

Plant disease resistance: insights from global expression profiling

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As a result of the widespread application of global mRNA expression profiling technology in the field of plant-pathogen interactions, we can now easily appreciate the magnitude and complexity of the plant response to pathogen infection. During resistant responses after infection of *Pseudomonas syringae* strains, more than 2000 genes among 8000 genes monitored substantially changed their mRNA levels within 9 hours in *Arabidopsis* leaves. Differences in gene expression patterns during resistance and susceptible responses could be mainly explained by quantitative and/or kinetic differences in expression changes. These observations suggest the following notions. (1) Plant defense responses are not highly specialized to a particular pathogen. Rather many defense mechanisms are turned on, and some of the mechanisms could be effective against a particular pathogen. This notion is supported by other expression profiling works that demonstrated substantial overlaps in expression changes during interactions with very different pathogens. (2) Regulatory mechanisms for gene expression changes are largely shared in resistant and susceptible responses. This notion is supported by the fact that mutations in many regulatory genes affect both resistant and susceptible responses. (3) Stronger and/or faster induction of a similar set of defense mechanisms is crucial in expressing resistance to certain pathogens. These notions further suggest that the regulatory mechanism for the response to pathogens may not be well understood if we employ a model with relatively independent signaling pathways specific to particular phenotype.