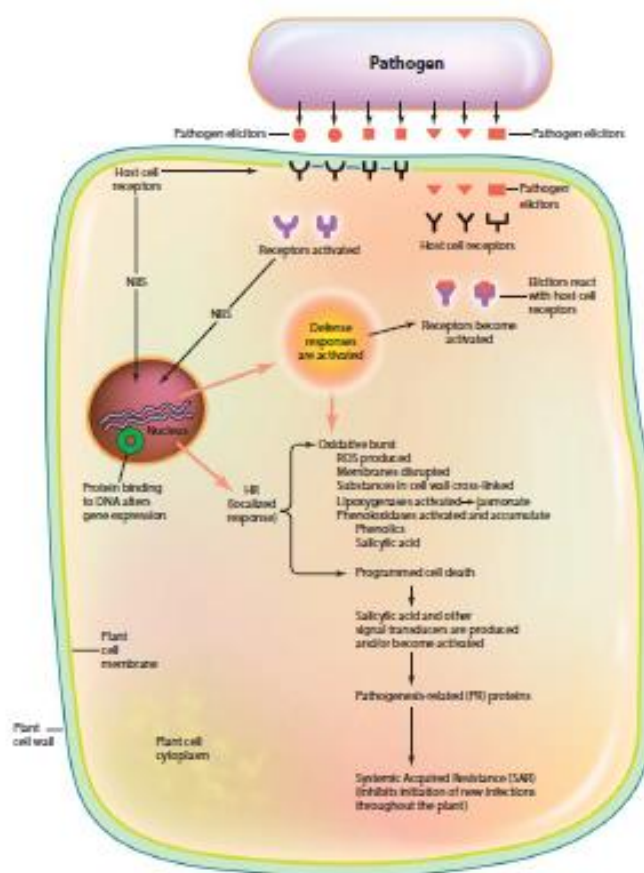


Genetics of Resistance through the Hypersensitive Response

The hypersensitive response is a localized self-induced cell death at the site of infection of a host plant by a race or strain of a pathogen that cannot develop extensively in this particular resistant plant cultivar. Thus, the plant species as a whole may be a host to the pathogen species, but individual cultivars (varieties) of the plant may be hosts (susceptible) or non-hosts (resistant) to a particular race or strain of the pathogen. Resistance through the hypersensitive response has been shown to be the result of gene-for gene systems in which an *a*-virulence (*avr*) gene in the pathogen corresponds to a resistance (*R*) gene in the host plant. Such gene-for-gene systems that provide resistance through the hypersensitive response occur in diseases caused by obligate intracellular pathogens, such as viruses and mollicutes, as well as in diseases caused by obligate and facultative pathogens, such as bacteria, fungi, and nematodes. Whatever the type of pathogen, it is believed that resistance through the hypersensitive response is the result of recognition by the plant of specific signal molecules, the **elicitors**, produced by the *a*-virulence genes of the pathogen and recognized by *R* gene-coded specific receptor molecules in the plant. Such recognition causes the activation of a cascade of host genes, which result in a burst of **oxidative reactions, disruption of cell membranes, and release of phenolic and other toxic compounds**, which then lead to the hypersensitive response, programmed cell death (**Programmed cell death** (or PCD) is the **death** of a **cell** in any form, mediated by an intracellular program, and is also referred to as **Cellular Suicide**. ... Recently a form of **programmed** necrosis, called necroptosis, has been recognized as an alternative form of **programmed cell death**), inhibition of pathogen growth, and thereby resistance. It also leads to the activation of numerous



other defense related genes that result in other types of resistance, including horizontal resistance and systemic acquired resistance.

Pathogen-Derived Elicitors of Defense Responses in Plants

Pathogen-produced elicitors that trigger defense responses in plants include a wide variety of molecules that seem to have little in common. Some elicitors are host specific, i.e., they induce defense responses leading to disease resistance only in specific host varieties, as is the case with elicitors produced by *avr* genes interacting with a matching R resistance gene in a host plant. Most elicitors are general or limited specificity elicitors in that they signal the presence of a potential pathogen to both host and non-host plants, although some general elicitors are recognized by a small number of plants.

General elicitors

Glucans, produced by *Phytophthora* and *Pythium*, derived from oomycete cell wall, induce phytoalexins
 Chitin oligomers, by higher fungi, from chitin of fungal cell wall, induce phytoalexins and lignification
 Pectin oligomers, by fungi and bacteria, from degraded cell wall, inhibit proteins and defense genes
 Harpins, by several gram-negative bacteria, part of type III secretion, cause HR and defense gene response
 Flagellin, by gram-negative bacteria, part of flagellum, cause callose formation and defense gene response
 Glycoproteins, by *Phytophthora*, induce phytoalexin production and defense gene response
 Glycopeptide fragments, by yeast, activate defense genes and ethylene production
 Ergosterol, by various fungi, the main sterol of higher fungi, causes alkalization in cell cultures
 Bacterial toxins, such as coronatine of *P. syringae*, toxin, disturbs salicylic acid, mimics jasmonic acid, and induces defense genes and defense compounds
 Sphinganine, the fumonisin analog, by *F. moniliforme*, toxin in necrotrophs, disturbs sphingolipid use, induces defense genes and programmed cell death (PCD)

Race-specific elicitors

avr gene products, Avr proteins, by fungi and bacteria, in some cases promoting virulence, HR, and PCD
 Elicitins, by *Phytophthora* and *Pythium*, scavengers of sterol, induce HR in tobacco
 Enzymes, e.g., endoxylanase, by *Trichoderma viride*, fungal enzymes, induce defense genes and HR
 Viral proteins, e.g., viral coat proteins, by TMV, structural component, HR in tobacco, tomato
 Protein or peptide toxins, e.g., victorin, by *Cochliobolus victoriae*, toxin for host, induces PCD in oat
 Syringolids (acyl glycosides), by *P. syringae* pv. *syringae*, signal compound for bacterium, HR in soybean, carrying the Rpg4 resistance gene

In nature, the elicitor molecule either reacts directly with the receptor protein encoded by the resistance gene R, or releases compounds or reacts with another host protein (endogenous elicitors), which then interacts with the R-coded receptor.

“Elicitors are compounds stimulating any type of plant defense. This broader definition of elicitors includes both substances of pathogen origin (exogenous elicitors and compounds released from plants by the action of the pathogen (endogenous elicitors))”

A-virulence (*avr*) Genes: One of the Elicitors of Plant Defense Responses

A-virulence (*avr*) genes, first identified by H. H. Flor in the 1950s, were only rather recently isolated from bacteria (1984) and fungi (1991), but since then numerous bacterial and fungal *avr* genes have been identified. The *avr* genes make a pathogen avirulent, that is unable to induce disease on a specific variety of the host plant because their protein product warns the plant of the presence and impending attack by the pathogen and the host plant then mobilizes its defenses and blocks infection by the pathogen. In this way, *avr* genes, by warning the host and thereby inhibiting infection by the pathogen, determine the host range of the pathogen at the species and at the race-variety level. As the gene-for-gene concept implies, in the majority of cases a matching dominant resistance gene (R) in the resistant host corresponds to each a-virulence gene in the pathogen. In some cases, however, because two independent resistance (R) genes may correspond to a single *avr* gene, there apparently are genes-for-gene interactions as well. Some *avr* genes, when transferred artificially to other pathovars, are active in the new pathovars, making the recipient pathogen unable to infect their previously susceptible hosts and, instead, causing the hypersensitive response in these plants. In some host–pathogen systems, *avr* genes determine not only which cultivars of a species the pathogen cannot attack, but also which plant species it can attack. For example, an *avr* gene (*avrBsT*) in the tomato-infecting group of strains of the bacterium *Xanthomonas campestris* pv. *vesicatoria*, the pathogen of bacterial spot in tomato and pepper, enables the bacterium to induce the hypersensitive response on all cultivars of pepper. Loss of *avrBsT* from such tomato-infecting strains allows these strains to cause disease on normally resistant pepper cultivars.

Several a-virulence genes and the proteins they code have been identified in and isolated from plant pathogenic fungi. These include especially the genes *avr2*, *avr4*, and *avr9* of strains of the fungus *Cladosporium fulvum* that are avirulent on tomato varieties carrying, respectively, the resistance loci Cf-2, Cf4, and Cf-9; and the gene *avrPi-ta* of the rice blast fungus, *Magnaporthe grisea*, which confers a-virulence to rice varieties containing the resistance gene Pi-ta. Similarly, several viral *avr* genes and their *avr* proteins have been obtained and studied, including those of the coat protein of potato virus X (PVX), the coat protein of turnip crinkle virus (TCV), and the replicase protein of tobacco mosaic virus (TMV).

Characteristics of avr Gene-Coded Proteins

The gene-for-gene model stipulates that for every dominant gene determining resistance in the host plant, there is a matching dominant gene in the pathogen that conditions a-virulence. The biochemical basis for explaining the gene-for-gene concept is the elicitor– receptor model according to which an a-virulence (*Avr*) gene of a pathogen encodes an elicitor (*Avr*) protein that is recognized by a receptor protein encoded by the matching resistance (*R*) gene of the host plant. The simplest way of recognition would be if the pathogen-produced elicitor interacted with the protein encoded by the matching resistance gene of the host. Recognition of the elicitor protein by the host plant leads to activation of a cascade of defense responses, which often include cell death around the infection site. The death of cells around the point of infection is known as the hypersensitive response and is characteristic of gene-for-gene-based resistance. Unlike *R* proteins, *Avr* proteins encoded by pathogen *Avr* genes share few common characteristics. Because most *Avr* genes continue to exist within a pathogen population, it would seem that in addition to acting as a-virulence factors, *Avr* genes probably have some additional function that is beneficial to the pathogen. From the few *Avr* genes for which a clear function for the pathogen has been demonstrated, it has now become generally accepted that their proteins carry out **two functions, one of them being a contribution toward the virulence of the pathogen**. Such a contribution appears to come about by the *Avr* proteins interacting with specific plant proteins, known as virulence targets, involved, for example, in host metabolism or in plant defense. Interaction of *Avr* proteins with such targets could enhance the availability of nutrients for the pathogen or could suppress defense responses by the host plant. To date, the *AvrD* protein, produced by the *AvrD* gene of the bacterial spot of tomato pathogen *P. syringae* pv. *tomato*, is the only *Avr* protein for which a biochemical function has been clearly defined. This function is the ability of the *AvrD* protein to direct the synthesis of low molecular weight syringolide elicitors, which elicit the hypersensitive response on soybean. A syringolide-binding protein has been identified in resistant soybean plants, possibly representing the protein of the matching *R* gene of the host plant. Proteins coded by pathogen *avr* genes (*Avr* proteins) seem to have some features in common. *Avr* proteins seem to be generally hydrophilic and, therefore, water soluble, lacking stretches of hydrophobic amino acids that would enable them to be anchored in cell membranes. *Avr* proteins also lack stretches of amino

acids known as “signal sequences” that would allow the proteins to be secreted into the external medium by the general secretory pathway. It appears, therefore, that *avr* gene proteins are produced and are either localized in the pathogen cytoplasm or they are secreted through membrane pores formed by proteins coded for hypersensitive response and pathogenicity (*hrp*) genes, known as Hrp proteins (harpins). If they are secreted externally, the Avr proteins may act directly as elicitors. If they are localized in the pathogen cytoplasm, the *avr* gene proteins may act enzymatically to produce an elicitor molecule that is transported freely through the bacterial envelope. In either case, the elicitor reacts directly or indirectly with the product of the corresponding plant resistance R gene.