs a signal is transduced in-part by activation of reactive oxygen species (ROS) bursts. Such bursts play a role in cell-wall modification and induction of defense gene expression (defensins) and rapid apoptopic-like cell death. How innate immune and environmental defense pathways are related and differentiated are central questions addressed in the laboratory.

Sentinel components

The foreign agents that plant sentinels detect are called avirulent factors. They are produced by the pathogen and likely play a role in aiding pathogen colonization of the host. One type of plant sentinel are resistance genes that are composed of Toll and Il-1R-like domains (TIR) or alternatively a coiled coil (CC) domain in the N-terminus, followed by a nucleotide binding domains (NBD) juxtaposed to a section of leucine rich repeats (LRR). There are hundreds of such genes in the plant genome. Implying a high degree of diversification and specificity. In contrast, in animals the TIR-dependent innate immunity consists of a limited number of pattern recognition genes. We isolated a plant resistance gene of the CC-NBS-LRR type whose presence is essential for resistance to the fungal vascular disease caused by *Fusarium oxysporum* and followed the adaptive evolution of this resistance gene and its family. Adding to the complexity of resistance gene biology are recent reports that implicate alternative splicing in R-gene function. In an effort to understand the relationship of alternative splicing to the dynamics of stress, we have established a database of *Arabidopsis* splicing variants and have shown their regulation by specific kinases and by environmental stress.

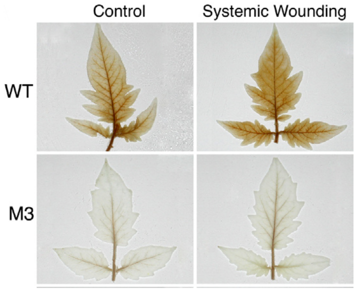

Fig.1 *ROS production in the systemic leaf of wild type (WT) and Rboh antisense plants (M3) without (control) or with wounding. Brown precipitates of DAB (3,3'-diaminobenzidine) reveal H_2O_2 that accumulates in normal systemic leaves 5 h after wounding but not in M3 mutant leaves.*

Signal transponders in pathogen and environmental stress

Activation of Toll defense responses in *Drosophila* requires processing of ligands by proteases that are rendered active during pathogenesis. The processing of these proteases is regulated by a class of serpins (serine protease inhibitors) that can form suicide substrates with their cognate substrate. In an analogous fashion, serpin homologs in plants are being investigated for their role in the plant defense and wound response.

Plant respiratory burst oxidase homologs (*Rboh*) play a key role in plant defense and are homologs of the human neutrophil pathogen-related gp91^{phox}. Antisense technology diminished Rboh activity which resulted in a change of the general cellular redox milieu and also compromised wound-induced gene expression. Extending these observations by transcriptome analysis revealed both Rboh-dependent and independent wound-induced gene induction pathways. The antisense plants also showed remarkably different developmental programs. They acquired a highly branched phenotype, switched from indeterminate to determinate growth habit and had fasciated-type reproductive organs implying a role for Rboh as hormone signaling transponder. The regulation of Rboh activity is part of our ongoing research.

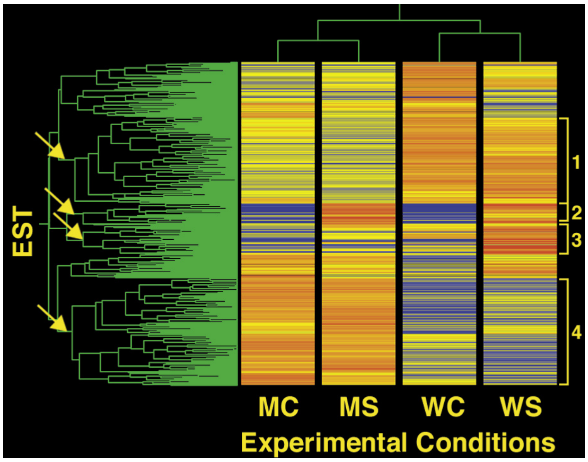

Fig.2 *Transcriptome analysis using a microarray grid containing 12,000 tomato EST. The leaves of non-wounded plants and the systemic leaves of wounded plants are compared in wild type and mutant Rboh lines. The double clustering analysis reveals changes in transcripts that are influenced in the control and wounded state in wild type and mutant plants. MC, mutant control leaf; MS, mutant systemic leaf; WC, wild type control leaf; WS, wild type systemic leaf. The arrows and numbers (brackets) indicate groups of genes with similar behavior.*

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Acknowledgements:

Our work is supported by the Israel Science Foundation, Minerva Foundation (Germany), Fundacion Antorchas (Argentina) and the United States-Israel Binational Research and Development Fund.