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Commentary

The molecular mechanisms responsible for resistance in plant–pathogen interactions of the gene-for-gene type function more broadly than previously imagined

R. James Cook

Department of Plant Pathology, Washington State University, Pullman, WA 99164

Molecular biology is making it possible to identify both the genes and the gene products involved in infection and disease and then to direct control strategies at these genes and gene products. Understandably, the vast majority of this kind of research and development continues to be directed at human diseases, but some of the most remarkable advances and biggest surprises have come from studies of plant diseases. Of course, plants, not having a circulatory system and ability to make antibodies, depend on very different defense strategies than those used by animals. Plants with ability to resist infection by a particular pathogen are referred to as "resistant" to that pathogen, and pathogens lacking the ability to attack a particular plant are referred to as "avirulent" on that plant. Research begun shortly after the rediscovery of Mendel's laws showed that resistance is heritable and plant breeders have been breeding varieties of crop plants with disease resistance ever since. Unfortunately for agriculture, the pathogen is adaptive by its ability to continually evolve strains that defeat the resistance genes deployed in crop plants by plant breeders. This has led to the treadmill of continually updating and replacing varieties with different genes or combinations of genes for resistance in response to the ever-changing pathogen populations. In one of the most important scientific contributions to plant biology in this century, H. H. Flor showed for flax rust that, for every gene that conditions resistance in the plant, there is a corresponding and complementary gene that conditions avirulence in the pathogen (1). Flor's gene-for-gene model, which he proposed about 50 yr ago, has since explained the genetics of disease phenotypes incited by plant-pathogenic viruses, bacteria, fungi, and nematodes as well as the success or failure of certain plant–insect interactions. The picture now emerging is that the products of resistance genes in gene-for-gene systems serve as receptors for specific ligands produced by the pathogen, either directly or indirectly through expression of avirulence genes, and that this specific receptor-ligand recognition event, in turn, through signal transduction, elicits a complex cascade of defensive responses observed as the resistant phenotype (2).

The first breakthrough in our understanding of the molecular biology of gene-for-gene interactions came about 15 yr ago with the cloning of an avirulence gene from a bacterial pathogen of soybean, *Pseudomonas syringae* pv. *glycinea* (3). This was followed by the discovery that an avirulence gene from a bacterial pathogen of tomato, *P. syringae* pv. *tomato*, when transferred to and expressed in *P. syringae* pv. *glycinea*, triggered the resistant phenotype in soybean, which was not known to carry the resistance gene corresponding to this particular avirulence gene (4). This was one of the first clues that plants as different as tomatoes and soybeans may have functionally if not structurally similar genes for resistance to related pathogens. The next surprise has come during the past 5 yr with the cloning of resistance genes of the gene-for-gene type [reviewed by Staskawicz *et al.* (2)]. Remarkably, a gene from *Arabidopsis thaliana* for resistance to two bacterial pathogens, a gene from tobacco for resistance to a virus, a gene from tomato and one from flax for resistance to respective fungal pathogens of these plants, and a gene from sugar beet for resistance to a nematode (5) all are similar, having protein products with regions or motifs of characteristic nucleotide-binding sites and leucine-rich repeats. The paper in this issue of the *Proceedings* by Rossi and associates (6) is but the latest surprise; it reports that the *Mi* gene for resistance in tomato to the root knot nematode, *Meliodogyne incognita*, not only belongs to the nucleotide-binding leucine-rich repeat family of plant resistance genes, it is the same gene in tomato for resistance to specific isolates of the potato aphid, *Macrosiphum euphoribiae*.

Gene-for-gene relationships have long been known for certain plant–insect interactions, e.g., wheat and Hessian fly, but the work of Rossi *et al.* (6) provides the first example of an insect resistance gene of the nucleotide-binding leucine-rich repeat family of resistance genes. No gene-for-gene relationship has been demonstrated for the potato aphid on tomato, but the fact that the *Mi* gene confers resistance against some but not other isolates of the potato aphid is typical of plant–pest interactions that fit the gene-for-gene model. The actual process by which the plant, once triggered into its defense mode, prevents feeding by aphids and nematodes, or contains would-be pathogens, undoubtedly varies greatly with the organism, but it is becoming increasingly more apparent that the early events of recognition and initiation of the defense response through signal transduction are fundamentally similar for higher plants and pests as dissimilar as viruses, bacteria, fungi, nematodes, and insects.

The ability of pathogens and presumably insect pests such as aphids to adapt to varieties of crop plants with resistance conferred by one or more genes for resistance is almost invariably because of their ability to avoid the recognition event rather than tolerate the cascade of events responsible for resistance. Rarely, if ever, do strains emerge with insensitivity to this cascade of defense responses. Some progress has been made with genetic modifications intended to accelerate, intensify, or otherwise improve on the effectiveness of resistance to pathogens that avoid the recognition conferred by specific resistance genes, such as the transfer of genes for production of chitinases or glucanases known to play roles in the defense response triggered by the receptor-ligand signal transduction mechanism (2). For certain nonspecialized pathogens, such as the *Rhizoctonia* and *Pythium* species responsible for seedling blights and root rots of a wide range of higher plants, this may be the most viable option by which to produce resistant or tolerant varieties (7). However, for diseases caused by the more specialized pathogens, such as cereal rusts, late blight of potato, and many other potentially devastating diseases, the resistance triggered by early recognition leads to an efficient

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and nearly immune response with obvious benefits to growers and consumers alike. The rapid increase in our knowledge of these genes, their products, and the molecular interactions responsible for early recognition opens enormous possibilities for both classical breeding and genetic transformations aimed at cost-effective, durable, and environmentally friendly disease and pest control.

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