

DIVERSITY OF *MELOIDOGYNE* SPP. PARASITIZING PLANTS IN MARTINIQUE ISLAND, FRENCH WEST INDIES

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ABSTRACT

Quénéhervé, P., M. Godefroid, P. Mège, and S. Marie-Luce. 2011. Diversity of *Meloidogyne* spp. parasitizing plants in Martinique Island, French West Indies. *Nematropica* 41:191-199.

To assess the presence of root-knot nematodes, *Meloidogyne* spp, 96 root and soil samples were collected in 24 locations in Martinique. This study followed a previous survey that primarily focused on assessing the sanitary risk linked to the presence of root-knot nematodes on dessert bananas. The aim of the present study was to extend the *Meloidogyne* species survey to a wider range of crops and associated weeds as a first step in introducing efficient integrated control of root-knot nematodes in the different cropping systems in Martinique. Soil and root samples were collected from 31 host plants belonging to 15 botanical vegetable crops, weeds and fruits trees. In addition, seven soil samples were collected in natural forests. Polyacrylamide gel electrophoresis (PAGE) revealed 12 different esterase phenotypes among the 76 *Meloidogyne* isolates collected. Six esterase phenotypes were linked to five previously identified species (*M. incognita*, *M. arenaria*, *M. enterolobii*, *M. exigua*, *M. javanica*) and one species recorded for the first time in Martinique (*M. paranaensis*), and five esterase phenotypes belonged to five unknown species, referred to in this study as *Meloidogyne* sp1 to sp 5. Intra-specific variability was also observed within *M. arenaria* populations since both malate-dehydrogenase phenotypes N1 and N3 were observed. This study confirms the high diversity of *Meloidogyne* in Martinique Island including species that are potentially harmful to crops.

Key words: enzymatic profile, *Meloidogyne enterolobii*, *Meloidogyne paranaensis*, root-knot nematode, nematode survey.

RESUMEN

Quénéhervé, P., M. Godefroid, P. Mège, and S. Marie-Luce. 2011. Diversidad de especies de *Meloidogyne* que parasitan plantas en la isla de Martinica, Antillas francesas. *Nematropica* 41:191-199.

Se colectaron 96 muestras de suelo y raíz en 24 localidades en Martinica, con el fin de evaluar la presencia de nematodos agalladores, *Meloidogyne* spp. Este trabajo es el seguimiento a un estudio previo en donde se evaluó el riesgo fitosanitario asociado a la presencia de nematodos agalladores en plantaciones de banano. El objetivo del presente trabajo fue incluir más cultivos y malezas asociadas como un primer paso para desarrollar métodos eficientes de control integrado de *Meloidogyne* en distintos sistemas de cultivo en Martinica. Se colectaron muestras de suelo y raíz de 31 plantas hospedantes pertenecientes a 15 cultivos, malezas o árboles frutales. Además se colectaron siete muestras de bosques naturales. La electroforesis en gel de poliacrilamida (PAGE) mostró 12 fenotipos de esterases diferentes en los 76 aislamientos de *Meloidogyne* colectados. Seis de estos fenotipos corresponden a especies previamente identificadas (*M. incognita*, *M. arenaria*, *M. enterolobii*, *M. exigua*, *M. javanica*) y a una especie registrada por primera vez en Martinica (*M. paranaensis*), y cinco de los fenotipos de esterases pertenecen a cinco especies desconocidas, a las cuales nos referimos en este estudio como *Meloidogyne* sp1 a sp 5. También se observó variabilidad intraespecífica en las poblaciones de *M. arenaria* pues se observaron los fenotipos N1 y N3 de malato-deshidrogenasa. Este estudio confirma la alta diversidad de *Meloidogyne* en Martinica, la cual incluye especies potencialmente dañinas a los cultivos.

Palabras clave: *Meloidogyne enterolobii*, *Meloidogyne paranaensis*, nematodos agalladores, perfil enzimático.

Root-knot nematodes (Nematoda: Heteroderidae) are a major group of plant parasitic nematodes that have a serious effect on yield and quality in a wide range of economically important crops. They represent a huge threat to crop production worldwide (Sasser, 1979; Luc *et al.*, 2005). *Meloidogyne* species are widespread in all cultivated areas including tropical areas. The majority are polyphagous endoparasites that prevent normal assimilation of nutrients by roots (Luc *et al.*, 2005). In addition, their presence is often associated with harmful fungi or bacteria. *Meloidogyne incognita* is the most commonly encountered species in tropical and subtropical regions, but many other species may occur in single or mixed populations (Trudgill *et al.*, 2000).

In recent decades, the characterization of *Meloidogyne* spp. has been considerably facilitated by new biochemical and laboratory techniques. Due to the difficulty involved in accurately identifying *Meloidogyne* species using morphological measurements and observations of perineal patterns of females, identifying esterase and malate-dehydrogenase phenotypes obtained after electrophoretic separation of protein extracts has become a useful tool in species identification of *Meloidogyne* (Esbenshade and Triantaphyllou, 1985; 1990; Fargette, 1987; Carneiro *et al.*, 2000). Today this technique is a widely used routine technique for the identification of *Meloidogyne*.

In Martinique, many studies have been conducted either to inventory *Meloidogyne* associated with weeds in different cropping systems (Quénéhervé *et al.*, 1995; 2006) or to identify *Meloidogyne* at the species level (Carneiro *et al.*, 2000; Cofcewicz *et al.*, 2004; 2005). Among these studies, Cofcewicz *et al.* (2005) conducted a nematode survey to assess the sanitary

risk linked to the presence of root-knot nematodes on dessert bananas (*Musa acuminata* cv Cavendish). Eight different *Meloidogyne* species were identified in Martinique, representing a potential threat to many fruit and market-gardening crops (Quénéhervé and van den Berg, 2005), and underlining the need to carefully monitor this genus to protect crops from endemic species or accidental introductions. It is in this context that this study of *Meloidogyne* species was extended to a wider range of crops and associated weeds as a first step to efficient integrated control of these root-knot nematodes in the different cropping systems.

Ninety-six root and soil samples were collected in 24 locations in Martinique from vegetable crops, weeds and fruits trees of respectively 17, 14 and 3 different host plant species, for a total of 31 host plants belonging to 15 botanical families. In addition, seven soil samples were collected from natural forests.

Adult females of root-knot nematodes were dissected directly from plant roots and analysed by electrophoresis. Corresponding egg masses were used as inoculum on tomato plants (*Lycopersicon esculentum* cv. Caraïbo) in PVC microcosms filled with steam sterilized soil and allowed to develop in controlled climate chambers. Bioassay studies using tomato as a host were used to detect *Meloidogyne* spp. in soil samples. The tomatoes were grown in a climate chamber for 45 days prior to dissection of mature root-knot female nematodes from the tomato roots.

At least 10 mature females from each isolate (originating either from plant or soil samples) were used for biochemical analysis. The dissected females were individually macerated in a 0.6 µl extraction solution containing 20% sucrose, 2% Triton X-100 and

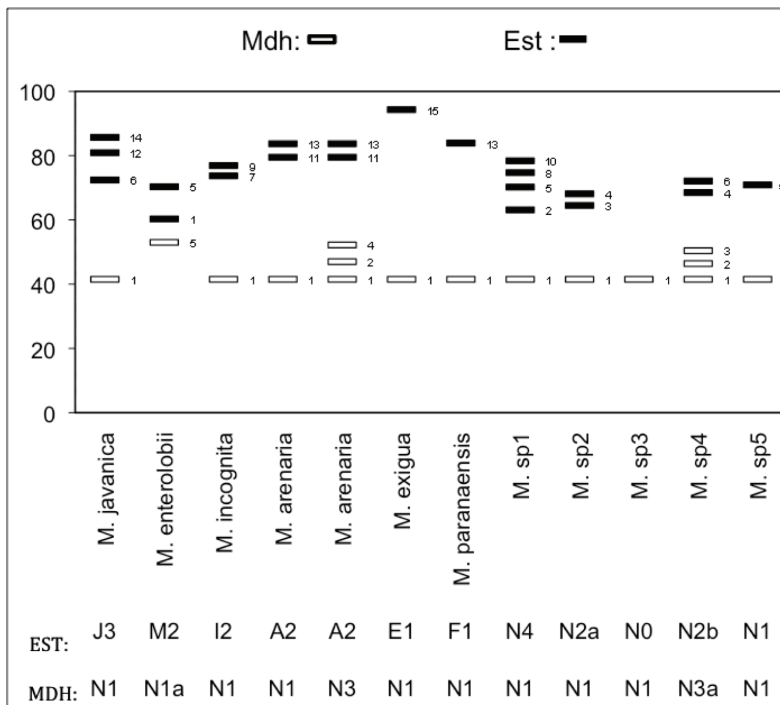


Fig. 1. Esterase (Est) and malate-dehydrogenase (Mdh) phenotypes obtained by electrophoresis from 96 root and soil samples from various host plants in Martinique

0.01% bromophenol blue. Electrophoretic separation of esterases (EST) and malate-dehydrogenases (MDH) was performed using an automated polyacrylamide gel electrophoresis Phatsystem® before staining. All gels included two females of either *M. javanica* or *M. enterolobii* as internal standards to facilitate the comparison of the relative mobility of the electrophoretic bands of *Meloidogyne* spp. isolates. Following Esbenshade and Triantaphyllou (1985), one or several letters and the number of bands were used to designate the enzyme phenotype of each isolate (Table 1). In parallel, some female perineal patterns were mounted in water agar and observed under a stereomicroscope.

Esterase phenotypes (EST)

Electrophoresis revealed 15 EST bands and 12 different EST phenotypes were identified among the 76 *Meloidogyne* isolates collected (Table 1, Fig. 1). Six phenotypes were linked to already known species and five EST phenotypes belonged to unknown species denoted here as *Meloidogyne* sp1 to sp 5.

The most frequent EST phenotype I2 (Rm: 73.7; 76.9) was specific to *Meloidogyne incognita*. A total of 27 plant species belonging to 15 botanical families were found to be hosts of this nematode species. Single populations of *M. incognita* parasitized different vegetable or aromatic crops including eggplant (*Solanum melongena*), sweet pepper (*Capsicum annuum*), hot pepper (*Capsicum chinense*), tomato (*Lycopersicon esculentum*), okra (*Abelmoschus esculentus*), pumpkin (*Cucurbita maxima*), lettuce (*Lactuca sativa*), cabbage (*Brassica oleracea*), parsley (*Petroselinum sativum*) and Spanish thyme (*Plectranthus amboinicus*). *Meloidogyne incognita* was found associated on the eight following weeds *Cnicus benedictus*, *Vernonia cinerea*, *Ageratum conyzoides*, *Cleome viscosa*, *Leonotis nepetifolia*, *Malachra fasciata*, *Peperomia pellucida*, and *Spemacoce prostata*.

We detected the EST phenotype M2 (Rm: 60.3; 40.7) belonging to *Meloidogyne enterolobii*, in 12 plant species belonging to seven botanical families. The vegetable hosts of *M. enterolobii* were celery (*Apium graveolens*), parsley, cucumber, watermelon (*Citrullus latanus*), hot pepper, Cayenne pepper (*Capsicum frutescens*) and tomato. Four spontaneous weeds (*Chamaesyce hypericifolia*, *Leonotis nepetifolia*, *Physalis peruviana*, and *Urena lobata*) were also found infected by this species of root-knot nematode. All guava plants (*Psidium guajava*) sampled in this survey were infected by a single population of *M. enterolobii*, except in one case there was a mixed population with *M. incognita*. The root-knot nematode *M. enterolobii* was also detected in natural forest soil.

Meloidogyne arenaria is characterized by the EST phenotype A2 (Rm: 79.5; 83.7) and was found infecting 12 host plants belonging to eight botanical families. Its presence was detected in a single population on carrot

(*Daucus carota*), pumpkin (*Cucurbita maxima*), basilic (*Ocimum basilicum*), and cucumber and on two weeds *Solanum torvum* and *Malachra alceifolia*. *Meloidogyne arenaria* was also found in mixed populations with *M. incognita* on papaya (*Carica papaya*), green onion (*Allium fistulosum*), sweet pepper, and on two weeds *Malachra alceifolia* and *Chamaesyce prostrata*.

The EST phenotype J3 (Rm: 72.3; 80.9; 85.7) specific to *Meloidogyne javanica* was found in mixed populations with *M. incognita* on cucumber and with *M. incognita* and *M. arenaria* on Spanish thyme.

The EST phenotypes F1 (Rm: 83.8) of *Meloidogyne paranaensis* and E1 (Rm: 94.3) belonging to *M. exigua* were detected once in soil from natural forests.

The N4 atypical phenotype (Rm: 63.1; 70.5; 74.7; 78.4) linked to the unknown species denoted *Meloidogyne* sp1 was found in roots of dessert banana (*Musa acuminata* cv. Cavendish) and in mixed populations with *M. enterolobii* on hot pepper.

The phenotype N2a (Rm: 64.5; 68.3) belonging to an unknown denoted *Meloidogyne* sp 2 was found in mixed population with *M. incognita* on cucumber.

The phenotype N0 without EST bands named *Meloidogyne* sp 3 was found mixed with *M. incognita* on Spanish thyme. This atypical phenotype was also observed in a different soil sample from a natural forest.

The N2b phenotype (Rm: 68.4; 72.2) was consistently detected in several populations denoted *Meloidogyne* sp 4 in soils cultivated with sugarcane (*Saccharum officinarum*).

The EST phenotype N1 (Rm 70.5) detected in populations denoted *Meloidogyne* sp 5 which was found on the roots of the common weed *Vernonia cinerea*.

Malate-dehydrogenase phenotypes (MDH)

Less variability was observed within MDH phenotypes than EST phenotypes among the 76 different *Meloidogyne* spp. isolates; we detected five MDH bands allowing four MDH phenotypes to be distinguished. This observation is in accordance with those made in previous studies (Esbenshade and Triantaphyllou, 1985; Carneiro *et al.*, 1996; Cofcewicz *et al.*, 2005; Brito *et al.*, 2008; 2010).

Intra-specific variability was observed within *M. arenaria* populations since both MDH phenotype N1 (Rm: 41.5) and N3 (Rm: 41.5; 46.7; 52.2) were observed. With the exception of three isolates from cucumber, papaya and Spanish thyme, all isolates showed the N3 phenotype.

The MDH phenotype N1a (Rm: 53) was found in populations characterized by the EST phenotype M2 typical of *M. enterolobii*.

The unknown species denoted *Meloidogyne* sp 4 was characterized by the MDH phenotype N3a (Rm: 41.5; 46.7; 50.4).

With the exception of *M. enterolobii* N1a, *M. arenaria* N3 and *M. sp4*, all isolates were characterized by the MDH phenotype N1.

Table 1: Species of *Meloidogyne* identified according to esterase and malate-dehydrogenase phenotypes on 15 botanical families from Martinique.

<i>Meloidogyne</i> Species	EST phenotypes	MDH phenotypes	Botanical families	Host Plant Species	Common Names	Type of crop
<i>M. arenaria</i> N1 A2		N1	Cucurbitaceae	<i>Cucumis sativus</i> *	Cucumber	Vegetable crop
<i>M. arenaria</i> N1, A2, A2, I2 <i>M. arenaria</i> N3, <i>M. incognita</i>		N1, N3, N1	Caricaceae	<i>Carica papaya</i>	Papaya	Fruit tree
<i>M. arenaria</i> N1, I2, A2, J3 <i>M. incognita</i> , <i>M. javanica</i>		N1, N1, N1	Lamiaceae	<i>Plectranthus amboinicus</i>	Spanish thyme	Vegetable crop
<i>M. arenaria</i> N3 A2		N3	Apiaceae	<i>Daucus carota</i>	Carrot	Vegetable crop
A2		N3	Cucurbitaceae	<i>Cucurbita maxima</i>	Pumpkin	Vegetable crop
A2		N3	Lamiaceae	<i>Ocimum basilicum</i>	Basilic	Vegetable crop
A2		N3	Malvaceae	<i>Malachra alceifolia</i>		Weed
A2		N3	Solanaceae	<i>Solanum torvum</i>	Turkey berry	Weed
A2		N3				Natural forest*
<i>M. arenaria</i> N3, A2, I2 <i>M. incognita</i>		N3, N1	Apiaceae	<i>Apium graveolens</i>	Celery	Vegetable crop
A2, I2		N3, N1	Euphorbiaceae	<i>Chamaesyce prostrata</i>	Ground spurge	Weed
A2, I2		N3, N1	Liliaceae	<i>Allium fistulosum</i>	Green onion	Vegetable crop
A2, I2		N3, N1	Malvaceae	<i>Malachra alceifolia</i>	Yellow leafbract	Weed
A2, I2		N3, N1	Solanaceae	<i>Capsicum annuum</i>	Sweet pepper	Vegetable crop
<i>M. arenaria</i> N3, A2, M2 <i>M. enterolobii</i>		N3, N1a	Apiaceae	<i>Apium graveolens</i>	Celery	Vegetable crop
<i>M. exigua</i> E1		N1				Natural forest*
<i>M. incognita</i> I2		N1	Apiaceae	<i>Apium graveolens</i>	Celery	Vegetable crop
I2		N1	Apiaceae	<i>Petroselinum sativum</i>	Parsley	Vegetable crop
I2		N1	Asteraceae	<i>Ageratum conyzoides</i>	Goat weed	Weed
I2		N1	Asteraceae	<i>Cnicus benedictus</i>	St. Benedict's thistle	Weed
I2		N1	Asteraceae	<i>Lactuca sativa</i>	Lettuce	Vegetable crop
I2		N1	Asteraceae	<i>Vernonia cinerea</i>	Inflammation bush	Weed
I2		N1	Brassicaceae	<i>Brassica oleracea</i>	Cabbage	Vegetable crop
I2		N1	Capparaceae	<i>Cleome viscosa</i>	Jasmin del rio	Weed
I2		N1	Caricaceae	<i>Carica papaya</i>	Papaya	Fruit tree
I2		N1	Cucurbitaceae	<i>Cucurbita maxima</i>	Pumpkin	Vegetable crop
I2		N1	Lamiaceae	<i>Leonotis nepetifolia</i>	Lion's tail	Weed
I2		N1	Lamiaceae	<i>Ocimum basilicum</i>	Basilic	Vegetable crop

Table 1: Species of *Meloidogyne* identified according to esterase and malate-dehydrogenase phenotypes on 15 botanical families from Martinique.

<i>Meloidogyne</i> Species	EST phenotypes	MDH phenotypes	Botanical families	Host Plant Species	Common Names	Type of crop
	I2	N1	Lamiaceae	<i>Plectranthus amboinicus</i>	Spanish thyme	Vegetable crop
	I2	N1	Malvaceae	<i>Abelmoschus esculentus</i>	Okra	Vegetable crop
	I2	N1	Malvaceae	<i>Malachra fasciata</i>	Roadside leafbract	Weed
	I2	N1	Piperaceae	<i>Peperomia pellucida</i>		Weed
	I2	N1	Poaceae	<i>Saccharum officinarum</i> *	Sugarcane	Sugarcane
	I2	N1	Rubiaceae	<i>Spemacoce prostata</i>		Weed
	I2	N1	Solanaceae	<i>Capsicum annuum</i>	Sweet pepper	Vegetable crop
	I2	N1	Solanaceae	<i>Capsicum chinense</i>	Hot pepper	Vegetable crop
	I2	N1	Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	Vegetable crop
	I2	N1	Solanaceae	<i>Solanum melongena</i>	Eggplant	Vegetable crop
<i>M. incognita</i> , <i>M. javanica</i>	I2, J3	N1, N1	Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber	Vegetable crop
<i>M. incognita</i> , <i>M. enterolobii</i>	I2, M2	N1, N1a	Myrtaceae	<i>Psidium guajava</i>	Guava tree	Fruit tree
<i>M. incognita</i> , <i>M. sp2</i>	I2, N2	N1, N1	Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber	Vegetable crop
<i>M. incognita</i> , <i>M. sp3</i>	N0, I2	N1, N1	Lamiaceae	<i>Plectranthus amboinicus</i>	Spanish thyme	Vegetable crop
<i>M. incognita</i> , <i>M. sp4</i>	I2, N3	N1, N3a	Poaceae	<i>Saccharum officinarum</i>	Sugarcane	Sugarcane
<i>M. enterolobii</i>	M2	N1a	Apiaceae	<i>Apium graveolens</i>	Celery	Vegetable crop
	M2	N1a	Apiaceae	<i>Petroselinum sativum</i>	Parsley	Vegetable crop
	M2	N1a	Cucurbitaceae	<i>Citrullus lanatus</i>	Watermelon	Vegetable crop
	M2	N1a	Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber	Vegetable crop
	M2	N1a	Euphorbiaceae	<i>Chamaesyce hypericifolia</i>		Weed
	M2	N1a	Lamiaceae	<i>Leonotis nepetifolia</i>	Lion's tail	Weed
	M2	N1a	Malvaceae	<i>Urena lobata</i>		Weed
	M2	N1a	Myrtaceae	<i>Psidium guajava</i>	Guava tree	Fruit tree
	M2	N1a	Solanaceae	<i>Capsicum chinense</i>	Hot pepper	Vegetable crop
	M2	N1a	Solanaceae	<i>Capsicum frutescens</i>	Cayenne pepper	Vegetable crop
	M2	N1a	Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	Vegetable crop

Table 1: Species of *Meloidogyne* identified according to esterase and malate-dehydrogenase phenotypes on 15 botanical families from Martinique.

<i>Meloidogyne</i> Species	EST phenotypes	MDH phenotypes	Botanical families	Host Plant Species	Common Names	Type of crop
	M2	N1a	<i>Solanaceae</i>	<i>Physalis angulata</i>	Cow pops	Weed
	M2	N1a				Natural forest*
<i>M. enterolobii</i> , <i>M. sp1</i>	M2, N4	N1a, N1	<i>Solanaceae</i>	<i>Capsicum chinense</i>	Hot pepper	Vegetable crop
<i>M. paranaensis</i>	F1	N1				Natural forest*
<i>M. sp1</i>	N4	N1	<i>Musaceae</i>	<i>Musa paradisiaca</i>	Plantain	Fruit tree
<i>M. sp3</i>	I2	N1	<i>Asteraceae</i>	<i>Vernonia cinerea</i>	Inflammation bush	Weed
	N0	N1	<i>Lamiaceae</i>	<i>Plectranthus amboinicus</i>	Spanish thyme	Vegetable crop
	N0	N1				Natural forest*
<i>M. sp4</i>	N3	N3a	<i>Poaceae</i>	<i>Saccharum officinarum</i> *	Sugarcane	Sugarcane
<i>M. sp5</i>	N1	N1	<i>Asteraceae</i>	<i>Vernonia cinerea</i>	Inflammation bush	Weed

(*) *Meloidogyne* isolates extracted from soil sample.

This present survey completes the previous study by Cofcewicz *et al.* (2005) and probably reflects the biodiversity of *Meloidogyne* spp. in Martinique and should provide the basis for integrated control of root-knot nematodes on crops. Samples were collected from market-garden crops, fruit trees, weeds and natural forests in different locations in the island. Potentially pathogenic species such as *M. cruciani* and *M. hispanica* were previously detected on *Musa* spp. by Cofcewicz *et al.* (2005) and the samples collected for the present study confirmed the additional presence of *M. enterolobii*, *M. exigua*, *M. paranaensis*, and of five unknown species.

Among the root-knot nematode species detected for the first time in Martinique on bananas (Cofcewicz *et al.*, 2005), *M. hispanica* and *M. cruciani* can be considered as potentially harmful parasites of other cultivated crops. Tomato is the most susceptible vegetable crop to *M. hispanica* (Hirschmann, 1986), while infected aubergine plants have been found in West Africa but no information on pathogenicity was provided (Trudgill *et al.*, 2000). *Meloidogyne cruciani* was described in the Caribbean on tomato in the US Virgin Islands. This species has been shown to infect tobacco and vegetable crops including cabbage, watermelon, sweet potato, maize and sweet pepper (Garcia-Martinez *et al.*, 1982). This species has also been detected in Argentina on aubergine (Doucet and Pinochet, 1992).

Meloidogyne enterolobii was detected for the first time in Martinique on the Mi-1 gene resistant tomato (Carneiro *et al.*, 2000) representing a potential risk for

economically important crops. This species, primarily described from a population sampled in China (Yang and Eisenback, 1983), is now regarded as a senior synonym of *M. mayaguensis* (Xu *et al.* 2004; Randig *et al.*, 2009) described later in one population in Puerto Rico (Rammah and Hirschmann 1988). This species is now found in Brazil, Venezuela, USA, Trinidad and Tobago, Cuba, Florida, Burkina-Faso, Senegal, Ivory Coast, Malawi, South Africa, (Brito *et al.*, 2004; Carneiro *et al.*, 2001; Decker and Rodriguez-Fuentes, 1989; Fargette and Braaksma, 1990; Trudgill *et al.*, 2000; Willers, 1997a). Recently, this plant parasitic species was also detected in greenhouses in Europe, including in France and Switzerland so vigilance is required to avoid its introduction and establishment in field crops (Block *et al.*, 2002; Kiewnick *et al.*, 2008). *Meloidogyne enterolobii* can parasitize a large number of host plants and can overcome plants' genetic resistance as exemplified by Mi-1, N and Tabasco genes on tomato, pepper and sweet pepper (Brito *et al.*, 2007). In this context, controlling this nematode species by using resistant varieties is not challenging. Furthermore, *M. enterolobii* is also responsible for a serious disease on *Psidium guajava* leading to plant death. The high pathogenicity of this species for guava trees has already been described in Brazil and South Africa, where control requires use of nematicides (Souza *et al.*, 2006; Willers, 1997b). During the present survey, *M. enterolobii* was found on a large number of garden plants and most of the guava trees sampled were infested with *M. enterolobii*. Due to its pathogenicity

and virulence, this species represents a serious threat to market garden and fruit crops in Martinique where this species is already denoted as the guava root-knot nematode. Considering the risk of introduction and dissemination of this pest in the European region, *M. enterolobii* was recently added to the EPPO Alert List (EPPO, 2008).

Meloidogyne paranaensis was detected in a single soil sample collected in a natural forest. This is the first report of this nematode in Martinique. Up to now, this species was only described in one population on *Coffea arabica* in Paraná state in Brazil where it caused major damage (Carneiro *et al.*, 1996) and in coffee fields in Guatemala and Hawaii (Anzueto *et al.*, 1991; Carneiro *et al.*, 2004). Campos and Villain (2005) suggested a large-scale survey for the accurate detection of *M. paranaensis* in the Americas because of possible confusion between *M. incognita* and *M. paranaensis*.

Tobacco, tomato, watermelon and the medicinal tea plant Yerba mate (*Ilex paraguariensis*) have been shown in experimental tests to be suitable hosts for *M. paranaensis* but this species has never been detected in the field (Carneiro *et al.*, 1996; Inserra *et al.*, 2003; Santiago *et al.*, 2000). In Martinique, this harmful species could spread to some economic crops and therefore constitutes a potential risk.

Meloidogyne exigua, responsible for diseases in coffee plantations in South and Central America, was previously detected in Martinique (Sasser, 1972; Scotto la Massèse, 1969) on bitter orange (*Citrus aurantium*), tea (*Camelia sinensis*) and coffee trees (*Coffea arabica*). Thus, its native presence in one soil sample from a natural forest was not surprising. Host plants for *M. exigua* include numerous crops such as cucumber, watermelon, pepper, tomato, sugarcane and coffee (Lordello, 1964; Moraes *et al.*, 1972). Eventhough *M. exigua* is mainly known for its high pathogenicity on coffee, it could spread to other economically important crops cultivated in Martinique.

In parallel with these known species, atypical phenotypes belonging to unknown species were also detected in soil and root samples. Lack of information limits the evaluation of the phytosanitary risk they represent and further studies are thus necessary. For example, the root-knot nematode *Meloidogyne* sp 4 was systematically found in soils where sugarcane was cultivated but to date, no information concerning its possible pathogenicity or range of host plants is available to estimate its potential impact on crops in Martinique. The root-knot nematode *Meloidogyne* sp 3 did not present major esterase band similarity to an unknown species detected on *Musa* spp. in Guadeloupe (Cofcewicz *et al.*, 2005). With the notable exception of *Meloidogyne* sp 4 on sugarcane, none of these other atypical phenotypes were found to be abundant.

Thus, further sampling, accurate identification and host tests focused on these new records of *Meloidogyne* species are indispensable as chemical control is reduced

and cultural practices involving fallow, green manures and crop rotations become increasingly used.

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