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## Chapter 3

# Taxonomy, Morphology and Phylogenetics of Coffee-Associated Root-Lesion Nematodes, *Pratylenchus* spp.

Zafar A. Handoo, Lynn K. Carta and Andrea M. Skantar

**Abstract** This review includes a synthesis of information on eight species of root-lesion nematodes (*Pratylenchus* spp.) that parasitize coffee or inhabit its rhizosphere. It includes a table of important morphological characters, a diagnostic key, photographs of anterior ends and tails of specimens from the USDA nematode collection, and a phylogenetic tree based on ribosomal DNA with drawings of scanning electron microscopic face-patterns. Information sources are evaluated and future research needs are outlined.

**Keywords** Diagnostic key · phylogeny · taxonomy · phylogenetic tree · evolution

### 3.1 Introduction

Root-lesion nematodes (*Pratylenchus* spp.) are among the most common and damaging to coffee (*Coffea* sp.) aside from root-knot nematodes and a few other genera. The genus *Pratylenchus* is comprised of 97 valid species of worldwide distribution and economic importance, which parasitize a wide variety of plant species. Members of this genus are called root-lesion nematodes because they produce lesions on feeder roots and occasionally on other underground plant parts as a result of their feeding. They are sometimes referred to as meadow nematodes due to their frequent occurrence in that environment.

The first described root-lesion nematode was *Tylenchus pratensis* De Man (de Man, 1880), which was redescribed and illustrated by De Man (1884). The genus name *Pratylenchus* was established by Filipjev in 1936, with *P. pratensis* (de Man) Filipjev as the type species. Sher and Allen (1953) first put the taxonomy of the genus on a basis familiar to modern taxonomists. Loof (1960; 1978; 1991) reviewed in detail the anatomy, morphology, distribution, systematics, variability and identification of the genus, and presented a key to its species. Key and comprehensive compendia including histories of the morphological work performed

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used to distinguish them are body length, head shape and number of annules, length of stylet, shape of stylet knobs, structure of lateral field, presence/absence and shape of spermatheca, length and structure of posterior uterine branch, shape of female tail terminus, presence or absence of males and shape and length of spicule and gubernaculum. Loof (1991) discussed these characters in detail, with particular emphasis on the intraspecific variation that limits their reliability. Table 3.1 contains updated morphometric data for the most important diagnostic characters of the coffee-associated *Pratylenchus* species. Figures 3.1 through 3.4 contain photomicrographs of female's heads and tails.

Identification of *Pratylenchus* species is hampered by the similarity among species in some cases, and by the significant intraspecific variability of both morphological and morphometric diagnostic characters in other cases. Several authors have described morphological variations within species that make it difficult to separate species accurately using traditional microscopy. Variable features include tail shape, the number of annules in the ventral part of tail, the lateral field throughout the body (Corbett and Clark, 1983), and the presence of one supplementary lip annule in some specimens (Baujard et al., 1990). This situation has prompted researchers to discover alternate methods and features for more accurate identification. Although not considered routine, SEM is a technique sometimes used for morphological analysis (see for example Sher and Bell, 1975; Corbett and Clark, 1983; Trett and Perry, 1985; Baujard et al., 1990; López and Salazar, 1990; Sakwe and Geraert, 1994; Inserra et al., 1998; 2005a; Duncan et al., 1999; Hernández et al., 2001; Carta et al., 2001; 2002). Fortunately, for taxonomic purposes, SEM has shown the stability and reliability of several nematode surface features, with the lip and face region, lateral field, and tail receiving the most attention (see for example Anderson and Townshend, 1980; Inserra et al., 2005a). In an SEM study of the surface features of nine *Pratylenchus* species the lip region has been demonstrated to be a particularly good taxonomic character; species have been separated into three groups according to the pattern of the first lip annule and the oral disc (Hernández et al., 2001).

### 3.2.2 *The Coffee-Associated Root-Lesion Nematodes, Pratylenchus spp.*

The eight species listed below have been reported from the roots of coffee (Campos et al., 1990). However, a recently described species from northern Europe, *P. brzeskii* Karssen, Waeyenberge and Moens, is morphologically similar to *P. coffeae* and *P. loosi* (Karssen et al., 2000), species both known to parasitize coffee in more southern climates and difficult to distinguish by morphology (Pourjame et al., 1999). To our knowledge, *P. brzeskii* has not been examined for possible parasitism on coffee. This closely related species is another indication that *P. coffeae* and relatives represent a densely populated species complex (Campos and Villain, 2005). Uncertainty about the identity of some amphimitic *Pratylenchus* populations has been recorded from Brazil (Siciliano-Wilcken et al. 2002a,b; Silva and Inomoto,



**Table 3.1** Compendium of eight *Pratylenchus* species known to parasitize coffee. Values represent range, average

Species	Body length (mm)	Stylet length ( $\mu\text{m}$ )	No. lip annules	a <sup>a</sup>	b	c	V%	No. tail annules	Tail shape <sup>b</sup>	Tail terminus	Spicule length ( $\mu\text{m}$ )	Gubernaculum length ( $\mu\text{m}$ )	Spermatheca	Males
<i>P. brachyurus</i>	0.39-0.75	17-22	2	15-29	5-10	13-28	82-89	15-21	SCYL,	SMO	16-17	5-6	Empty	Very rare
	0.59	20.7		23	8	25	85.6	18.5	TRC, SHM, SMO					
<i>P. coffeae</i>	0.46-0.70	15-18	2	21-30	5-8	17-27	76-82	17-24	HEM-BLP,	IND,	15-18	4.2-6	Large, broadly oval to round	Common
	0.53	16.5		25	6.5	22	80	20	SMO	TRC, BR, 16.5				
<i>P. panamaensis</i> (= <i>P. gutierrezii</i> )	0.43-0.55	16-18	2	15-24.9	3.5-4.5	17-25	74-84	18-23	SCYL	BLR,	15.5-21	3.2-4.4	Oval to round	Common
	0.5	16.8		19.8	3.9	19.9	80	21		ANN	16.8	3.7		
<i>P. goodeyi</i>	0.40-0.68	14-17	4	24-37	5.5-7.3	14-18	73-75	21	SC	TP,	15.5-21	5-6	Large, oblong	Common
	0.52	15.7		32	6.5	16.5	74		SMO					
<i>P. loosi</i>	0.48-0.64	14-18	2	28-36	5.7-7.1	18-25	79-85	27-34	NAR, SA	NAR,	16-20	4-7	Oval	Common
	0.57	16.5		32	6.4	21	82.5		SMO		17.5	5.5		

2002), Guatemala (Villain et al., 1998; Villain, 2000), El Salvador and Costa Rica (Herve, 1997; Duncan et al., 1999) based on host range and genetic information.

Drawings of *Pratylenchus* species other than *P. goodeyi* and *P. pratensis* (see below) may be found at the USDA website (<http://ars.usda.gov/Main/docs.htm?docid=9866>) and at the University of Nebraska websites <http://nematode.unl.edu/pratkey7.htm#pratkey7>, <http://nematode.unl.edu/pracoff.htm>, <http://nematode.unl.edu/ploos.htm> and <http://nematode.unl.edu/prapse.htm>.

### **3.2.2.1 *Pratylenchus coffeae* (Zimmermann, 1898) Filipjev and Schuurmans Stekhoven, 1941**

The taxonomy of *P. coffeae* (Fig. 3.1 A–H) has been the subject of numerous studies (Sher and Allen, 1953; Loof, 1960; 1978; 1991; Roman and Hirschmann, 1969; Siddiqi, 1972; Rashid and Khan, 1978; Bajaj and Bhatti, 1984; Inserra et al., 1996; 1998; 2001; Mizukubo, 1992; Duncan et al., 1999; Ryss, 2002a; Van Den Berg et al., 2005).

This species is the most widespread and damaging on coffee. It occurs in the Dominican Republic, El Salvador, Guatemala, Puerto Rico, Costa Rica, Brazil, India, Southeast Asia, Barbados, Martinique, Tanzania, Madagascar, Indochina, Java, Indonesia and Venezuela. On other hosts this species is found throughout the tropics and in many subtropical regions. Specific locations include Japan, Australia, South Africa, Brazil, Oman (Campos and Villain, 2005) and southern parts of the United States (Norton et al., 1984).

### **3.2.2.2 *Pratylenchus brachyurus* (Godfrey, 1929) Filipjev and Schuurmans Stekhoven, 1941**

The taxonomy of *P. brachyurus* (Fig. 3.1 I–P) has been advanced by authors in Europe and the Americas (Sher and Allen, 1953; Loof, 1960; 1978; 1991; Roman and Hirschmann, 1969; Corbett, 1976; Corbett and Clark, 1983; López and Salazar, 1990; Hernández et al., 2001; Ryss, 2002a).

In South America, this was one of the first root-lesion nematodes known on coffee (Campos and Villain, 2005). It is found primarily in the tropics and subtropics, and specifically in Australia, Brazil, Peru, USA, Turkey, West Africa, South Africa and Japan. In some areas of Brazil it may be more widespread than *P. coffeae* (Campos and Villain, 2005).

### **3.2.2.3 *Pratylenchus loosi* Loof, 1960**

Taxonomic and morphological studies of *P. loosi* (Fig. 3.2 A–H) have been published in various review papers (Seinhorst, 1977; Loof, 1978; 1991; Inserra et al., 1996; 2001).

This species has been reported on coffee in Sri Lanka (Hutchinson, 1963 cited by Whitehead, 1968). On other hosts its geographic distribution includes Sri Lanka, India, Japan (Seinhorst, 1977; Campos and Villain, 2005), Korea (Park et al., 2002),

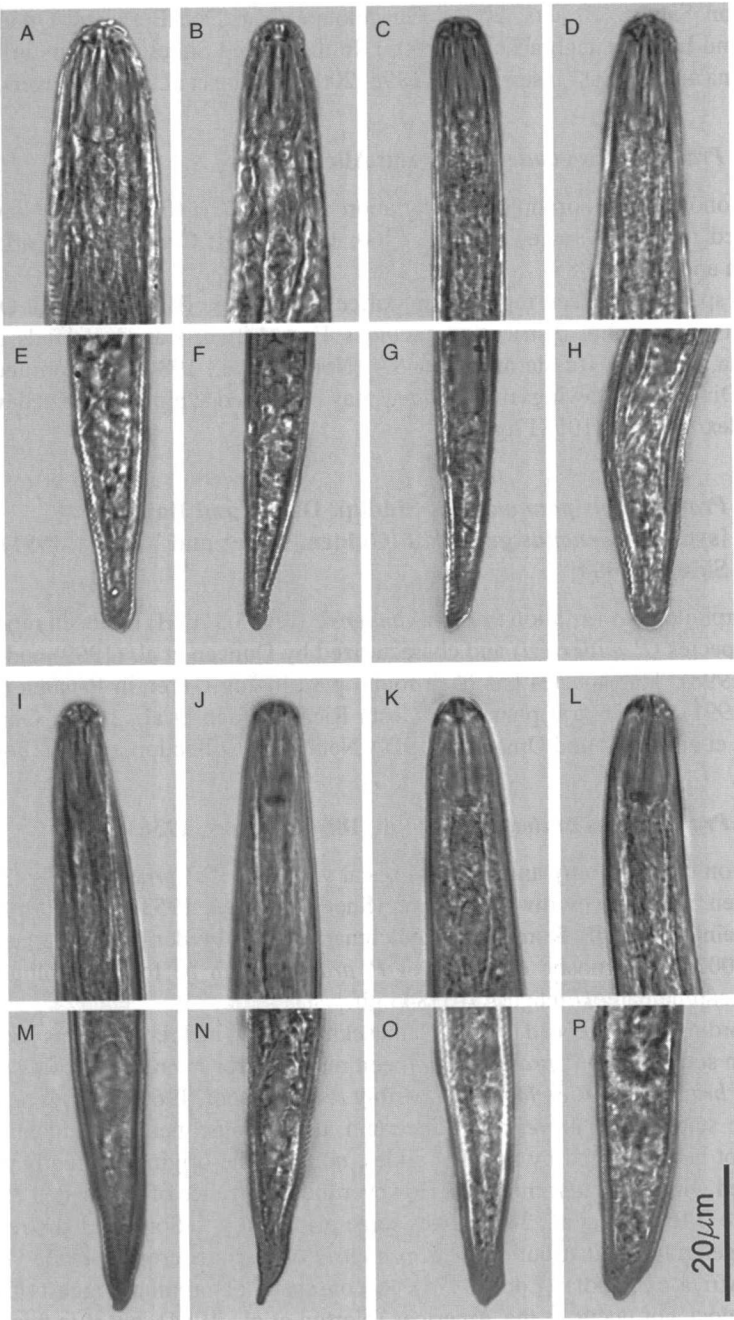


Fig. 3.2 Photomicrographs of female heads and tails, showing variations in tail shape. (A–H) *P. loosi*, (I–P) *P. goodeyi*. (Photos by Z. A. Handoo)

American Samoa (Brooks, 2004), Guadeloupe (Van Den Berg and Quénéhervé, 2000) and Iran (Hajieghrari et al., 2005). In the United States, it occurs in Florida, Louisiana and Kansas (Inserra et al., 1996; 2001; Norton et al., 1984; Powers, 2008).

#### **3.2.2.4 *Pratylenchus goodeyi* Sher and Allen, 1953**

The taxonomy and morphological variation of *P. goodeyi* (Fig. 3.2 I–P) have been described in various reviews (Loof, 1960; 1978; 1991; Corbett and Clark, 1983; Machon and Hunt, 1985).

This species has been reported on coffee in Tanzania (Bridge, 1984). On other hosts, its geographic distribution includes East Africa, Canary Islands, Kenya, Tanzania, England, Russia and the USA (Norton et al., 1984; Machon and Hunt, 1985). Diagnostic drawings of *P. goodeyi* may be viewed at [plpnmweb.ucdavis.edu/Nemaplex/images/G105S12.gif](http://plpnmweb.ucdavis.edu/Nemaplex/images/G105S12.gif).

#### **3.2.2.5 *Pratylenchus panamaensis* Siddiqi, Dabur and Bajaj, 1991 [syn. *Pratylenchus gutierrezii* (Golden, López and Vilchez, 1991) Siddiqi, 2000]**

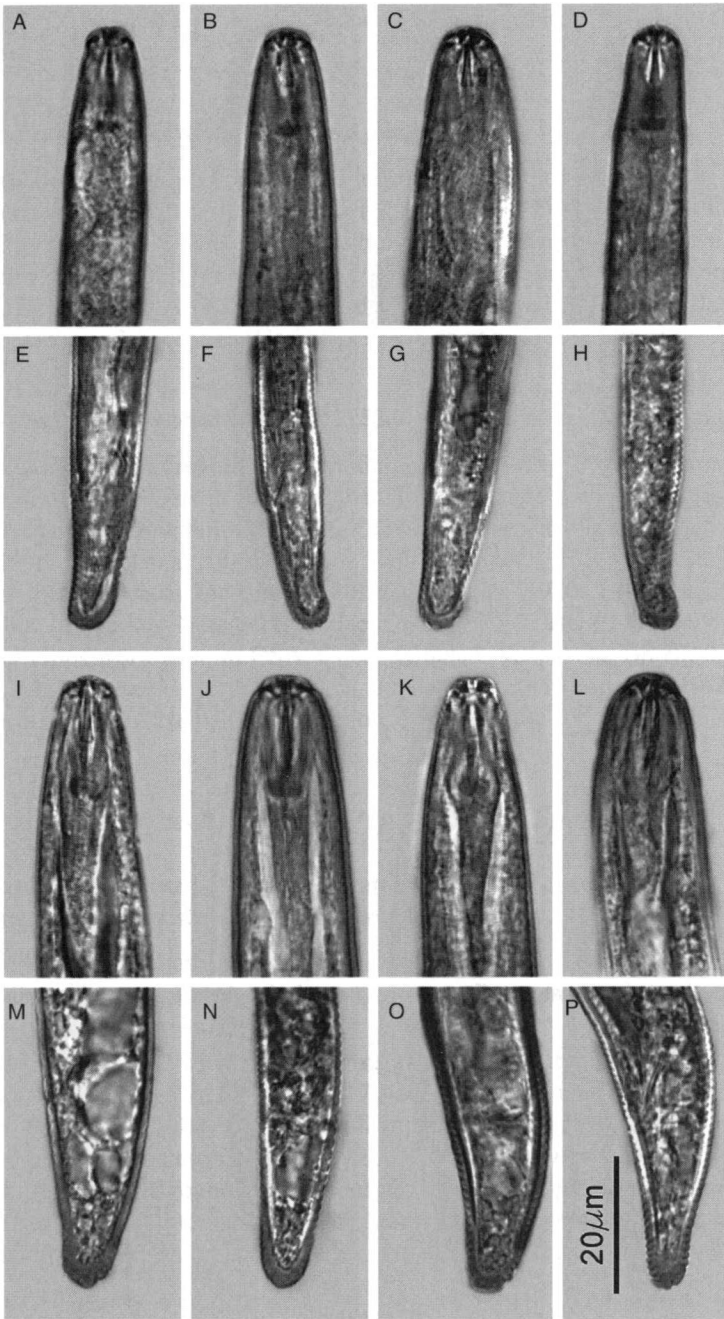
The morphological variation in *P. panamaensis* (Fig. 3.3 A–H) has been reported as a new species (*P. gutierrezii*) and characterized by Duncan et al. (1999) and Inserra et al. (1998). This species has been found parasitizing coffee in Panama (Siddiqi et al., 1991), the central plateau of Costa Rica (Golden et al., 1992), Guatemala (Inserra et al., 1998) and Oman (in USDA Nematode Collection, entry #1546).

#### **3.2.2.6 *Pratylenchus pratensis* (de Man, 1880) Filipjev, 1936**

Studies on the taxonomy and morphological variation of *P. pratensis* (Fig. 3.3 I–P) have been advanced by diverse authors (Sher and Allen, 1953; Loof, 1960; 1974; 1978; Seinhorst, 1968; Roman and Hirschmann, 1969; Frederick and Tarjan, 1989; Ryss, 2002a). Diagnostic drawings of *P. pratensis* can be found at [plpnmweb.ucdavis.edu/nemaplex/images/G105S45.gif](http://plpnmweb.ucdavis.edu/nemaplex/images/G105S45.gif).

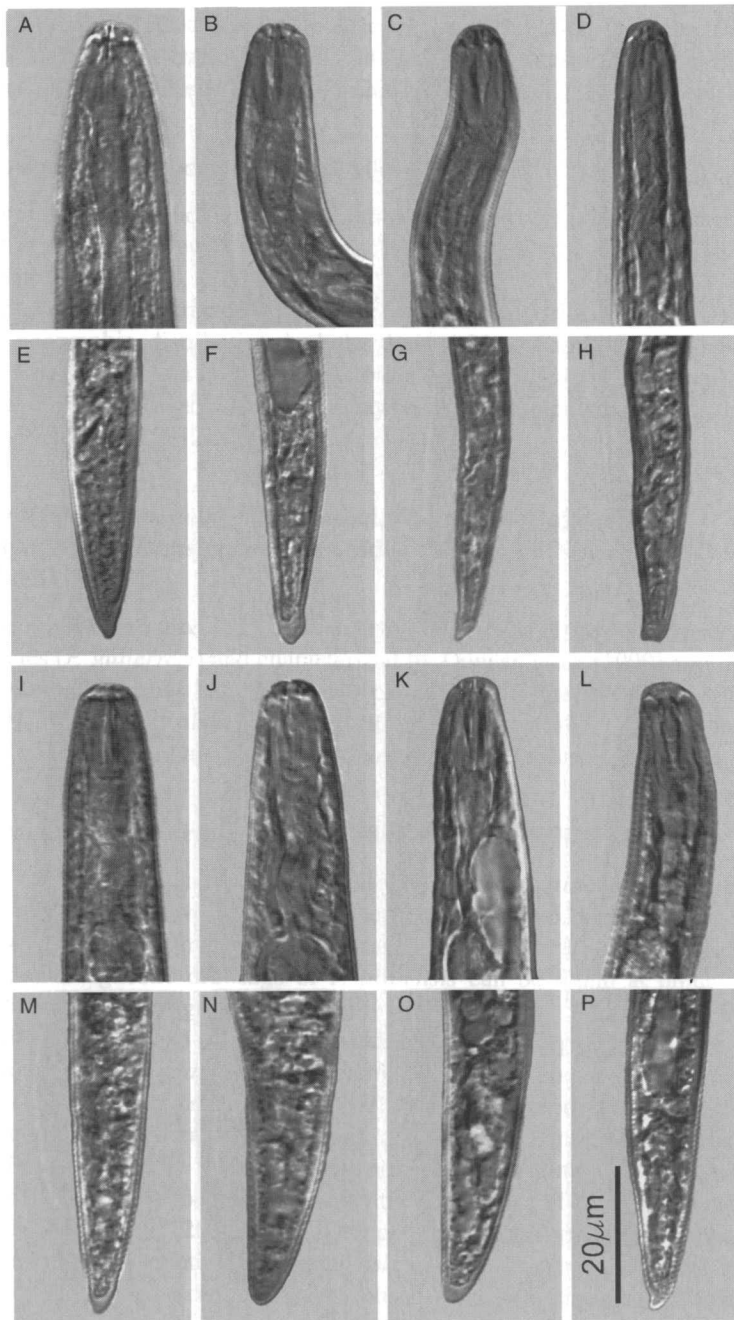
According to Whitehead (1968), Somasekhar (1959) had reported this species on coffee in south India. *P. pratensis* has been mistaken for *P. crenatus* Loof, *P. penetrans*, *P. brachyurus*, *P. coffeae* and possibly *P. loosi* (Loof, 1960; 1974). The coffee-parasitic status of *P. pratensis* is uncertain also because nematode identification could not be confirmed by voucher slides, nor was the original coffee population examined with molecular methods. However the occurrence of the related *P. vulnus* on coffee (Monteiro et al., 2001) gives some plausibility to Somasekhar's report.

The geographic distribution of *P. pratensis* on various crops includes Europe, South Africa and India (Loof, 1974). A consensus of opinion suggests that this species does not occur in the Americas (Norton et al., 1984), but it is fairly common in Europe (Peña et al., 2007). However, the morphologically similar species *P. pratensisobrinus* Bernard occurs in Alaska (Bernard, 1984) and *P. pseudo-pratensis* Seinhorst in Konza Prairie, eastern Kansas (USA) (Powers, 2008). This



**Fig. 3.3** Photomicrographs of female heads and tails, showing variations in tail shape. (A–H) *P. panamaensis*, (I–P) *P. pratensis*. (Photos by Z. A. Handoo)





**Fig. 3.4** Photomicrographs of female heads and tails, showing variations in tail shape. (A–H) *P. vulnus*, (I–P): *P. zeae*. (Photos by Z. A. Handoo)

issue will not be satisfactorily resolved until molecular sequences are available for *P. pratensis*-like taxa.

### 3.2.2.7 *Pratylenchus vulnus* Allen and Jensen, 1951

The taxonomy and morphological variations in *P. vulnus* populations (Fig. 3.4 A–H) have been described in several reviews (Corbett, 1974; Doucet et al., 1996; 1998; 2001; Gao et al., 1999). This species has been recently discovered on coffee in Brazil (Monteiro et al., 2001). It has also been found on other crops in Southern Europe, Russia, Egypt, South Africa, India, Japan, China, Philippines, New Zealand, USA, Mexico, Cuba and Argentina (Corbett, 1974; Gao et al., 1999; Lax et al., 2004).

### 3.2.2.8 *Pratylenchus zaeae* Graham, 1951

The taxonomy and morphological variation of *P. zaeae* (Fig. 3.4 I–P) have been described in various papers in the more than 50 years since it was described (Roman and Hirschmann, 1969; Fortuner, 1976; Olowe and Corbett, 1983, 1984a,b; Troccoli et al., 1996; Inerra et al., 2005a).

This species occurs on coffee in Brazil (Ferraz, 1980; Campos, 2002) and Colombia (in USDA Nematode Collection, entry #4686). It is also distributed on other crops worldwide in USA, Cuba, Trinidad, Venezuela, Brazil, throughout Africa, Madagascar, Egypt, Iraq, India, Japan, Australia (Fortuner, 1976) and in Indonesia (in USDA Nematode Collection, entry #2356).

## 3.2.3 Key to Coffee-Associated *Pratylenchus* Species

- 1 Lip region composed of 2 annules (rarely three) ..... 2
- 1a Lip region composed of 3–4 annules ..... 5
- 2(1) Tail terminus smooth ..... 3
- 2a Tail terminus annulated or indented ..... *P. panamaensis* (= *P. gutierrezii*)
- 3(2) Lip region low, with outer margins angular; stylet typically 19–22  $\mu\text{m}$  long (in Loof (1960) range is 17–22, but 17 very rare) with massive rounded knobs; V% = 82–89; tail subcylindrical, with truncate to subhemispherical or broadly rounded terminus; males rare. .... *P. brachyurus*
- 3a Lip region high, roundly convex; stylet less than 18  $\mu\text{m}$  long, V% = 76–85; tail narrowly rounded to subacute with hemispherical to bluntly pointed, truncate smooth terminus ..... 4
- 4(3a) V% = 78(76–82); a = 25(21–30); tail terminus truncate or broadly rounded, occasionally indented ..... *P. coffeae*
- 4a V% = 82(79–85); a = 32(28–36); tail terminus narrowly rounded to subacute ..... *P. loosi*

- 5(1a) Tail terminus smooth ..... 6  
 5a Tail terminus annulated; stylet 12–16  $\mu\text{m}$  long; lip region with three annules; V% = 76–80; tail subcylindrical with obtuse to rounded asymmetrical annulated terminus ..... *P. pratensis*
- 6(5) V% = 66–76..... 7  
 6a V% = 78 – 84; body slender, a = 25–40; spermatheca oval, oblong filled with sperm, posterior uterine sac long, tail terminus bluntly pointed to narrowly rounded; males common ..... *P. vulnus*
- 7(6) Lip region low with 3 annules; stylet 15–17  $\mu\text{m}$  long with broad, anteriorly flattened knobs, tail terminus narrowly rounded to subacute; males extremely rare ..... *P. zeae*  
 7a Lip region high with 4 annules; stylet 16–17  $\mu\text{m}$  long with rounded flattened knobs; tail sharply conical with dorsal tail contour characteristically sinuate anterior to terminus; tail terminus with a small terminal peg; males common ..... *P. goodeyi*

### 3.3 Phylogenetic Trees and Molecular Characterization

Based on morphological data, Ryss (2002a,b) have presented multi-entry and mono-entry keys and diagnostic relationships within *Pratylenchus* sp., along with proposals for phylogeny and evolution of this genus. Also, a morphological tree for a somewhat different set of taxa has been constructed using cladistic methods (Carta et al., 2002). Not surprisingly, these morphological frameworks are often inconsistent with some molecular phylogenetic trees inferred from 28S rDNA sequences (Al-Banna et al., 1997; Duncan et al., 1999; Carta et al., 2001; De Luca et al., 2004). This is partly due to a more limited and different set of species used in the molecular studies, and also due to selection of outgroups, which can have a major impact on branching order (Carta et al., 2001).

The first phylogenetic study of some *Pratylenchus* species with *Radopholus* sp., *Hirschmanniella* sp. and *Nacobbus* sp. demonstrated a polyphyletic tree using the D3 segment of rDNA (Al-Banna et al., 1997). A second study on the *P. coffeae* species complex subdivided and defined many populations into genetic units using both D2 and D3 rDNA regions (Duncan et al., 1999). A study conducted using more *Pratylenchus* species and different outgroups has restored *Pratylenchus* monophyly (Carta et al., 2001). An analysis of sequences of multiple individuals of one or more populations of *P. thornei* Sher and Allen, *P. neglectus* (Rensch) Filipjev and Schuurmans Stekhoven, *P. mediterraneus* Corbett, *P. pinguicaudatus* Corbet and *P. vulnus* has demonstrated high variability among individuals of *P. neglectus* (De Luca et al., 2004). A different assemblage of taxa using variously coded morphological characters has been used to construct trees (Ryss, 2002b; Carta et al., 2002) with different topologies from molecular trees; these differences cannot simply be attributed to differences in species composition.



While the number of sequences and taxa used for testing hypotheses of relationships within the genus *Pratylenchus* has grown through the last decade, it is clear that molecular trees will continue to require expansion, clarification and eventual integration with morphological data.

Molecular methods are often essential to confirm species identity, as with the discovery of *P. jaehni* Inserra, Duncan, Troccoli, Dunn, Santos, Kaplan and Vovlas, which has been revealed from a 28S rDNA phylogeny (Duncan et al., 1999; Inserra et al., 2001). While straightforward PCR-RFLP diagnostics are available for some coffee-parasitic *Pratylenchus* species (Pourjame et al., 1999), many such tests have not been validated with multiple populations or related species. Obtaining the DNA controls necessary for this standardization may also present a challenge, as some species may be difficult to obtain or require labor-intensive culture methods to maintain. Nevertheless, when characterizing potentially new or economically important populations, the generation of gene sequences for comparison with those in GenBank® is highly recommended.

To construct a phylogenetic tree of the coffee-associated *Pratylenchus* spp., 28S and 18S rDNA sequences have been obtained either from GenBank® or our own unpublished data. For the 28S rDNA D2-D3 region these include the following species and GenBank® accession numbers: *P. panamaensis* (= syn. *P. gutierrezii*) isolate K1, AF170440; *P. loosi* isolate N1, AF170437; *P. coffeae* isolate M1, AF170435; *P. zaeae*, AF303950; unpublished sequence for peanut-parasitic *P. brachyurus* NL8 isolate from Florida; *Radopholus similis* (Cobb) Thorne, outgroup D3, U47558. ClustalW alignments (Thompson et al., 1994) have been made for sequences of 28S D2-D3 rDNA from the five *Pratylenchus* species from coffee listed previously plus two species from other hosts (*P. hexincisus* Taylor and Jenkins, AF303949 and *P. pseudocoffeae* Mizukubo, AF170444) plus two outgroups: *Meloidogyne exigua* Göldi, AF435804 and *Hirschmanniella pomponiensis* Abdel-Rahman and Maggenti, DQ077795.

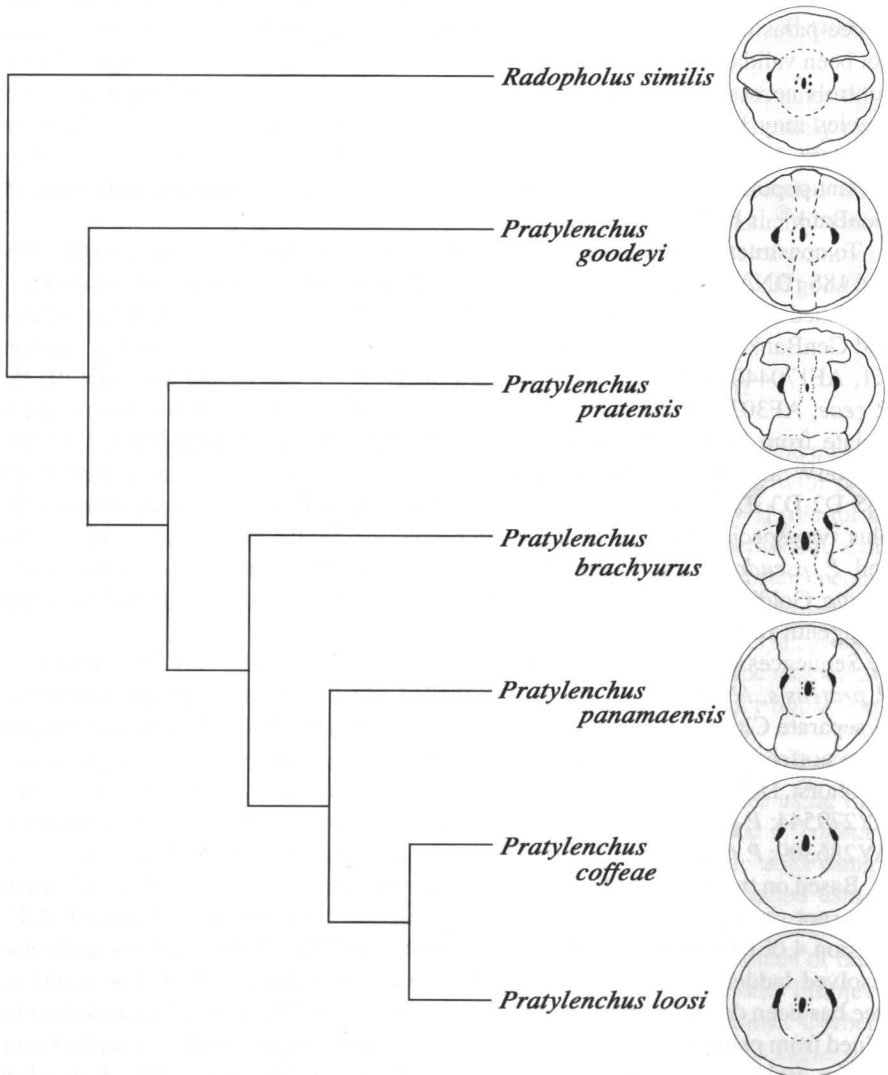
Sequences for 18S rDNA include: *P. brachyurus*, AY279545; *P. goodeyi*, AJ966498; *P. pratensis*, AY284611; *P. vulnus*, AY286311 and *R. similis*, outgroup, AJ966502. A separate ClustalW alignment has been made for 18S rDNA of these five species from coffee, plus seven from other hosts: *P. crenatus*, AY284610; *P. cf. flakkensis* Seinhorst, DQ080595 (species unconfirmed); *P. hexincisus*, AY919242; *P. neglectus*, AY279544; *P. penetrans*, AY286308; *P. scribneri* Steiner in Sherbakoff and Stanley, AY286309; *P. thornei*, AJ966499, plus one outgroup (*R. similis*, AJ966502).

Based on the branch order in the two corresponding rDNA trees with overlapping taxa (not shown), a single synthetic composite has been constructed using PAUP\* version 4.0b10 (Swofford, 1998), with parenthetical NEXUS tree format as an unresolved ladder-like topology in TreeView ver. 1.6.6 (Page, 1996). The resulting tree has been decorated with face views drawn from SEM images of nematodes obtained from published literature: *R. similis* (Sher and Bell, 1975), *R. neosimilis* Sauer (Sauer, 1985), *P. zaeae* (Baujard et al., 1990; López and Salazar, 1990), *P. goodeyi* (Corbett and Clark, 1983; Hernández et al., 2001), *P. vulnus* (Corbett and Clark, 1983; Sauer, 1985; Hernández et al., 2001), *P. pratensis* (Corbett and Clark, 1983), *P. brachyurus* (Corbett and Clark, 1983; Baujard et al., 1990; López and Salazar,



1990), *P. gutierrezii* (Golden et al., 1992; Inserra et al., 1998; Duncan et al., 1999), *P. loosi* (Corbett and Clark, 1983; Baujard et al., 1990; Duncan et al., 1999; Pourjame et al., 1999; Inserra et al., 2001) and *P. coffeae* (Corbett and Clark, 1983; Inserra et al., 1998; Duncan et al., 1999; Inserra et al., 2001).

The schematic phylogenetic tree of coffee-associated nematodes, including drawings based upon SEM face views, is shown in Fig. 3.5. Compared to a previous



**Fig. 3.5** Synthetic composite tree of six root-lesion nematode species derived from 28S rDNA and 18S rDNA trees with overlapping taxa, based on branch order and constructed with PAUP and TreeView. Scanning electron microscopic face views were drawn from the literature

molecular tree based solely on the D3 region of the 28S rDNA (Carta et al., 2001), the phylogenetic position of *P. brachyurus* inferred from the composite tree is more distant from *P. coffeae* and relatives than before. This updated position for *P. brachyurus* is more in line with the phylogenetic tree position based on morphology (Ryss, 2002b). In addition, *P. pratensis* and *P. coffeae* also appear highly divergent in the synthetic tree, unlike their position within the same clade in the morphological tree (Ryss, 2002b). The topology of the tree in Fig. 3.5 is congruent with the one shown in the most recent molecular phylogeny of this group (Inserra et al., 2007).

### 3.4 Concluding Remarks

Integrated studies on the morphological variation of *Pratylenchus* populations combined with molecular sequencing should result in improved methods of species delimitation. Of particular concern is the presence in the literature of nematode SEM face images that are sometimes variable and of poor quality, in part due to the use of formalin-fixed and dried specimens. This problem could be solved through more widespread application of low temperature-SEM (LT-SEM), a technique that reveals morphological features undistorted by chemicals and drying under pressure (Carta et al., 2003). Rapid cryo-fixation has revealed distinguishing features in root-lesion nematode faces even to the subspecies level (Carta et al., 2002). Determination of the number of lip annules is another serious problem, especially when few specimens are available for examination. This situation may improve through the use of new microscopic technology, such as the modular, high-resolution CytoViva® condenser (CytoViva Inc., Auburn, USA), with a cardioid annular ring that can achieve more than twice the resolution of standard circular condensers (Vainrub et al., 2006).

Increases in speed and capability and decreases in cost should lead to more frequent use of DNA sequencing by diagnostic labs for routine or selective species verification. Rapid new pyrosequencing technology, which generates short fragments (Shendure et al., 2004), may drive the development of rapid new diagnostics which are based upon short DNA fragments from multiple molecular markers.

Comparative pathogenicity studies have not been conducted for most coffee-parasitic root-lesion nematodes (Campos and Villain, 2005). Such studies would be highly desirable to assist in pest management decisions after a nematode species has been identified in a field. Systematic comparisons among species parasitizing either *C. arabica* L. (a commodity representing about 75% of world coffee exports, mostly in South and Central America) or the easier grown *C. canephora* Pierre ex Froehner (about 25% of exports, mostly grown in Africa and Asia) (Anonymous, 1986; Campos and Villain, 2005), would be especially valuable.

A concerted international research effort to centralize collection, preservation and molecular analysis of specimens, with satellite locations to perform morphology and pathogenicity studies, could greatly advance effective crop management of coffee-parasitic *Pratylenchus* species.

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