

Biochemical and Molecular Methods of Identifying *Meloidogyne* Species: Symposium Introduction¹

RICHARD S. HUSSEY²

Root-knot nematodes belonging to the genus *Meloidogyne* are the most economically important group of plant-parasitic nematodes. Their worldwide distribution, extensive host ranges, and interaction with other plant pathogens in disease complexes rank them among the top plant pathogens affecting the world's food supply (5). Even though only four *Meloidogyne* species—*M. incognita*, *M. javanica*, *M. arenaria*, and *M. hapla*—account for approximately 95% of all root-knot nematode infestations of agricultural land (6), accurate identification of these species based on morphology is not a simple task. Unfortunately, however, precise identification is required to effectively implement nonchemical management strategies. Our inability to readily identify *Meloidogyne* species is a major obstacle to the application of such strategies (3).

In the 1960s and early 1970s the availability of economical and effective soil fumigants often simplified nematode management. Consequently, nematologists were lulled into a false sense of security by managing nematode diseases with these chemicals which typically made it unnecessary to identify the *Meloidogyne* species present in infested fields. With these nematicides now removed from use (1), nematologists can no longer provide effective advisory recommendations without accurate identification of species within this genus. Nonchemical management strategies for root-knot nematodes, e.g., host resistance or crop rotation, are becoming

more important in agriculture. Effective application of these management practices requires accurate and often rapid identification of individual species of root-knot nematodes. Unfortunately, nematode diagnostic laboratories usually are unable to provide *Meloidogyne* species identification on a timely basis.

Species identification in the genus *Meloidogyne* is particularly difficult. The second-stage juvenile is the life stage most readily extracted from soil samples submitted to diagnostic laboratories, but species identification by morphology cannot be made based solely on this life stage. If host plants are available, adult females can be dissected from galled roots for species identification; otherwise, different life stages can be obtained only by inoculating susceptible plants with juveniles. In addition to a considerable delay in determining the species, this approach also requires glasshouse space for growing plants.

The difficulty encountered in distinguishing *Meloidogyne* species has led nematologists to focus on novel approaches to the taxonomy of this genus. Initial efforts were directed at biochemical and serological methods (2). These early studies illustrated that biochemical identification of *Meloidogyne* species has considerable potential. More recently, developments in molecular biology and biotechnology are being evaluated for their application to nematode diagnosis. These new techniques are already widely used for the diagnosis of other plant pathogens (4). Widespread acceptance of new diagnostic methods in nematology probably will require that the procedures utilize stages of nematodes normally recovered from soil samples by diagnostic laboratories. A goal for these new diagnostic techniques should be the

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² Professor, Department of Plant Pathology, University of Georgia, Athens, GA 30602.

use of specific probes for rapid identification of the four major *Meloidogyne* species once second-stage juveniles have been detected in a sample.

Nematology faces many challenges in the future; improvements in identification of plant-parasitic nematode species and pathotypes should rank high among them. The future for readily and reliably identifying *Meloidogyne* species for diagnostic purposes relies on the development and application of the diagnostic approaches discussed in the following papers. Recent developments in biochemical, serological, and molecular methods for identifying *Meloidogyne* species are presented. These techniques have the potential to revolutionize nematode identification, even where routine identification of host races or pathotypes is required.

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