

Focus: Plant Interactions with Bacterial Pathogens

The incorporation of resistance genes into agronomically important crop plants is the most economically effective method for controlling plant disease. This biological disease control strategy is heritable and, therefore, inexpensive and permanently available once introduced (Keen et al., 1993).

In 1993, Noel Keen and colleagues wrote an insightful review that outlined the benefits to be gained if only cloned resistance genes were available for deployment against plant pathogens. Practically before the ink was dry, the doorway to a new era opened with the news from Steve Tanksley's laboratory at Cornell that the tomato *PTO* gene conferring resistance to strains of the bacterial pathogen *Pseudomonas syringae* pv *tomato* carrying the corresponding avirulence gene *AvrPto* was a kinase (Ronald et al., 1992; Martin et al., 1993). This discovery was quickly followed by cloning and functional characterization of a number of diverse classes of genes for resistance to other bacterial pathogens, including intracellular proteins carrying nucleotide-binding sites and Leu-rich repeat motifs (NBS-LRRs; Bent et al., 1994; Mindrinos et al., 1994; Whitham et al., 1994) and extracellular pattern recognition receptors (PRRs; Song et al., 1995).

Many plant pathologists now recognize two broad classes of the plant immune system termed pathogen-triggered immunity controlled by PRRs and effector-triggered immunity controlled by NBS-LRRs (Chisholm et al., 2006; Jones and Dangl, 2006). PRRs respond to microbe- or pathogen-associated molecular patterns that are highly conserved within a class of microbes such as flagellin (Medzhitov and Janeway, 1997; Gómez-Gómez and Boller, 2000). The NBS-LRR proteins recognize pathogen effectors, typically secreted by type III secretion systems.

This focus issue provides an update on the tools now in hand to combat bacterial pathogens and the insights gained in the ensuing years. With complete genome sequences of several host and pathogen partners now available, there are literally hundreds of candidate genes with potential applications in crop protection. These include genes with sequence similarity to known NBS-LRR genes and PRRs as well as genes controlling plant responses to hormones involved in disease resistance responses. In addition to well-established players including jasmonic acid, ethylene, and salicylic acid, Lamb and coworkers report in the current issue that altered expression of genes controlling abscisic acid synthesis can increase resistance to certain pathogens while increasing susceptibility in others. Bent and coworkers note that the ability of plants to respond rapidly with global changes in physiology was recognized decades before any cloned genes were available; and while there are

“few truly new questions” to be asked, focusing attention on underexplored niches in research and biology is likely to amplify the information to be gained.

On the pathogen side, Collmer and colleagues consider that the greatest impact of a genomics approach has been the discovery that pathogens express many genes encoding many known or predicted effectors. They suggest that the greatest challenge will be to define how they work together to facilitate access to their host plants. Discovery of the “HRP” cluster and its relationship with the *Yersinia* outer membrane proteins in 1986 led quickly to the recognition that type III secretion is a central player in plant pathogenesis (Galan and Collmer, 1999). Expression of a single secreted protein, harpin, could confer the ability to induce the cell death response that is a hallmark of disease resistance, and harpin was soon made available for commercial disease control (Wei et al., 1992). This rapid translation of discovery into application made it appear that solutions to plant disease would be forthcoming with great efficiency. At present, exactly how or even where in the cell (or outside the cell, as the case may be) harpin may function remains under investigation. Michelmore and colleagues used a global profiling analysis to show that many effectors, like harpin, can trigger defense responses in diverse species. On the other hand, functional redundancy means that most are dispensable and, as White and coworkers put it, challenges for the future include establishing whether they work as “wrecking balls or guided missiles” in subverting plant metabolism. The *Agrobacterium* system continues to be in a class by itself with regard to insights into cross-species transport and transformation, fundamental plant physiology and development, as well as applications ranging from basic research to crop improvement.

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**Martha Hawes
Pamela Ronald
Monitoring Editors
*Plant Physiology***