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Pratylenchus quasitereoides n. sp. from cereals in Western Australia

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Abstract

Pratylenchus quasitereoides **n. sp.** is described from Western Australia. It is characterized by 2 external incisures in the head cuticle, 4 lateral incisures at mid body, stylet length 17 µm to 19 µm, *V* greater than 75%, PUS less than 2 body diameters long and crenate tail terminus. Molecular data confirm the separation of the new species from morphologically similar and sympatric congeners. The host range also differs from *P. teres* as well as the sympatric *P. neglectus*, *P. thornei* and *P. penetrans*. Reproduction rates on oat and lupin differed between the new species and *P. neglectus*. The species was originally described as *P. teres*, but the species concept of *P. teres* now encompasses a considerable range of different attributes spread over two described subspecies and three variant populations. The new species differs from all these subspecies and populations in at least two characters. It differs from all populations of *P. teres teres* most notably in having four rather than 6 lateral lines and a more posterior vulva. It differs from *P. teres vandebergae* in having a longer stylet and longer overlap of the intestine by the oesophageal glands. Characters which can be used under low magnification to separate the new species from the closest sympatric congeners (*P. thornei* and *P. crenatus*) are discussed.

Key words: 28S, *Avena sativa*, cereal, D3, host, lupin, *Lupinus angustifolius*, molecular biology, morphology, oat, *P. teres*, *P. neglectus*, *P. thornei*, reproduction rate, Root Lesion Nematode, rRNA, taxonomy

Introduction

Recently, *Pratylenchus teres* Khan and Singh 1974 was redescribed from Western Australia (Riley & Wouts 2001), having been originally described from Punjab, India. It was also redescribed from the Caribbean and South Africa at about the same time as Western Australia (Carta *et al.* 2002; van den Berg & Queneherve, 2000). Since the original find in Western Australia, many additional specimens have been located which allow a better evaluation of the variability in characteristics among the Western Australian populations relative to the variability in the *P. teres* found elsewhere. They have also given better understanding of the differences between the Western Australian populations and the *P. teres* found elsewhere. These differences are sufficient to differentiate the Western Australian population as a new species, which is described herein as *Pratylenchus quasitereoides* n.sp. Phylogenetic analyses of 28S rRNA also suggest the new species is separate from *P. teres* and other morphologically-similar congeners, as well as sympatric congeners. There are also differences between the new species and others in host relationships.

Material & methods

Specimens of the new species were obtained from several collections between 1998 and 1999, including the first

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collection from which *P. teres* was identified in West Australia. All were extracted by Whitehead Tray (Whitehead & Hemming 1965), heat killed, fixed using FA4:1 (Hooper 1986a), and transferred to anhydrous glycerol by the glycerol-ethanol method (Seinhorst 1959). Body structures were measured along the midline using a Zeiss Axioskop compound microscope with Differential Interference Contrast (DIC) or Phase Contrast (for hard structures such as the stylet). To measure straight structures up to 50 µm, an ocular graticule at x1000 magnification was used, or, for curved structures and those more than 50 µm, a map-measuring wheel was used on a camera lucida drawing at the magnification which fitted the structure into a single field of view. Abbreviations for morphometric indices not defined explicitly follow Hooper (1986b). Where indices use diameters, the maximum diameter of the portion of the body around a structure is used unless explicitly stated otherwise.

DNA was prepared by cutting a single nematode in distilled water with a heat-sterilized fine needle, then transferring the nematode immediately into a microcentrifige tube containing 10 µl of Worm Lysis Buffer (10mM Tris-HCl pH8.3, 50 mM KCl, 2.5mM $MgCl_2$, 0.45% Tween 20, 0.45% NP40, 0.01% gelatin , 60 µg ml^{-1} proteinase K). The tube was then immersed in liquid N for 2 minutes, heated to 65°C for 10 minutes, boiled for 10 minutes, and finally placed on ice while 2–8 µl of DNA suspension was removed using a micropipette. The primers of Nunn *et al.* (1996) (5'-GACCCGTCTTGAAACACGGA-3' and 5'-TCGGAAGGAACCAGCTACTA-3') were used to sequence a portion of the D3 subunit of 28S rRNA, the region most used in the diagnosis of species in the genus *Pratylenchus* (Palomares-Rius *et al.* 2010, Subbotin *et al.* 2008, Taheri *et al.* 2013). DNA was amplified in a 50 µl reaction volume containing 10 mM Tris pH8.4, 50 mM KCl, 1.5mM $MgCl_2$, 0.05% Tween 20, 0.05% NP40, 0.4µM of each primer, 25 µM each of dATP, dCTP, dGPT and dTTP. The mix was heated to 94°C for 5 minutes, then 2.5 U of *Taq* polymerase was added, followed by 35 cycles of 94°C for 1 minute, 55°C for 90 seconds, and 72°C for 75 seconds.

Ten sequences for the new species were obtained from specimens from five locations within Western Australia and South Australlia. Sequence data for comparison were obtained by searching the GenBank database for the same portion of rRNA for all the species of *Pratylenchus* known to occur in Western Australia (Riley & Wouts 2001), and for the closest morphological species, *Pratylenchus teres*: a total of 29 sequences from 8 species. A sequence from *Zygotylenchus guevari* (Tobar-Jimenez 1963) Braun & Loof 1966 was used as an outgroup because this species was the closest species in another genus from the subfamily Pratylenchidae that had a sequence from the same region available. GenBank identifiers for the all sequences used are listed in Figure 2.

Sequence analysis was by MEGA 5.2.1 (Tamura *et al.* 2011). Alignments were by ClustalW (Thompson *et al.* 1994) using the default parameters. Evolutionary history was inferred from cladograms constructed using four combinations of clustering algorithms and evolutionary distance metrics:

- Neighbour-Joining (Saitou & Nei 1987) using number of differences (Nei & Kumar 2000) (*NJ-ND*);
- Neighbour-Joining (Saitou & Nei 1987) using maximum composite likelihoods (Tamura *et al.* 2004) (*NJ-MCL*);
- Minimum Evolution (Rzhetsky & Nei 1992) using the Close-Neighbour Interchange algorithm (Nei & Kumar 2000) at search level 1 and an initial tree generated using Neighbour Joining (*ME*); and
- Maximum Likelihood based on the Tamura-Nei model (Tamura & Nei 1993) with the initial tree for the heuristic search obtained automatically by applying Neighbour-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood approach, then selecting the topology with the superior log-likelihood value (*ML*).

All trees were consensus trees inferred from 1000 bootstrap replicates (Felsenstein 1985).

The bionomics of the new species were compared experimentally with those of the morphologically most similar sympatric described congeners: *P. neglectus* (Rensch 1924) Filipjev & Schuurmans Stekhoven 1941; *P. thornei* Sher & Allen 1953; and *P. penetrans* (Cobb 1917) Filipjev & Schuurmans Stekhoven 1941 (Collins *et al.* 2013, Vanstone 2007). Bionomic data for the morphologically most similar allopatric congener *P. teres* was obtained from the literature (Cadet *et al*., 1994; Carta *et al*., 2002; Khan & Singh, 1974; van den Berg & Queneherve, 2000).

Multiplication rates on lupins and oats for *P. quasitereoides* **n. sp.** and *P. neglectus* were compared using ratios of initial to final nematode populations from 36 field trial sites across the cropping region of Western Australia in the Crop Variety Testing, Cereal and Pulse Breeding Programs of the Department of Agriculture Western Australia

(Department of Agriculture Western Australia 2005). Samples of soil of approximately 200 g were taken with a trowel at sowing (May-June) and in mid spring (September-October) and returned to a central laboratory for processing. Nematodes were extracted using a mister (Hooper, 1986a) and the relevant species were counted under x50 magnification. Multiplication factors were calculated as final population divided by initial population, and ratios less than one were regarded as non-hosts.

Systematics

Pratylenchus quasitereoides n. sp.

(Table 1, Fig. 1)

Measurements and morphometrics of the holotype female and paratypes are presented in Table 1.

Adult female: Body vermiform, tapering to anterior and posterior ends, maximum diameter at about oesophago-intestinal junction, with slight reduction in diameter near vulva.

Cuticle thin (about 0.5–1.0 µm), with external transverse striae spaced about 1 µm apart, lacking internal transverse striae, radial striation, punctation and longitudinal markings. Lateral field conspicuous, with three incisures from posterior end of stylet to about level of median oesophageal bulb, four incisures over most of body then two incisures at the phasmids; outer incisures straight, inner incisures straight and continuous; inner field without markings; outer fields of equal width to inner. Cuticular pores absent. Anterior cephalid just anterior to junction of conus and shaft, posterior cephalid just anterior to posterior end of shaft. Excretory pore just anterior to nerve ring, duct prominent, sclerotized. Hemizonid visible anterior to excretory pore, in similar longitudinal position to oesophago-intestinal junction. Hemizonion just posterior to excretory pore.

Head 8 µm long (0.28 times head diameter), tapering little anteriorly, flat, angular, not dorsoventrally flattened, lacking longitudinal division, consisting of three annules of which the middle is widest. A shallow, rounded constriction about 0.5 µm deep located behind head, 2–2.5 µm from anterior extremity. Cephalic framework thick, sclerotized, extending anteriorly to anterior-most annule. Stoma very thin walled, with stylet. Stylet 18–19 µm long, straight. Conus and shaft lengths equal. Knobs at posterior of shaft large, rounded, with anterior face at slightly obtuse angle to shaft (105–115°), posterior face at slightly greater angle to shaft (120–130°), creating indentation at posterior end of stylet.

Dorsal oesophageal gland orifice 3–4 µm from posterior end of stylet. Median expansion of oesophagus spindle-shaped, diameter 11 µm (50–60% of body diameter), with sclerotized hemispheroid valves of diameter about 3 µm (20–30% of the oesophagus diameter), located 55–61 µm from anterior of body (65–85% of the distance to the oesophago-intestinal junction). Oesophageal glands large, free in body cavity, offset to ventral side, with three nuclei, dorsal cell and nucleus larger than subventrals. Circumoesophageal nerve ring located 15–20 µm behind valves (80–90% of distance between anterior of body and oesophago-intestinal junction). Intestinal fasciculi absent. Anus clearly visible. Post-anal sac absent.

Anterior genital branch outstretched, located ventrally to the intestine, spermatheca not strongly differentiated, round, without constrictions, without sperm. Posterior genital branch short, 0.5–1.8 body diameters long, consisting of uterine sac and a small amount of incomplete or non-functional ovarial tissue. Vulva without cuticular thickening, indented from a small protuberance on the ventral body surface. Vaginal cuticle thickened, sclerotized over most of length, smooth, directed radially, lumen narrow over entire length.

Tail cylindroid-ellipsoid, tapering very little in anterior half, more rapidly in posterior half, slightly concave ventrally, with slightly thickened cuticle on posterior surface only, with 20 to 28 external transverse striae extending around the rounded terminus. Phasmids pore-like, located nearly opposite each other, posterior to anus, in middle of lateral field.

Adult male: Not found.

Juvenile: Similar to adult female but lacking reproductive structures.

Type locality and host. Katanning, Western Australia (33°17'S 117°35'E), cultivated wheat (*Triticum aestivum* L.). Collectors: I Riley & S Kelly. Collected on 01 October 1998.

Type designations. Holotype adult female: specimen no 89, Australian National Insect Collection Nematode Collection, Canberra, Australia. Paratypes: 16 adult females: specimen nos 90-105, ANIC Nematode Collection, Canberra, Australia.

TABLE 1. Measurements and morphometric indices for *Pratylenchus quasitereoides* **n. sp.**

Measure [a] or morphometric index [b]	holotype	Paratypes mean	Paratypes S.D.	Paratypes Minimum	Paratypes Maximum
N	1	16	16		
total body length	605	656	50.9	569	741
maximum diameter	19	23	2.4	19	27
stylet L	19	18	0.6	17	19
stylet base to dorsal oesophageal gland orifice	3	3	0.3	3	4
anterior of body to anterior of median oesophageal bulb	61	59	2.3	55	62
anterior of body to median oesophageal valve	71	65	3	59	70
anterior of body to nerve ring	79	75	2	70	78
oesophageal gland lobe length	68	64	7	48	71
anterior genital branch length	140	175	20	147	232
posterior genital branch length	34	21	10	10	41
vagina length	7.5	7.0	1.4	6.0	10.0
tail length	37	35	4	27	43
number of tail annules	28	25	2	22	28
body diameter at anus	12	15	1.2	12	16
distance of right phasmid posterior to anus	19	18	3.6	14	25
distance of left phasmid posterior to anus	16	18	3.1	14	25
a	31.2	28.7	3.6	22.8	39.4
a’	29.3	27.2	3.5	21.7	37.5
b	7.0	7.3	0.7	6.3	8.7
b’	6.5	7.0	1.5	4.9	10.1
c	16.2	18.8	2.1	15.9	22.5
c’	3.1	2.3	0.3	2.0	3.1
V	76	78	1.9	75.0	82
V’	80.6	82.5	1.8	80.0	86.6
p	3.0	3.1	0.4	2.6	4.0
lateral field width / body diameter	0.27	0.26	0.04	0.20	0.34
head length / diameter	0.28	0.22	0.02	0.18	0.25
stylet L / head diameter	2.34	1.95	0.22	1.55	2.25
median oesophageal bulb diameter / body diameter	0.61	0.57	0.04	0.50	0.65
valve diameter / median oesophageal bulb diameter	0.24	0.28	0.02	0.25	0.30
anterior of body to nerve ring / anterior of body to oesophago-intestinal junction	0.91	0.83	0.03	0.78	0.88
posterior genital branch length / body diameter at vulva	1.9	1.1	0.5	0.4	2.0
vagina length / body diam	0.42	0.32	0.14	0.00	0.51
spermatheca length / spermatheca diameter	1.2	1.0	0.2	0.6	1.3
rectum length / anal diameter	1.0	1.1	0.3	0.6	1.5
tail taper anterior half [c]	0.27	0.24	0.04	0.28	0.17
tail taper posterior quarter [d]	0.56	0.60	0.05	0.50	0.67

[a]—in µm. [b]—abbreviations follow Hooper (1986b). [c]—diam at 50% tail length / diam at anus. [d]—diam at 75% tail length / diam at anus.

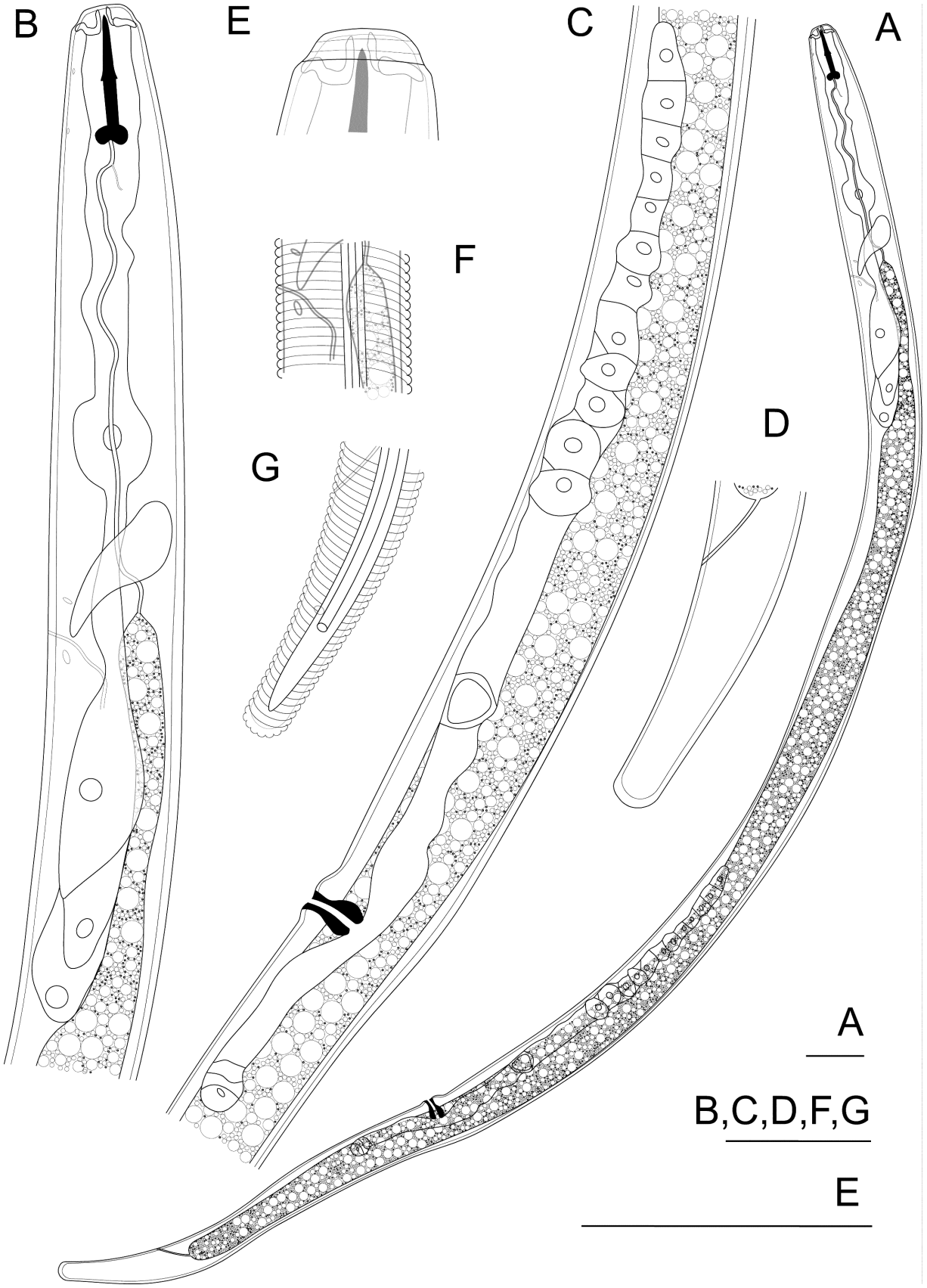

FIGURE 1. *Pratylenchus quasitereoides* **n. sp.** adult female. A—whole body, B—head and oesophagus (median focus), C—reproductive system, D—tail, E—head surface, F—body surface at oesophago-intestinal junction, G—tail surface. Scale bars represent 20 µm.

TABLE 2. Tabular compendium of diagnostic features of *P. quasitereoides* n. sp. differing from other species or species populations from the genus *Pratylenchus*. Only species differing from *P. quasitereoides* in less than 4 primary characters are listed[a].

species or population	head incisures	Stylet length [b]	lateral incisures	V	PUS length [b]	Tail terminus	Other differences[c]
P. quasitereoides	3	17–19	4	75–82	0.5–1.8	annulated	
P. teres sensu Loof (1992)	3	16–18	6	69–78	1	annulated	
P. teres Amritsar pop (Khan and Singh, 1974)	3	16–18	6	69–78	1.1–1.4[d]	annulated	
P. flakkensis	2	17	4	73–77	1.3–1.6	annulated	SF,OG
P. fallax	3	16–17	4	77–81	0.9–1.6	annulated	SF,OG
P. pratensis	3	12–16	4	76–80	>1	annulated	SF,OG,SL
P. convallariae	3	16–17	4	76–81	1.4–2.0	annulated	SF,OG,TA
P. crenatus	3	14–18	6	78–86	1.0–2.0	annulated	OG
P. yassini	3	16–19	4	71–76	1.5–2.5	annulated	SL,LLC
P. kasari	3	16–18	4	75–81	1.8–2.3[e]	annulated	SF,SL,LLC
P. morettoi	3–4	14–19	4	73–80	>2.5	annulated	SF,OG,TA
P. thornei	3	15–19	4	74–79	1.5	smooth	SF
P. pinguicaudatus	3	16–20	4	78–81	<1	smooth	LLC
P. andinus	3	15–18	4	78–85	1.3–1.5	smooth	LLC,TA
P. delattrei	3	16–18	4	73–81	1.2–1.4	smooth	OG
P. alleni	2	13–15		77–84	1–3	smooth –annulated	SF
P. loosi	2	14–18		79–85	0.8–1.3	smooth	SF
P. wescolagricus	4	17–20		78–82	1	smooth	

……*continued on the next page*

TABLE 2. (Continued)

species or population	head incisures	Stylet length [b]	lateral incisures	V	PUS length [b]	Tail terminus	Other differences[c]
P. coffeae	2	14–19		76–84	0.8–4	smooth	SF
P. agilis	2	16–18	4	76	1.0–1.4	smooth	
P. pratensisobrinus	3	15–17	4	75–80	1.6–2.7	annulated	SF,TA
P. teres vandenbergae	3–4	15–16	4	71–77	1.3–1.9	annulated	OG,LLC
P. subpenetrans	3	15–17	4	77–83	1.5	smooth	SF
P. ventroprojectus	3	14–16		78–80	0.9–1.8	smooth – annulated	SF,SL
P. ekrami	3	11–13		77–83	>1	smooth	SF
P. mediterraneus	3	14–16		77–80		smooth	SF
P. pseudopratensis	3–4	15		76–80		smooth	SF
P. cruciferus	3	15–16	4	76–81	0.7–1.4	smooth	
P. sensillatus	3	15–17	4	77–81	>1	smooth	
P. sefaensis	3	13–16	4	77–81		smooth	
P. australis	3	18–20		77–83		smooth	
P. teres Solan pop (Khan and Singh, 1974)	3	17–18	6	72–75		annulated	OG
P. teres type (Ludhiana) pop (Khan and Singh, 1974)	3	17–18	6	70–77	1–1.2	annulated	
P. mulchandi	3	16–20	4	75–78		smooth	
P. vulnus	3–4	13–19	4	77–82	1.5–4.5	smooth	SF,SL
P. bolivianus	3	17–20	4	77–83	>2.5	smooth	OG

[a] shaded cells represent differences from *P. quasitereoides* n. sp.; [b] in µm; [c] SF=spermatheca full (of sperm), males common; OG=length of oesophageal gland overlap of intestine; SL=spermatheca length relative to diameter; TA=number of tail annules; LLC=lateral lines crenate; [d] calculated from diagram in original description; [e] <1.8 in Loof (1992), 1.8 in Ryss (1982: original description), 2.0–2.3 in Ryss (2002)

Diagnosis. *Pratylenchus quasitereoides* **n. sp.** is characterized by having three annules (two external incisures) in the head cuticle, four lateral incisures at mid body, stylet 17–19 µm long, morphometric index *V* greater than 75%, PUS less than 2 body diameters long and tail terminus crenate.

Morphological relationships. *P. quasitereoides* **n. sp.** differs from all other species in the genus by at least two morphological characters, except for the Amritsar population of *P. teres* (as documented by Khan and Singh 1974) and Loof's (1992) concept of *P. teres* (Table 2). The main difference between *P. quasitereoides* **n. sp.** and these taxa is that *P. quasitereoides* **n. sp.** has 4 rather than 6 lateral lines. *P. quasitereoides* **n. sp.** differs from the Amritsar population of *P. teres* in the following characteristics additional to those presented in Table 2:

- mean position of vulva relative to total body length (morphometric index *V* = 78 for *P. quasitereoides* **n. sp.** *vs* V = 70 for the Amritsar population of *P. teres*); and
- mean body length (L = 656 µm for *P. quasitereoides* **n. sp.** *vs* L = 550 µm for the Amritsar population of *P. teres*).

There is some small overlap in the ranges of the two characters, but the differences are based on 16 and 17 adult female specimens of the two species, so there is a high probability that the differences are real, particularly in the case of the morphometric index *V* (Geraert 1968).

The species concept of *P. teres* implicit in the key of Loof (1992) encompasses a very broad range of characteristics. Not all characters were used in the key, so additional differences between the species concepts may exist, most notably in the mean position of the vulva and body size. The species concept of *P. teres* was further expanded by Carta *et al.* (2002). The biological basis for such gradual expansion of species definitions and its implications for the taxonomy of the genus *Pratylenchus* will be discussed at length in a forthcoming publication. More general considerations of the relationships between morphological, biological, genetic and ecological species concepts in nematodes will also be discussed elsewhere.

For identification at low magnifications, two species may be confused with *P. quasitereoides* **n. sp.**: *P. thornei* has the ventral side of the body indented between the vulva and anus, a longer PUS and a wider tail than *P. quasitereoides* **n. sp.**; *P. crenatus* is generally smaller (although there is some overlap), has a shorter oesophageal gland lobe, and a longer PUS. *Pratylenchus quasitereoides* **n. sp.** shares a very prominent excretory pore with *P. crenatus* (Karssen & Bolk 2000).

Molecular relationships. Cladistic analyses of the sequences for *P. quasitereoides* **n. sp.** and 29 sequences from nine other species in the genus for which the same section of the genome was available used 180 positions in the final data set. All species were in separate, well-supported clades (Fig. 2). Identical consensus tree topologies were obtained from all methods, with support levels for the species clades only differing slightly (86–100% for *NJ-ND*, 80–100% for *NJ-CML*, 75–99% for *ML*, and 86–100% for *ME*).

To put the genetic differences in context, *P. quasitereoides* n.sp. differed by 0–10 bp among 4 populations, which was similar to the differences among 8 populations of *P. thornei* and slightly less than the differences among 5 populations of *P. penetrans* (0–12 bp). Similar variation in this gene region has been observed in other species of *Pratylenchus* (Hodda pers. comm.).

Ecological relationships. *P. quasitereoides* **n. sp.** has been found in Western Australia from Carnamah (29°41'S 115°53'E) to Tambellup (34°02'S 117°38'E) (Collins *et al.* 2013, Riley & Kelly 2002, Riley & Wouts 2001, Vanstone 2007), as well as in South Australia (J. Nobbs, SARDI, personal communication). All populations recorded previously as *P. teres* in Western Australia seem to be the new species *P. quasitereoides*. No known specimens from Western Australia or anywhere else in Australia should be called '*P. teres'* now that *P. quasitereoides* **n. sp.** has been described. *P. teres* has been found in widely separated locations elsewhere in the world (Carta *et al.* 2002, Khan & Singh 1974; van den Berg & Queneherve, 2000).

No endemic species in the genus *Pratylenchus* are known in Australia other than *P. quasitereoides* n.sp (Hodda & Nobbs 2008). The genus *Pratylenchus* contains a few apparently widespread species and many species with geographic distributions apparently restricted to various small regions of the world (Ryss 2002, Siddiqi 2000). The restricted distribution is not unusual.

P. quasitereoides **n. sp.** has been found on wheat (*Triticum aestivum* L.), oat (*Avena sativa* L.), barley (*Hordeum vulgare* L.), chickpea (*Cicer arietinum* L.), lupin (*Lupinus angustifolius* L.) and canola (*Brassica napus* L.) (Collins *et al.* 2013, Riley & Kelly 2002, Riley & Wouts 2001, Vanstone 2007). By contrast, *P. teres* has never

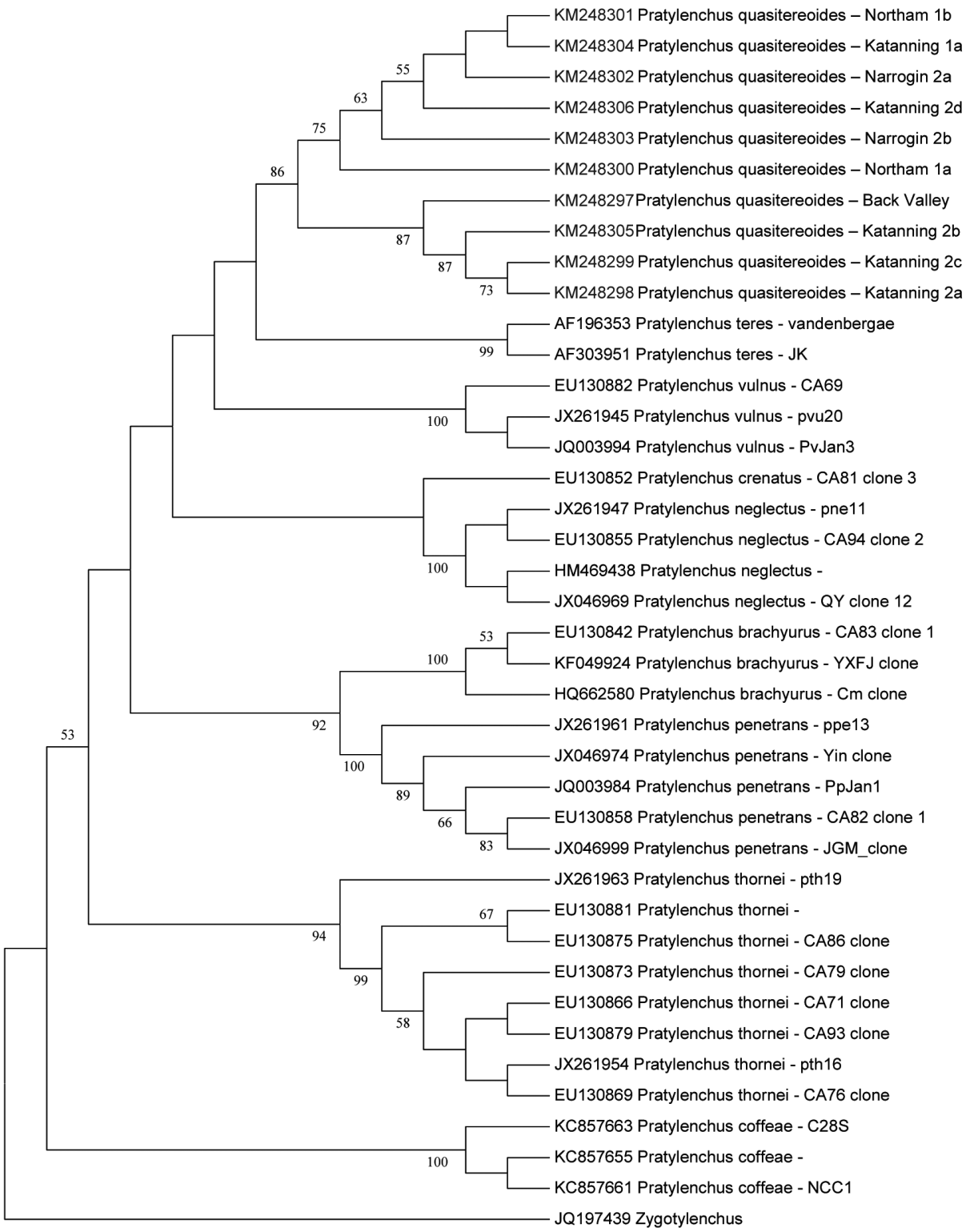

FIGURE 2. Bootstrap consensus cladogram inferred using the Neighbor-Joining method on number of nucleotides different (*NJ-ND*). The percentages of replicate trees in which the associated taxa clustered together in 1000 bootstrap replicates are shown next to the branches where >50%. The tree is rooted with a sequence from *Zygotylenchus guevari*. Genbank identifier precedes species name and population or subspecies designation.

been found on these hosts (Table 3). The sympatric congeners *P. neglectus, P. thornei* and *P. penetrans* have many of the same plant species as hosts as *P. quasitereoides* n.sp, but all have been found on additional hosts (Table 3).

Multiplication factors for *P. neglectus* and *P. thornei* on lupin and oats are generally less than 1, but generally greater than 1 for *P. quasitereoides* **n. sp.** (Vanstone *et al.* 2005). On the same varieties of lupin and oats, reproduction rates of *P. quasitereoides* **n. sp.** (1.6 and 8.1, respectively) were much greater than those of *P. neglectus* (1.0 and 1.6, repectively). However, different varieties have different host status to *P. quasitereoides* n.sp. as well as for *P. neglectus* and *P. thornei* (Collins *et al.* 2013, Vanstone 2007, Vanstone *et al.* 2005).

Etymology. The name indicates the similarity of the new species with *P. teres* from the suffix "oides", and that the species has been known as *P. teres* "quasi". The species epithet is mostly Latin neuter, but the suffix is Greek (as with the generic name), and chosen for euphony above the Latin "similis".

TABLE 3. Hosts of the most common species of *Pratylenchus* in Western Australia, plus *P. teres* sensu stricto.

Host	*P. quasitereoides* **n. sp.**	*P. teres*	*P. neglectus*	*P. thornei*	*P. penetrans*
barley (*Hordeum vulgare* L.)	X		X	X	X
wheat (*Triticum aestivum* L.)	X		X	X	X
oat (*Avena sativa* L.)	X		X		X
chickpea (*Cicer arietinum* L.)	X		X	X	X
lupin (*Lupinus angustifolius* L.)	X				X
canola (*Brassica napus* L.)	X		X	X	X
potato (*Solanum tuberosum* L.)		X			
mustard (*Brassica juncea* L.)		X	X	X	
safflower (*Carthamus tinctorius* L.)		X			
cotton (*Gossypium hirsutum* L.)		X			
pearl millet (*Pennisetum glaucum* (L.))		X			
sugar cane (*Saccharum officinarum* L.)		X			
tobacco (*Nicotiana tabacum* L)		X			
medic (*Medicago* spp.)			X		
durum (*Triticum durum* L.)			X		X
common vetch (Vicia *sativa* L.)			X	X	
field pea (*Pisum sativum* L.)					X
faba bean (*Vicia faba* l.)					X
triticale (*Triticum* x *Secale*)					X

References

Braun, A.L. & Loof, P.A.A. (1966) *Pratylenchoides laticuada* n. sp., a new endoparasitic phytonematode. *Netherlands Journal of Plant Pathology*, 72, 241–245.
http://dx.doi.org/10.1007/BF02650210

Cadet, P., van den Berg, E., Delatte, A. & Fiard, J.-P. (1994) Comparaison de quelques peuplements nematologiques des Petites Antilles. *Biogeographica*, 70, 125–138.

Carta, L.K., Handoo, Z.A., Skantar, A.M., van Biljon, J. & Botha, M. (2002) Redescription of *Pratylenchus teres* Khan & Singh, 1974 (Nemata: Pratylenchidae), with the description of a new subspecies from South Africa, and a phylogenetic analysis of related species. *African Plant Protection*, 8, 13–24.

Cobb, N.A. (1917) A new parasitic nema found infesting cotton and potatoes. *Journal of Agricultural Research*, 11, 27–33.

Collins, S.J., Kelly, S., Hunter, H., MacLeod, B., Debrincat, L., Teasdale, J., Versteeg, C. & Zhang, Z. (2013) P. teres*—WA's home grown Root Lesion Nematode (RLN) and its unique impacts on broadacre crops*. 2013 WA Crop Updates, GRDC & DAFWA, Perth., 4 pp.

Department of Agriculture Western Australia (2005) *Annual Report 2003–2004*. Western Australian Department of Agriculture, Perth, 121 pp.

Felsenstein, J. (1985) Confidence-limits on phylogenies—an approach using the bootstrap. *Evolution*, 39, 783–791.
http://dx.doi.org/10.2307/2408678

Filipjev, I.N. & Schuurmans Stekhoven, J.H. (1941) *A manual of agricultural helminthology*. E. J. Brill, Leiden, 878 pp.
Geraert, E. (1968) Morphometric relations in nematodes. *Nematologica*, 14, 171–182. http://dx.doi.org/10.1163/187529268X00390
Hodda, M. & Nobbs, J.M. (2008) A review of current knowledge on particular taxonomic features of the Australasian nematode fauna, with special emphasis on plant feeders. *Australasian Plant Pathology*, 37, 308–317. http://dx.doi.org/10.1071/AP08024
Hooper, D.J. (1986a) Extraction of free-living stages from soil. *In*: Southey, J.F. (Ed.), *Laboratory methods for work with plant and soil nematodes*. 6th ed. Her Majesty's Stationery Office, London, pp. 5–30.
Hooper, D.J. (1986b) Drawing and measuring nematodes. *In*: Southey, J.F. (Ed.), *Laboratory methods for work with plant and soil nematodes*. 6th ed. Her Majesty's Stationery Office, London, pp. 87–94.
Karssen, G. & Bolk, R.J. (2000) An additional character useful for the identification of *Pratylenchus crenatus* Loof 1960 (Nematoda: Pratylenchidae). *Nematology*, 2, 695–697. http://dx.doi.org/10.1163/156854100509556
Khan, E. & Singh, D.B. (1974) Five new species of *Pratylenchus* (Nematoda : Pratylenchidae) from India. *Indian Journal of Nematology*, 4, 199–211.
Loof, P.A.A. (1992) The family Pratylenchidae Thorne, 1949. *In*: Nickle, W.R. (Ed.), *Manual of Agricultural Nematology*. Marcel Dekker, New York, pp 363–421.
Nei, M. & Kumar, S. (2000) *Molecular Evolution and Phylogenetics*. Oxford University Press, New York, 333 pp.
Nunn, G.B., Theisen, B.F., Christensen, B. & Arctander, P. (1996) Simplicity-correlated size growth of the nuclear 28S ribosomal RNA D3 expansion segment in the crustacean order Isopoda. *Journal of Molecular Evolution*, 42, 211–223. http://dx.doi.org/10.1007/BF02198847
Palomares-Rius, J.E., Castillo, P., Liebanas, G., Vovlas, N., Landa, B.B., Navas-Cortes, J.A. & Subbotin, S.A. (2010) Description of *Pratylenchus hispaniensis* n. sp from Spain and considerations on the phylogenetic relationship among selected genera in the family Pratylenchidae. *Nematology*, 12, 429–451. http://dx.doi.org/10.1163/138855409X12559479585043
Rensch, B. (1924) *Aphelenchus neglectus* sp. n., eine neue parasitare Nematodenart. *Zoologischer Anzeiger Leipzig*, 59, 277–280.
Riley, I.T. & Kelly, S.J. (2002) Endoparasitic nematodes in cropping soils of Western Australia. *Australian Journal of Experimental Agriculture*, 42, 49–56. http://dx.doi.org/10.1071/EA01054
Riley, I.T. & Wouts, W.M. (2001) *Pratylenchus* and *Radopholus* species in agricultural soils and native vegetation in Southern Australia. *Transactions of the Royal Society of South Australia*, 125, 147–153.
Ryss, A.Y. (1982) [New phyto nematode species of the genus *Pratylenchus* in the Estonian SSR, USSR.] *Eesti NSV Teaduste Akadeemia Toimetised Bioloogia*, 31, 22–29.
Ryss, A.Y. (2002) Genus *Pratylenchus* Filipjev: multientry and monoentry keys and diagnostic relationships (Nematoda: Tylenchida: Pratylenchidae). *Zoosystematica Rossica*, 10, 241–255.
Rzhetsky, A. & Nei M. (1992) A simple method for estimating and testing minimum-evolution trees. *Molecular Biology and Evolution*, 9, 945–967.
Saitou, N. & Nei, M. (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4, 406–425.
Seinhorst, J. W. (1959) A rapid method for the transfer of nematodes from fixative to anhydrous glycerine. *Nematologica*, 4, 67–69. http://dx.doi.org/10.1163/187529259X00381
Sher, S.A., Allen M.W. (1953) Revision of the genus *Pratylenchus* (Nematoda: Tylenchidae). *University of California Publications in Zoology*, 57, 441–470.
Siddiqi, M.R. (2000) *Tylenchida: Parasites of plants and insects*. CABI, New York, 833 pp.
Subbotin, S.A., Ragsdale, E.J., Mullens, T., Roberts, P.A., Mundo-Ocampo, M. & Baldwin, J.G. (2008) A phylogenetic framework for root lesion nematodes of the genus *Pratylenchus* (Nematoda): Evidence from 18S and D2-D3 expansion segments of 28S ribosomal RNA genes and morphological characters. *Molecular Phylogenetics and Evolution*, 48, 491–505. http://dx.doi.org/10.1016/j.ympev.2008.04.028
Taheri, Z.M., Maafi, Z.T., Subbotin, S.A., Pourjam, E. & Eskandari, A. (2013) Molecular and phylogenetic studies on Pratylenchidae from Iran with additional data on *Pratylenchus delattrei*, *Pratylenchoides alkani* and two unknown species of *Hirschmanniella* and *Pratylenchus*. *Nematology*, 15, 633–651.
Tamura, K., Nei M. & Kumar, S. (2004) Prospects for inferring very large phylogenies by using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)*, 101, 11030–11035. http://dx.doi.org/10.1073/pnas.0404206101
Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011) MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution*, 28, 2731–2739. http://dx.doi.org/10.1093/molbev/msr121

Tamura, K. & Nei, M. (1993) Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution*, 10, 512–526.

Thompson, J.D., Higgins, D.G. & Gibson, T.J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research*, 22, 4673–4680.
http://dx.doi.org/10.1093/nar/22.22.4673

Tobar-Jimenez, A. (1963) *Pratylenchoides guevarai* sp. nuevo, nematode tylenchido relacionado con el cipres (*Cupressus sempervirens* L.). *Revista Iberica de Parasitologia*, 23, 27–36.

van den Berg, E. & Queneherve, P. (2000) *Hirschmanniella caribbeana* sp. n. and new records of *Pratylenchus* spp. (Pratylenchidae: Nematoda) from Guadeloupe, French West Indies. *Nematology*, 2, 179–190.
http://dx.doi.org/10.1163/156854100509079

Vanstone, V. A. (2007) Root Lesion and Burrowing Nematodes in Western Australian cropping systems. *DAFWA Bulletin*, 4698, 1–19.

Vanstone, V.A., Kelly, S.J., Hunter, H.F. & Gilchrist, M.C. (2005) *Rotations for nematode management.* 2005 WA Crop Updates, GRDC & DAFWA, Perth, 7 pp.

Whitehead, A.G. & Hemming, J.R. (1965) A comparison of some quantitative methods of extracting small vermiform nematodes from soil. *Annals of Applied Biology*, 55, 25–38.
http://dx.doi.org/10.1111/j.1744-7348.1965.tb07864.x