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Contemporary Approaches to the Study of Host–Parasite Interactions: An Introduction[1]

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Elucidating the biochemical basis of host–parasite relationships will be instrumental in the success of biologically based control in agriculture. This challenge is an ambitious one, but several central themes emerge regarding the roles of both parasite- and host-derived molecules. These include their contribution to nematode attraction, recognition, and reproduction as well as the response of plant hosts. Identification of the gene products involving such fundamental biological processes as nematode behavior and sex determination, although not usually considered as direct participants at the host–parasite interface, will also expand our knowledge of host–parasite interactions and provide alternative strategies for pest management.

The complex nature of plant–nematode interactions and the obligate parasitism of many phytopathogenic nematodes have combined to hinder progress on elucidating mechanisms involved in events such as feeding site initiation and plant responses. With the adoption of molecular biology techniques to plant nematology, new lines of research have been opened in these areas. Rapid advances in understanding the basic biology of the free-living nematode *Caenorhabditis elegans* will most certainly ease the tasks that lie ahead. Answers to such seminal questions as "What makes one nematode a parasite and another a saprophyte?" or "How does an infective second-stage juvenile recognize a host plant?" may now be accessible.

These ideas provided the basis for a symposium entitled Contemporary Approaches to the Study of Host–Parasite Relationships, presented at the Society of Nematologists' annual meeting held in Baltimore during July 1991. With respect to phytonematology, studies addressing the biochemistry of host–parasite relationships are in their infancy. Therefore, we chose three speakers that have made important inroads into the research areas described above irrespective of the specific experimental system employed, recognizing that their contributions will be directly applicable to plant nematologists pursuing similar interests.

One common theme conveyed by the three speakers was the use of molecular genetics to identify and isolate genes whose end products are involved in host–parasite interactions. The tools of molecular biology can be used in several contexts. Characterization of gene-coding regions can be directly used to predict the encoded polypeptide sequence, leading to possible structure-function assignments and to the design of synthetic proteins or antibodies that may ultimately become useful molecules in control strategies. Genes from one nematode, isolated and immortalized by molecular cloning procedures, can be used in nucleic acid hybridization experiments to identify similar DNA regions from other phytopathogenic nematodes. Finally, nematode-derived genes may be transferred among different isolates or

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into plant hosts by DNA-mediated transformation procedures, thereby conferring altered genetic traits to the recipient organism.

We anticipate that the genetic and molecular technologies developed for *C. elegans* can be extended to non-free-living nematodes (6). Moreover, the basic developmental and behavioral features of *C. elegans* are most likely shared with parasitic nematodes (2). The ability to manipulate sex determination genetically in phytopathogenic nematodes may provide a novel approach towards the control of nematode populations. At the Baltimore meeting, Patricia Kuwabara (3) of the University of Wisconsin-Madison described the suite of genes responsible for sex determination in *C. elegans* and provided a vivid example of how traditional and molecular genetic approaches are being used in combination to resolve this complicated developmental pathway. She identified one important gene in sex determination, *her-1,* as a possible gene to insert into a susceptible plant host, because its secreted, diffusible product apparently acts as a masculinizing agent. This strategy might thwart invasive female endoparasitic forms from establishing feeding sites.

Peter Lindgren and his co-workers (4) at the North Carolina State University exploited molecular genetics to study genes from the plant host point of view, in which genes participating in the hypersensitive response (HR) to bacterial phytopathogens were sought. They first demonstrated that several plant host defense mechanisms can be separated from the HR. Messenger RNA populations were next prepared from beans infected with Hrp^+ or Hrp^- *Pseudomonas syringae* pv. *tabaci* strains that were able to promote or unable to induce a HR, respectively. These mRNA preparations were converted in vitro into complementary DNA (cDNA) copies, and individual cDNA fragments were inserted into molecular cloning vector molecules. Clones specific to the HR mRNA population were next identified. These molecules should represent gene sequences expressed during the HR response. This strategy should serve as a paradigm for nematologists interested in determining which plant genes might be responsive to nematode infection.

Development of a simple, experimentally manipulable plant–nematode system will simplify investigation into host–parasite relationships. To this end, Paul Burrows (1) of the Rothamsted Experimental Station described experiments in which *Heterodera schachtii* was used to infect the well-characterized, genetically tractable plant host, *Arabidopsis thaliana* (5). Infection of *Arabidopsis* by second-stage juveniles induces a multinucleate syncytial feeding site. Using strategies similar to that of Lindgren, Burrows is addressing which plant host genes are regulated by cyst nematode infection. Given the success with bacterial and fungal pathogen systems and the ease with which *Arabidopsis* can be controlled in a laboratory setting, developments from the *Heterodera* experiments should be forthcoming at a rapid pace.

The reiterative message echoed by the three symposium speakers addresses the great promise for molecular genetics in dissecting the biochemistry of nematode–plant host relationships. Within the next few years, genes and their encoded protein end products that contribute to pathogenicity and host response will be identified and their functions will be subsequently elucidated. Moreover, employing "reverse genetics," or placing foreign genes in new contexts, may reveal novel strategies for biological control. Recombinant genes encoding nematicidal activities (such as peptide antagonists to neurotransmitters) may be fused with plant gene control (promoter) regions that are responsive to nematode infection. These constructs can then be used to create transgenic plants, with the nematicidal agent expressed exclusively upon infection, perhaps only in root cells comprising the feeding site.

The imaginative approaches addressed at the symposium represent only a fraction of the avenues that "contemporary approaches to host–parasite relationships" might traverse. Based on the information presented in Baltimore during July 1991, the future will be filled with surprises and success.

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