

became accepted, that the search for host-coded proteins involved in the viroid-incited pathogenic response (PR proteins) commenced in a systematic way.

The first report implicating proteins in viroid pathogenesis was the detection in PSTVd-infected tomato leaves of two proteins with molecular weights 155 and 195 kDa (Zaitlin and Hariharasubramanian, 1972). Five years later, two low molecular weight polypeptides of 15 kDa (CEVd-P1) and 18 kDa (CEVd-P2) were detected in leaves of CEVd-infected *Gynura aurantiaca* (Conejero and Semancik, 1977b).

Enhanced levels of analogous polypeptides were found when the search was extended to additional host plants (Etrog citron, tomato cv. "Rutgers", potato cv. "Marijke") infected with CEVd (Conejero *et al.*, 1979). These polypeptides showed slight variation in size, depending on the host. This fact could be compatible with a viroid-specified nature of these polypeptides and a host-dependent processing reaction. Nevertheless, in one host, *G. aurantiaca*, such polypeptides were also detected in naturally senescing plants, indicating that they were not translation products of the viroid RNA, nor of any mRNA exclusively related to the viroid-host interaction. This finding also excluded the possibility proposed by Matthews (1978) that the polypeptides might be specified by viroid complementary sequences.

Later, the accumulation of several low molecular weight polypeptides was reported for a number of plants infected with several viroids (CEVd, PSTVd, cucumber pale fruit viroid (CPFVd), CSVd) and, in the case of tomato, infected by tobacco mosaic virus (TMV) and cucumber mosaic virus, and the fungus *Cladosporium fulvum* (Camacho-Henriques and Sanger, 1982a,b). More recently, an enhanced level of a high molecular weight protein (140 kDa) was also found in tomato plants infected with TPMVd (Galindo *et al.*, 1984). In addition, decreases in a number of protein species in the range of 14 kDa to 45 kDa were found in different hosts infected by CSVd. Decreased levels of four polypeptides (14.5 kDa to 105 kDa) were associated with pathogenesis in tomato leaves infected either by viroids, viruses or *Cladosporium fulvum* (Camacho-Henriquez and Sanger, 1982b).

All these observations strengthened the idea that the enhanced occurrence of certain proteins which accompanies viroid infection is a host response that may be generalized beyond this particular type of host-pathogen interaction. Thus, these proteins were considered to belong to the class of "pathogenesis-related" or "PR" proteins where the definition includes all proteins which are stimulated in plants as a consequence of pathologically altered metabolism (Van Loon, 1983).

The finding that the polypeptides associated with viroid infection are not specified by the viroid but result from a disease-induced alteration of host metabolism (Conejero *et al.*, 1979; Camacho-Henriquez and Sanger, 1982a,b), prompted the search for other proteins as possible components of the pathological response, as had been described for other systems (Van Loon and Van Kammen, 1970; Gianinazzi *et al.*, 1970). Since the non-denaturing electrophoresis system (Davis, 1964) normally used to detect tobacco PRs excluded basic proteins, a system with the capability of separating cationic proteins (Reisfield *et al.*, 1962) was also tested. This approach led to the detection of ten PR proteins (C1 to C10) in tomato plants infected with CEVd (Granell *et al.*, 1987). Only four cationic PR proteins could be detected in CEVd-infected *G. aurantiaca* (Semancik and Conejero, 1987), again emphasizing the specificity of host control in the biosynthesis of proteins. The basic nature of nine of the tomato proteins contrasts with most PR proteins described so far (Van Loon, 1985). However, the tomato PR proteins do share with tobacco PR proteins the characteristics of being preferentially extracted at low pH and resistant to proteinase digestion (Granell *et al.*, 1987). The tomato PR protein C2, which increases most dramatically, corresponded to the polypeptide previously described as tomato CEVd-P1 (Conejero *et al.*, 1979) or p14 (Camacho-Henriquez and Sanger, 1982b). The basic nature of this protein has been pointed out (Camacho-Henriquez and Sanger 1984) and recently confirmed by sequencing (Lucas *et al.*, 1985). The 69 kDa polypeptide most probably coincides with the 70 kDa polypeptide reported for tomato infected with TPMVd (Diener, 1987) while some of the other SDS-detected proteins matched those reported for tomato infected with PSTVd (Camacho-Henriquez and Sanger, 1982b). These PR proteins were also induced by Ag⁺ and ethephon treatments in association with necrotic (localized) lesions or non-necrotic (systemic, viroid-like) reactions (Granell *et al.*, 1987) indicating that their accumulation is not correlated with necrosis. As already discussed, these findings gave support to the idea that PR proteins are components of a non-specific response of the host mediated by ethylene (Granell *et al.*, 1987).

Biological significance of the PR proteins. The discovery of these proteins posed a number of questions, among which their biochemical function and biological role are the most important, not only for understanding of viroid pathogenesis but also as components of a system of response of plants to pathogenic or stress signals.

Even before the concept of PR proteins had been crystallized, attempts to unravel the biochemical activity displayed by viroid-induced proteins had been made with the

P1 protein from CEVd-infected *G. aurantiaca*. In these studies the potential activities of this protein as ribonuclease or hormone-binding protein were tested with no conclusive results (Flores *et al.*, 1978).

Recently, P-69 has been characterized as an alkaline cysteine proteinase (Vera and Conejero, 1988). It has also been found that P-32 and P-34 (C7 and C6 respectively of Granell *et al.*, 1987) are chitinases (García-Breijo *et al.*, 1989). Also, a β -1,3-glucanase activity has been assigned to a CEVd-induced PR protein in tomato (F García-Breijo, unpublished results).

Critical to the unravelling of the biological role of these proteins is their *in vivo* localization. The electrophoretic detection of PR proteins in extracts obtained by vacuum infiltration of tomato leaves infected with TMV (Parent and Asselin, 1984), treated with chemicals (Hooft van Huijsdijnen *et al.*, 1986), or after infection with *Cladosporium fulvum* (De Wit and Van der Meer, 1986) prompted the idea of the intercellular localization of PR proteins. Recently Carr *et al.* (1987) have reported the localization of PR1 in tobacco leaves by immunofluorescence. A more direct approach, the immuno-gold-EM technique applied to P1 (p14) (Vera *et al.*, 1988) and P69 (Vera *et al.*, 1989b) led to the discovery of two main locations: the vacuole, in association with inclusion bodies, (a newly described location) and the intercellular spaces of CEVd-infected tomato leaves.

We have already commented on the reputed resistance of PR proteins to degradation by endogenous proteases (Van Loon, 1985). Consistently, they have long half-lives (40-70 h) (Matsuoka and Ohashi, 1986), but there must be some turnover. The fact that they accumulate in the intercellular space (Van Loon, 1985) suggests that their degradation might also occur there. Following this idea, evidence has been obtained (Rodrigo *et al.*, 1989) that some tomato PR proteins are degraded upon incubation of intercellular washing fluids (IWF). This degradation occurs at acidic pH and it has been found that the enzyme responsible is a 37-kDa constitutive aspartyl endoproteinase with a pH optimum of 2.5-3.5. The selective hydrolysis of some of the pathogenesis-related proteins by the 37 kDa aspartyl proteinase lends credence to a possible rôle for this proteinase as part of the regulatory mechanism for the biological action of the PR proteins. The biological relevance of this enzyme in the PR metabolism is reinforced by the fact that an analogous enzyme has been isolated from IWF of tobacco plants (I Rodrigo, P Vera and V Conejero, unpublished results).

Although the biological role of most of these tomato PR proteins is as yet

unknown the following must be stressed:

1. Chitinases and β -1,3-glucanases can clearly be implicated in defence against pathogens such as bacteria and fungi, containing chitin or β -1,3-glucans as a component of their structure (Boller *et al.*, 1983).
2. The rôle of P69 proteinase (Vera and Conejero, 1988) either in symptom production or as a defence tool remains to be elucidated.
3. There is no evidence for any biological activity of P1 (p14), the most intensely accumulated PR protein in leaf tissue as a consequence of the viroid induced response. Nevertheless, P1 has been found in leaves from healthy (non-infected) plants and always in association with cell material undergoing disorganization (Vera *et al.*, 1988). This led these authors to propose the idea that P1 is involved in cell degeneration, either naturally activated as a normal event of the biological cycle of the plant (e.g. in lysogenous development of intercellular spaces (Esau, 1972; Fahn, 1972) or by cell ageing) or provoked by afflicting agents. The possible involvement of P1 in the resistance induced in the systemic reaction of the host or with some other biological role cannot be discarded. The biological significance of P1 is also sustained by the fact that this protein is synthesized as a pre-protein, then targetted to the vacuole and to the apoplast (Vera *et al.*, 1988; 1989a) in association with P69 (Vera *et al.*, 1989b). The vacuolar and apoplastic localization of chitinases have also been reported (Mauch and Staehelin, 1989).
4. The reported evidence to date indicates that ethylene is an intermediary step (second messenger) in the coordinate activation of PR synthesis as part of the response to viroid infection (Conejero and Granell, 1986; Granell *et al.*, 1987; Bellés and Conejero, 1989).

All this suggests that the viroid induced PR proteins, despite their different biochemical activities, might have the common biological role of being part of an adaptive response against potential aggressors from the environment.

Cell wall components. Three types of biochemical alterations of the cell wall can be considered for possible involvement in the response of the plant to viroid infection: those involved in limiting cell expansion; those implicated in altering the normal cell-to-cell communication and signalling in developmentally active cells and tissues; and breakdown products with the capability of becoming secondary pathogenic signals for neighbouring cells.

The effects of viroid infection on cell walls were realized in cytological studies.

These cytopathic effects received biochemical confirmation when a differential release of protoplasts from healthy and viroid infected tissues was attributed to abnormal β -1,3-glucan in viroid infected cells (Marton *et al.*, 1982).

More direct information was obtained with purified cell walls from healthy and CEVd-infected tomato cell suspension cultures. Enhanced levels of the key constituents of extensin, hydroxyproline and specific arabinosyl residues, were detected (Wang *et al.*, 1986), and taken to indicate an increased extensin content. An ethylene-induced accumulation of hydroxyproline rich proteins has also been found in diseased plants, and this accumulation has been correlated with the developmental alterations produced (Wang *et al.*, 1986).

A possible mechanistic relationship between the viroid-enhanced ethylene production and its effects in limiting cell expansion growth involving peroxidases and extensin has been outlined (Semancik and Conejero, 1987).

Finally, prominent protrusions have been detected on the surfaces of CEVd-infected cells (Wang *et al.*, 1986). Although the chemical nature of these structures has not yet been determined, it is possible that they are related to the alterations in cell wall composition. A possible relationship between the specific restriction of cell wall growth and the appearance of endocytic invaginations (plasmalemmasomes) reported in viroid-infected cells has also been suggested.

Individual specific reactions integrated in a general non-specific network system of response.

The idea that the whole metabolic structure of a plant consists of pathways of sequential steps which are interconnected in a highly reticulate network seems well accepted. This type of organization, together with cascade systems to amplify signals, permits synchronous control of many biochemical functions (Blowers and Trewavas, 1989). It also explains how very different pathogenic signals can elicit common responses (Fig. 1). Otherwise, it is difficult to explain how a viroid is able to elicit a response including coordinate expression of genes encoding chitinases, glucanases, etc. whose biological role is defence against infectious agents or stresses other than viroids.

One could hypothesize that these coordinately interconnected defence tools may have been built up in two steps: specific and individual development of each tool by coevolution with a given pathogen or with aggressive environmental conditions, and then the interlinking of the individual specific responses. Thus, what appears to be a non-specific response may result from evolutionary integration of specific individual

components. With this strategy, the battery of defensive weapons would be progressively enriched by new experiences. A prediction of this model would be the possible existence or future development of proteinases and nucleases against viruses and viroids.

The lack of specificity of this response could have biological advantages for the plant. This type of mechanism would broaden the scope of potential pathogens against which the plant would have acquired a certain degree of immunity after having been non-specifically triggered (Fig. 1).

AN INTEGRATIVE MODEL

How a response at the cellular level becomes a developmental disease: intracellular and intercellular stimulus-response processes

The general inhibition of growth in viroid infections is readily understandable. It is proposed that primary infection might occur in the region of differentiation of the procambial initials in the growing apex (Semancik and Conejero, 1987). Then, synthesis and release of ethylene is persistently enhanced during viroid infection resulting in inhibition of growth (Bellés *et al.*, 1989a).

It is more difficult to explain how the pathogenic response at the cellular level has effects at higher levels of organization, thus producing the distorted pattern of leaf development, for example. A precise system of cell-to-cell communication is required for the control of the normal pattern of growth and differentiation of the leaf. Failure or changes of some critical cell-to-cell connections, produced by alterations of the cell wall structure or other signalling events, could distort developmental patterns. A differential susceptibility of cells to becoming infected and to producing a pathogenic response would contribute to the macroscopical anisotropy of development. This hypothesis would also explain how different pathogenic agents such as a viroid (CEVd) and Ag^+ induce the same macroscopic syndrome, if both agents elicited the same general response in the cells. But we still need to explain how two agents with different pathways of access to cells ($AgNO_3$ is applied by spraying, viroids travel through the vascular system) incite indistinguishable developmental aberrations. This difficulty can be overcome if it is assumed that the same juvenile cells with a special reactivity and with the same developmental role are preferentially affected by both agents. We are dealing with an adaptive morphogenetic response to viroids which, following our

reductionist ideas, conveys information through common "informational channels". This is true not only at the cellular level (integrating membranes, common second messengers and coordinate activation of certain genes) but also at the supracellular level (commonality of morphogenetic information fluxes which can be distorted in the same way by alteration of certain especially susceptible key cells).

The model involves juvenile compatible cells which have the capacity to become infected and to display a pathogenic response (i.e. to undergo affliction and produce defence reactions) (Semancik and Conejero, 1987). Of these cells, a few would be the primary target cells: those at which the viroid molecules arrive from outside. Also, a small proportion of these cells would be infected by viroid molecules coming from other cells. But the bulk of infection is probably through cell division. The infected cells undergo a series of biochemical changes as a consequence of which they become physiologically and structurally altered. In the language of the signalling model, viroids as "primary signals" are amplified through replication, then "sensed", most probably at the membrane level, thus triggering a network of transductional events leading to cell response. The cell becomes a viroid-diseased cell, then transmits mismessages of aberrant developmental information horizontally, to other cells. Disease mismessages are also transmitted vertically by cell division.

All this conforms the developmental syndrome, which may also involve non-infected cells brought in by secondary signalling. This reflects the existence of a cascade system of signal transduction in the supracellular network, analogous to that at the cellular level (Fig. 2). In this case, one would predict, for example, that ethylene synthesis and PR protein production would occur in "secondarily stressed" but non-infected cells of infected leaves.

How does cellular response lead to a more resistant plant?

Apart from the known phenomena of specific cross-protection among viroids (interference with the establishment of a severe strain of a viroid by prior infection and specific interaction with an homologous milder strain) there are other possible mechanisms of resistance and protection in which signalling and response may be implicated. Chitinases, β -1,3-glucanases and other PR proteins potentially implicated in defence reactions have already been discussed and may have specific defensive significance (Vera *et al.*, 1989a,b; Mauch and Staehelin, 1989), although none is known against viroids. Non-specific physiological resistance may also occur as a consequence

of the stress imposed by infection in either infected or non-infected neighbouring cells which have been signalled. These cells lose the juvenile condition that enables them to be compatible and responsive to viroid infection. This may be the kind of protection produced by Ag^+ and ethephon treatments at low doses. The lack of specificity in the so-called cross-protection between non-homologous viroids (Niblett *et al.*, 1978) could also be an example of non-specific physiological resistance.

In systems reacting hypersensitively (which is not in general the case for viroid infections) there is another type of defensive phenomenon, the so-called induced systemic resistance (as in TMV infection of *N*-gene tobacco). The necrotic localized reaction in fully expanded inoculated leaves induces resistance to virus establishment in younger, upper leaves. Gianinazzi *et al.* (1970) and Van Loon and Van Kammen (1970) suggested that PR proteins could be involved in this phenomenon.

A similar reaction was observed in experiments following the mimicking procedure previously described for tobacco plants (Van Loon, 1977). Fully expanded leaves of *Gynura aurantiaca* plants were pricked with 0.2 M ethephon prior to infection with CEVd. This treatment impaired the establishment of viroid infection. This is taken as additional proof of the general scope of this mechanism of defence. In this case, however, no PR protein was associated with the induced resistance (JM Bellés, unpublished results). This is in accordance with the reported lack of correlation between acquired systemic resistance to viruses and PR proteins (for a review see Fraser, 1987).

CONCLUSIONS AND PROSPECTS

The model outlined in Figure 2 is an attempt to summarize and integrate the data and ideas that have been discussed in the preceding pages under the concept of host-pathogen interaction as a case of pathogenic signalling and homeostatic response in plants. Although the model has numerous gaps, these are due to lack of experimental data rather than to inconsistency with what is presently known. Deeper knowledge of many mechanistic details is still required, but the model provides a framework within which a number of questions relating to viroid pathogenesis can be considered.

1. How can some host plants actively replicate viroids without any visible pathological syndrome?

2. Why do viroids not "need" to act as messengers to incite disease?
3. How can viroids with very different primary structures produce indistinguishable disease syndromes on a given host?
4. Why is the intensity but not the type of syndrome expressed by the host modulated by the viroid structure?
5. How can the so called cross-protection between rather non-homologous viroids be explained?

Principally, we need to elucidate which is the initial pathogenic alteration or interference produced by viroid molecules; which are the steps leading to the signal that triggers the non-specific network of reactions forming the host response; which are the components of this informational flux; how it is connected with control of gene expression; and what kind of relationship exists between the pathogenic and defence reactions.

Viroids, as the simplest pathogens, offer unique opportunities to study these questions. These opportunities are enhanced by the ease with which viroid molecules can now be engineered. Studies with viroids may give insights into how plants interact with more complex pathogens such as viruses and fungi. However, a major obstacle to progress in studies of plant-viroid interactions is the lack of host systems which are genetically well-defined for variation in response, in terms of resistance/susceptibility and severity of the disease syndrome.

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