Redescription of the root-lesion nematode, *Pratylenchus globulicola* Romaniko, 1960 (Tylenchida: Pratylenchidae) from the Ural Federal District of Russia

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Accepted for publication 19 May 2022

Summary. A redescription of the root-lesion nematode, *Pratylenchus globulicola*, is given in this paper. It was originally described as a pest for legume crops in the Ural district, Russia, but was later considered by several taxonomists as a synonym of *P. penetrans*. In 2010 and 2011, new nematode material was obtained in the type locality from the type and other hosts and the extracted females and males were morphologically identified as *P. globulicola*. Neotype and neoparatypes are designated for this species. The species has four lip annuli, or four at one side and three at another side of the offset anteriorly flattened cephalic region, strongly sclerotised cephalic framework and strong stylet 14-15 µm long with anteriorly flattened basal knobs, DGO = 2.5-3.5 µm, pharyngeal glands lobe = 41 (29-54) µm, four equidistant, not areolated lateral field incisures, single genital tract and post-uterine sac (PUS) located to the right side from intestine, spermatheca spherical to oval, averaged 14 × 13 µm, filled with spherical to oval nucleic sperm of 3 µm in diam., distance from spermatheca to vagina = 41.9 (19-60) µm, vulva = 78 (72-82)%, PUS with three to four distal cellular elements, right to intestine, 24.4 (17-33) µm long or 1.2 (0.8-1.5) times of the vulval body diameter or 36 (23-49)% of vulva-anus distance, tail subcylindrical, bearing 11 (10-14) annuli on ventral side. Phasmids located slightly posterior to mid-tail. Tail tip smooth, flat in lateral view or rarely sub-hemispherical in ventral or dorsal orientation. The comparisons of ITS and D2-D3 expansion segments of the 28S rRNA gene sequences of *P. globulicola* revealed that those sequences are highly identical to corresponding gene sequences of *P. vovlasi* syn. n. *Pratylenchus vovlasi* syn. n. was proposed here as a junior synonym of *P. globulicola* based on analysis of morphological and molecular datasets. The rRNA gene sequences of *P. globulicola* clustered with the sequences of *P. pratensis* and *P. pseudopratensis*, forming the *Pratensis* clade.

Key words: Fabaceae, molecular phylogeny, *Pratylenchus*, Rosaceae, taxonomy.

Root-lesion nematodes of the genus *Pratylenchus* Filipjev, 1936 are migratory root endoparasites that are among the most widespread and destructive phytopathogenic nematodes of agricultural crops worldwide. The genus includes up to 105 valid species according to different authors (Ryss, 1988; Siddiqi, 2000; Castillo & Vovlas, 2007; Geraert, 2013; Hodda *et al.*, 2014; Ngyuen *et al.*, 2017, 2019; Singh *et al.*, 2018; Qing *et al.*, 2019, Handoo *et al.*, 2020; Powers *et al.*, 2021).

Presently, 13 valid *Pratylenchus* species: *P. crenatus* Loof, 1960, *P. emarginatus* Eroshenko, 1978, *P. fallax* Seinhorst, 1968, *P. flakkensis* Seinhorst, 1968, *P. gibbicaudatus* Minagawa, 1982, *P. globulicola* Romaniko, 1960, *P. kasari* Ryss, 1982, *P. neglectus* (Rensch, 1924) Filipjev & Schuurmans Stekhoven, 1941, *P. penetrans* (Cobb, 1917) Filipjev & Schuurmans Stekhoven, 1941, *P. pratensis* (De Man, 1880) Filipjev, 1936, *P. pseudopratensis* Seinhorst, 1968, *P. thornei* Sher & Allen, 1953 and *P. vulnus* Allen & Jensen, 1951 are reported from Russia (Ryss, 1988; Eroshenko & Volkova, 2005). Several species: *P. cerealis* Haque, 1966, *P. clavicaudatus* Baranovskaya & Haque, 1968, *P. obtusicaudatus* Romaniko, 1977, *P. stupidus* Romaniko, 1977,

 doi: 10.24412/0869-6918-2022-2-89-101
Published online 15 September, 2022

P. uralensis Romaniko, 1966, *P. variacaudatus* Romaniko, 1977 were originally described from Russia, but are presently considered as *species inquirendae* (Geraert, 2013).

A population of the root-lesion nematode, *Pratylenchus globulicola*, initially identified as *P. pratensis*, was reported from leguminous plants in the Chelyabinsk region, Russia by Romaniko (1960a, b). Romaniko (1957, 1958, 1960a, b, 1961, 1963, 1964, 1969) described the life cycle, embryogenesis, postembryogenesis, population dynamics, plant-host range, and pathogenicity of this population on legumes. He conducted experiments with the root-lesion nematodes at the Agrobiological station of the former Chelyabinsk Pedagogical Institute (now South Ural State Humanitarian Pedagogical University) and collected soil samples from pea fields in Chelyabinsk region, Etkulsky, Krasnoarmeisky, Sosnovsky and Oktyabrsky (Pisklovo) districts. Therefore, pea, *Pisum sativum* L., was selected as the type host and Oktyabrsky district, Chelyabinsk region, Russia was considered as the type locality for *P. globulicola*. In the original description, Romaniko (1960a) did not designate holotype and paratype specimens. However, in 1976, during an examination of the Nematode Collection at the Zoological Institute of the Russian Academy of Science, A.Yu. Ryss found two slides designated as 'holotype' (female) and 'allotype' (male) of this species with the following labels in Russian: 'Chelyabinsk, Exp. Field, *Pisum sativum* roots'. Unfortunately, in 1977 the slides were damaged during a loan and were subsequently considered unsuitable for examination. Thus, the type materials of *P. globulicola* were lost.

Presently, *P. globulicola* is listed as a valid *Pratylenchus* species by Siddiqi (1986, 2000) although other authors considered it as a synonym of *P. penetrans* (Loof, 1978, 1991; Luc, 1987; Ryss, 1988; Andrássy, 2007; Castillo & Vovlas, 2007; Geraert, 2013) or together with *P. penetrans*, as a synonym of *P. pratensis* (Frederick & Tarjan, 1989).

In 2010, 2011, and 2021, several nematological surveys of legume crops were conducted within the Chelyabinsk region with intensive sampling in Pisklovo and the Agrobiological Station of the South Ural State Humanitarian Pedagogical University in Chelyabinsk. Pisklovo settlement is located at the border of the two districts of Chelyabinsk region and now belongs to the Etkulsky district. Root-lesion nematodes similar to *Pratylenchus globulicola* were detected only at the Agrobiological Station, in a mixture of roots of *Pisum sativum* L., *Trifolium* sp. and *Ribes nigrum* L. No pea crops were found growing in Pisklovo and *P. globulicola* were not found in alfalfa and clover crops also growing in that region. The main objective of the present study was to revalidate and redescribe *P. globulicola* using an integrative approach based on morphological and molecular data and reconstruct the phylogenetic position of the recently recovered population from the type locality.

MATERIAL AND METHODS

Nematode samples. Soil and root samples of pea, black currant, clover, and alfalfa were collected during the surveys conducted in four districts of Chelyabinsk region of Russia, at locations indicated in V.I. Romaniko's articles (1957, 1960a, b, 1961) with intensive sampling in the Pisklovo, Chelyabinsk region (GIS: 54.576111N, 62.016111E) and Agrobiological Station of the South Ural State Humanitarian Pedagogical University, Chelyabinsk (GIS: 55.109967N, 61.401117E). Nematodes were extracted from roots and soil samples using a modification of Baermann's funnel technique (Ryss, 2015).

Morphological study. For morphological study, nematodes were fixed with hot TAF (2 ml of triethanolamine, 10 ml of formalin, 90 ml of distilled water) in a water bath (Ryss, 2017a). Nematodes were processed into pure glycerol using the express method and the permanent collection slides were prepared according to the 'cocktail' protocol (Ryss, 2003, 2017b). The nematodes were studied and photographed under a Leica DM-2500 microscope. Adobe Photoshop CS2 software was used for contrasting photos, ImageJ software was used for measuring nematodes (Collins, 2007), and MS Excel was used for calculations and statistical analysis of the measurements. Line drawing images were prepared with Adobe Photoshop and Adobe Illustrator using series of microphotographs at different optical levels.

Molecular and phylogenetic study. DNA was extracted from several specimens using the proteinase K protocol. DNA extraction and PCR protocols were according to Subbotin (2021a). The following primer sets were used in this study: (*i*) D2A (5'-ACA AGT ACC GTG AGG GAA AGT TG-3') and D3B (5'-TCG GAA GGA ACC AGC TAC TA-3') amplifying the D2-D3 expansion segments of 28S rRNA gene and (*ii*) TW81 (5'-GTT TCC GTA GGT GAA CCT GC-3') and AB28 (5'-ATA TGC TTA AGT TCA GCG GGT-3') amplifying the ITS rRNA gene. The successfully amplified fragments were sequenced using the primer pairs used in PCR. The new sequences for each gene were edited, compared with other sequences available in GenBank database, and

the relevant sequences were retrieved. New sequences were aligned using ClustalX 1.83 (gap opening 15.0 and gap extension – 6.66 for ITS rRNA gene and gap opening 5.0 and gap extension – 3.0 for the D2-D3 of 28S rRNA gene) with corresponding selected and published gene sequences of *Pratylenchus* spp. (Subbotin *et al.*, 2008; Troccoli *et al.*, 2008, 2021; Janssen *et al.*, 2017 and others). Sequence datasets were analysed with Bayesian inference (BI) using MrBayes 3.1.2 and PAUP 4.0 as described by Subbotin (2021b). The new sequences were submitted to the GenBank database under accession numbers: OM472924 (D2-D3 of 28S rRNA gene) and OM472925 (ITS rRNA gene).

RESULTS

Pratylenchus specimens were found in root samples of pea and black currant from the Agrobiological Station only. These nematodes were identified as *P. globulicola*. In Pisklovo, pea had not been cultivated in the region for many years and alfalfa was the only mass cultivated legume crop. Only three *Paratylenchus* spp. were found in alfalfa soil and root samples.

DESCRIPTION
Pratylenchus globulicola Romaniko, 1960
Figs 1 & 2

Morphometrics of the neotype female, and neoparatype females, males and juveniles are listed in Table 1.

Female. Body almost straight, cylindrical, slightly narrowing posterior to the vulva. Lip region flattened anteriorly, offset, 3.9 (3.0-4.5) µm high and 8.3 (8-9) µm wide, bearing four annuli or three annuli at one side and four annuli at the other side in lateral view. Cephalic framework strong and heavily sclerotised. Stylet strong, with anteriorly flattened basal knobs. Stylet conus 52 (47-57)% of the entire stylet length. Hemizonid just anterior to the excretory pore, two body annuli long. Excretory pore located at the level of or slightly posterior to the pharyngeal-intestinal valve. Median pharyngeal bulb spherical. Pharyngeal glands moderately wide, overlapping the intestine ventro-laterally. Pharyngeal lobe with a dorsal nucleus in anterior part of the lobe and ventro-sublateral nuclei near the tip of the pharyngeal lobe. Lateral field marked with four smooth, equidistant incisures becoming three or two in the distal end of tail, shortly posterior to the phasmid. Spermatheca round to oval, filled with spherical to oval sperm with nucleus 2 µm in diam. Vulva is a transverse slit, 6-8 µm long. In ventral view, vulva has four pairs of dilators; two of them attached laterally to dorsal and two to ventral vulval lip. Vagina short, perpendicular to ventral body wall. Post-uterine sac (PUS) with three to four distal cellular elements. Tail subcylindrical, truncate. Phasmids located slightly posterior to mid-tail. Tail tip smooth, flat in lateral view or rarely sub-hemispherical in ventral or dorsal orientation.

Male. Less abundant than females (one third of the population). Body shape similar to that of female, cylindrical throughout length, not narrowing posteriorly, except in tail. Lateral field with four smooth, equidistant incisures. Stylet and cephalic framework strongly developed, stylet knobs with anteriorly flattened basal knobs. Pharynx slightly less developed than that in females, with glands overlapping the intestine ventro-laterally, 3.5 (2.3-5.0) times the median bulb length. Spicules crescent-shaped, ventrally weakly sclerotised. Gubernaculum straight, smoothly Y-shaped. Tail conical, with smooth bursal alae enveloping tail and extending to the tail tip. Phasmid 'ribs' at mid-tail or slightly shifted posteriorly.

Juveniles. Preadult fourth-stage juveniles (J4) similar to adults with exception of genital structures. Juveniles have genital primordia occupying 22 (18-29)% of body length. Only 6 female J4 and 1 male J4 were collected. The male J4 differs from female J4 by a larger cloacal primordium (24 × 17 µm) near the posterior body terminus. Female J4 with distinct lens-shaped vulval primordium.

Host and locality. Mixture of roots of pea, *Pisum sativum* L. and black currant, *Ribes nigrum* L., Agrobiological Station of the South Ural State Humanitarian Pedagogical University (GIS: 55.109967N, 61.401117E); Chelyabinsk, Park Street B 4-km. Specimens were collected in July 2010.

Neotype and neoparatypes. Neotype female (Collection slide no. P4516) slide and several neoparatype slides containing 25 females, eight males, six female juveniles and one male juvenile (Collection slide no. P4514-P4521) deposited at the Zoological Institute of Russian Academy of Sciences (RAS).

Measurements of the Romaniko's type slides. In 1977, A.Yu. Ryss measured body lengths of holotype female (L = 483 µm) and allotype male (L = 450 µm).

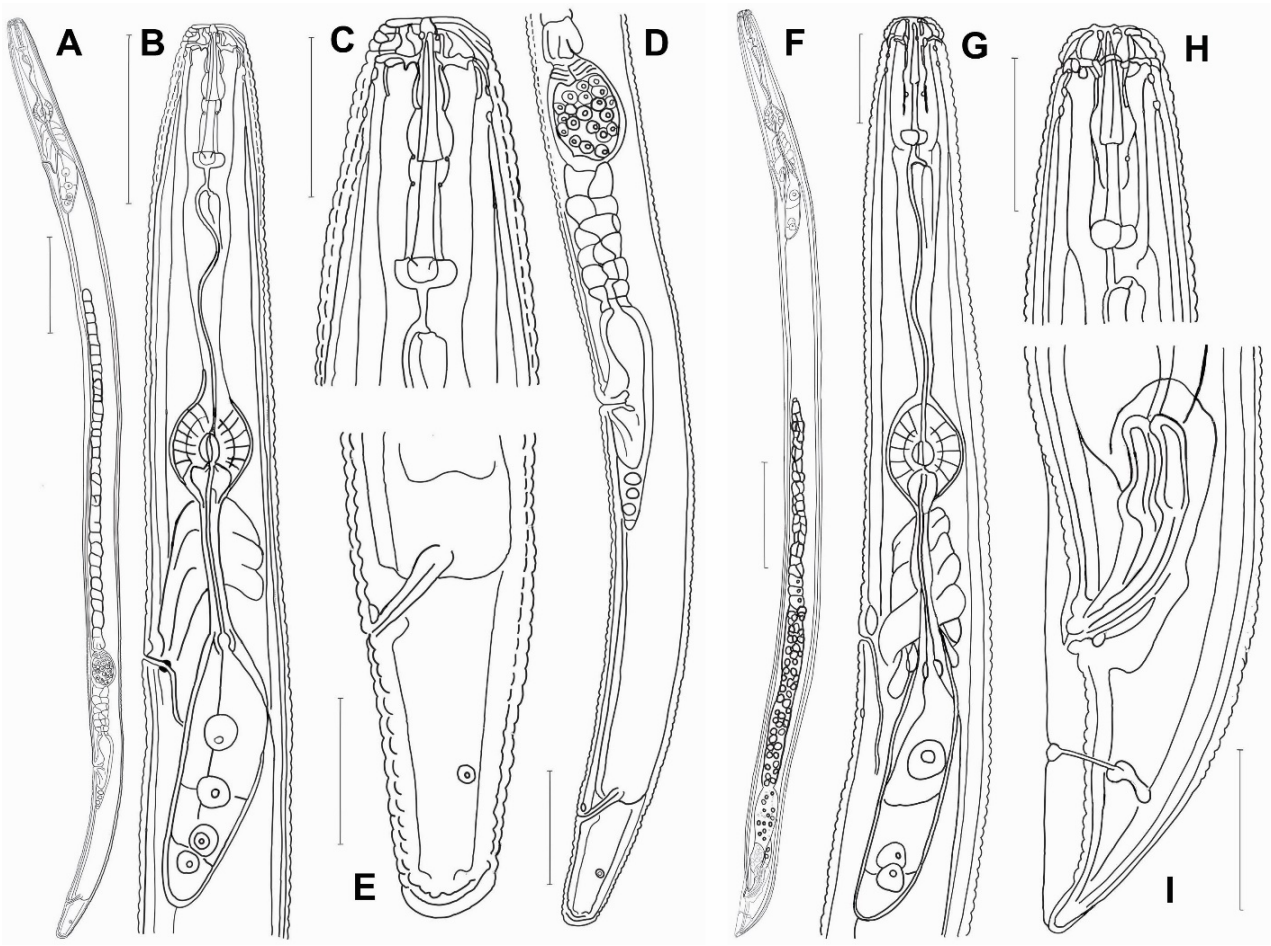

Fig. 1. *Pratylenchus globulicola* Romaniko, 1960. Line drawings. Female (A-E), male (F-I). A, F: Body outline; B, G: Anterior region; C, H: Cephalic region; D: Posterior region with genital system; E: Female tail; I: Male tail with spicules. Scale bars: A, F= 50 µm; B, D, G = 20 µm; C, E, H, I = 10 µm.

Molecular characterisation and phylogenetic relationships. Several alignments of the D2-D3 expansion segments of 28S rRNA gene sequences were generated for this study. The first alignment contained sequences of *Pratylenchus* species and *P. globulicola.* This alignment was 836 bp in length and contained 56 sequences of *Pratylenchus* and three sequences of the outgroup taxa. Phylogenetic relationships of *P. globulicola* with other *Pratylenchus* inferred from the first alignment are given in Figure 3. The second alignment contained 26 sequences of some populations of the *Pratensis* clade and other related species. Phylogenetic relationships of *P. globulicola* with other related species inferred from the second alignment are presented in Figure 4. In these trees the sequence of *P. globulicola* from Russia clustered with those of *P. globulicola* from Italy (= *P. vovlasi* syn. n.). Other alignments were generated to calculate genetic distances for four species. These analyses showed that maximal intraspecific sequence variation for *P. globulicola* (4 sequences from Italy and 1 sequence from Russia) was 1.8%, *P. pratensis* (4 sequences) – 1.0%, *P. vulnus* (65 sequences) – 2.6% and *P. kumamotoensis* (17 sequences) – 3.4%.

The ITS rRNA gene alignment contained 25 sequences of *P. pratensis, P. globulicola*, and by one sequence of *P. vulnus* and *P. kumamotoensis* and was 753 bp in length. Phylogenetic relationships of *P. globulicola* with related *Pratylenchus* species based on this dataset are given in Figure 5. Maximal intraspecific sequence variation for *P. globulicola* (six sequences from Italy and one sequence from Russia) was 3.4% and *P. pratensis* (17 sequences) – 5.9%.

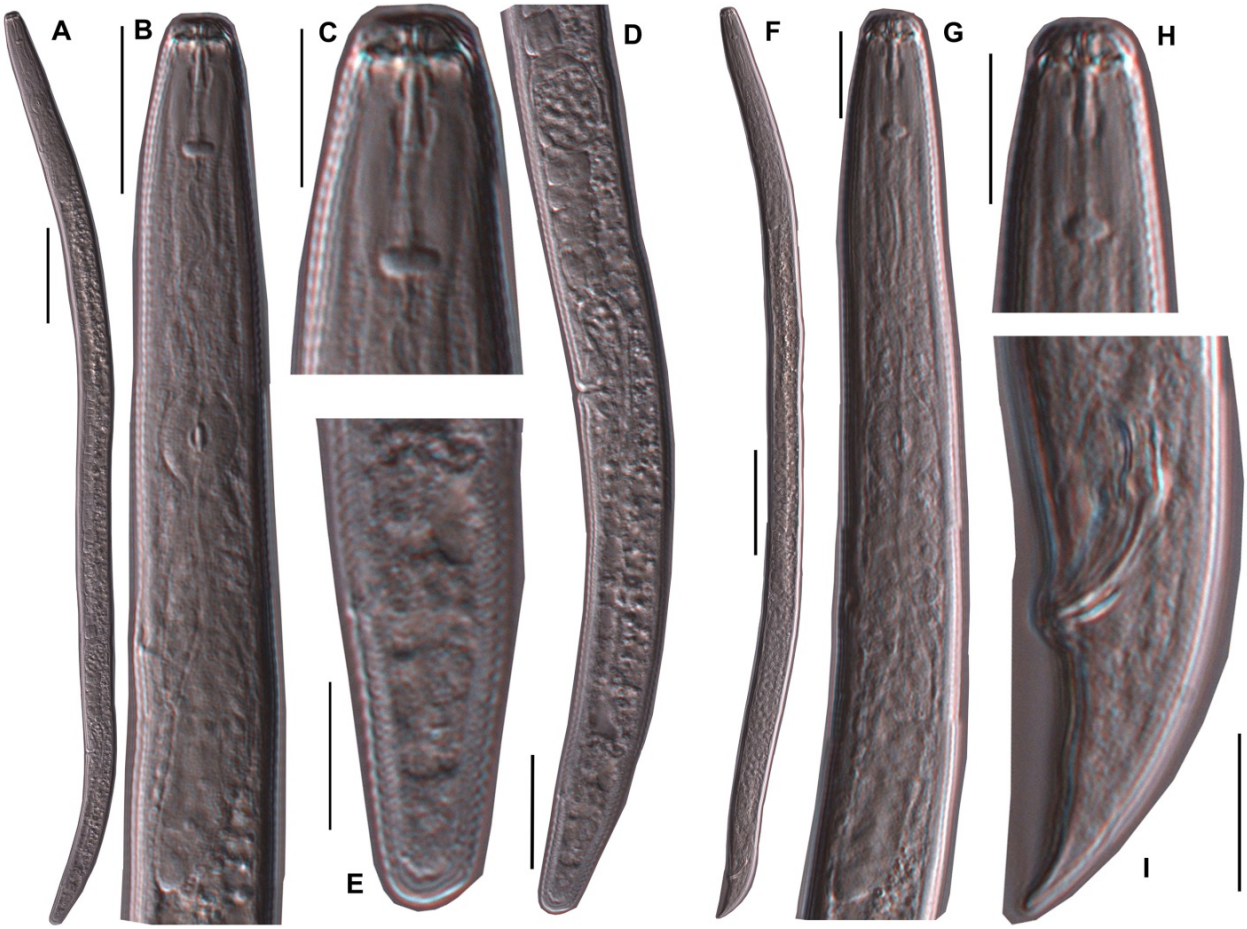

Fig. 2. *Pratylenchus globulicola* Romaniko, 1960. Microphotographs. Female (A-E), male (F-I). A, F: Body outline; B, G: Anterior part; C, H: Cephalic region; D: Posterior part with genital system; E: Female tail; I: Male tail with spicules. Scale bars: A, F = 50 µm; B, D, G = 20 µm; C, E, H, I = 10 µm.

Diagnosis and relationships. *Pratylenchus globulicola* is distinguished by four lip annuli or four annuli at one side and three at the other side in lateral view, an offset and anteriorly flattened cephalic region, strongly sclerotised cephalic framework, stylet (14-15) µm long, robust with anteriorly flattened basal knobs, DGO = (2.5-3.5) µm, median pharyngeal bulb spherical averaged 12 × 10 µm, pharyngeal glands lobe = 41 (29-54) µm, four equidistant incisures, non-areolated lateral field. Spermatheca round to oval, averaged 14 × 13 µm, filled with spherical to oval nucleic sperm of 3 µm diam. Vulva at 78 (72-82)%, PUS with three to four distal cellular elements, 24.4 (17-33) µm long; 1.2 (0.8-1.5) times vulval body diameter, and 36 (23-49)% of the vulva-anus distance, tail subcylindrical, truncate, bearing 11.7 (10-14) annuli on ventral side, tail tip smooth, flat. Phasmids located slightly posterior to mid-tail. According to the *Pratylenchus* spp. polytomous key of morphological characters (Castillo & Vovlas, 2007; Troccoli *et al.*, 2021) for *P. globulicola* code is: A23; B2; C2; D2; E2; F3; G2; H1; I3; J1; K1.

Pratylenchus globulicola belongs to the *Pratensis* group or clade according to morphological and molecular analyses. The *Pratensis* group presently includes only three species: *Pratylenchus pratensis*, *P. pseudopratensis* and *P. globulicola*. Two species: *P. vulnus* and *P. kumamotoensis* Mizukubo, Sugimura & Uesugi, 2007 are closely related with the *Pratensis* group (Figs 3 & 4).

Recently, *P. lentis* Troccoli, De Luca, Handoo & Di Vito, 2008 was synonymised with *P. pratensis*, based on the analyses of molecular, morphological and morphometric datasets by Janssen *et al.* (2017). Here we proposed a synonymisation of *P. vovlasi* Troccoli, Fanelli, Castillo, Liébanas, Cotroneo & De Luca, 2021 syn. n. (Troccoli *et al.*, 2021) with

Table 1. Morphometrics of *Pratylenchus globulicola* Romaniko, 1960. All measurements are in µm and in the form: mean ± s.d. (range).

Character	Female		Male	Female juvenile J4	Male juvenile J4	Female	Male
	Neotype	Neoparatypes	Neoparatypes	Neoparatypes	Neoparatype	Romaniko (1960a) Paratypes	Romaniko (1960a) Paratypes
n	1	25	8	6	1	?	?
L	448	433±55 (292-529)	416±23 (383-442)	319±51 (220-369)	377	540-770	480-530
a	18.7	22.3±4.0 (15.9-29.0)	23.8±4.7 (16.9-30.6)	20.3±2.8 (15.9-23.4)	15.7	24.0-28.5	24.0-26.5
b	5.7	6.2±0.7 (4.9-7.4)	5.9±0.5 (5.3-6.6)	5.5±0.6 (4.7-6.2)	5.8	8-9	7-8
b’	4.0	3.9±0.4 (3.1-4.9)	3.8±0.2 (3.5-4.3)	3.4±0.5 (2.8-4.2)	4.2	–	–
c	20.4	18.9±3.1 (14.5-26.2)	21.8±2.1 (19.4-25.9)	16.3±1.9 (14.4-19.2)	18.0	27-33	20.8-23.0
c’	1.5	1.8±0.2 (1.5-2.1)	1.5±0.3 (1.0-1.9)	1.7±0.2 (1.5-1.9)	1.2	–	–
V, (V) or T (%)	79.7	78±2 (72-82)	47±6 (41-58)	78±2 (76-81)	93	72.0-80.7	
Lip annuli	3 and 4	3 and 4	3 and 4	3 and 4	3 and 4	4	4
Stylet	14.5	14.2±0.7 (12.5-15.0)	13.6±0.8 (12.0-14.5)	11.7±1.0 (11-13)	14	12-14	12-14
Stylet base diam.	4.5	3.8±0.5 (3.0-4.5)	3.4±0.5 (2.5-4.0)	3.3±0.5 (3.0-3.5)	4	–	–
DGO	3.5	2.5-3.5	3.5	3.0-3.5	3.5	4	4
Cephalic region diam.	8.0	8.1±0.7 (6-9)	7.4±0.6 (7.0-8.5)	7.3±0.6 (6.0-7.5)	7.5	–	–
Cephalic region height	4.5	3.9±0.4 (3.0-4.5)	3.8±0.2 (3.5-4.0)	3.2±0.2 (3.0-3.5)	4	–	–
Median bulb length (L)	13	12.0±1.5 (9-15)	11.5±2.1 (9-15)	10.0±0.6 (9-11)	11	10	10
Median bulb diam. (D)	11	10.4±2.0 (8-15)	9.4±1.4 (7-12)	9	10	8	8
Median bulb L/D	1.2	1.2±0.1 (1.0-1.5)	1.2±0.1 (1.0-1.4)	1.1±0.1 (1.0-1.2)	1.1	–	–
Excretory pore from anterior	74	73.1±8.7 (57-100)	70.3±4.1 (64-75)	59.4±4.3 (53-65)	69	–	–
Pharynx	79	70.1±8.6 (54-88)	70.3±4.7 (65-77)	57.8±6.2 (47-66)	65	–	–
Anterior to gland lobe end	112	110.8±12.5 (90-138)	108.4±3.3 (102-112)	93.3±8.2 (80-103)	89	–	–
Gland lobe	33	40.7±6.7 (29-54)	38.2±4.2 (34-45)	35.5±6.3 (28-47)	24	–	–
Gland lobe / median bulb length	2.5	3.4±0.6 (2.4-4.5)	3.5±1.0 (2.3-5.0)	3.6±0.7 (2.5-4.7)	2.2	–	–
Max. body diam.	24	20.2±5.1 (12-28)	18.1±3.6 (12.5-23.0)	15.9±3.3 (12-21)	24	–	–
Spermatheca length (L)	18	13.8±3.7 (9-24)	–	–	–	–	–
Spermatheca diam. (D)	17	13.2±3.0 (9-20)	–	–	–	–	–
Spermatheca L/D	1.1	1.1±0.2 (0.8-1.5)	–	–	–	–	–
Sperm diam.	2.5	3.1±0.6 (2.5-4.0)	3.0±0.4 (2.5-3.5)	–	–	–	–
Vagina-spermatheca distance	40	41.9+9.6 (19-60)	–	–	–	–	–
Vagina-spermatheca/vulva-anus (%)	55	58+8 (42-73)	–	–	–	–	–
Vulva-anus distance	73	71.1±9.9 (48-88)	–	–	–	–	–
Post-uterine sac (PUS)	29	24.4±4.1 (17-33)	–	–	–	Less than vulval body diam.	–
Posterior genital branch/vulval diam.	1.2	1.2±0.2 (0.8-1.5)	–	–	–	<1	–
Posterior genital branch/vulva-anus distance (%)	40	36±6 (23-49)	–	–	–	–	–
Genital primordium (juveniles)				71.0±21.6 (45-98)	89	–	–
Gen. primordium/L (%)				22±5 (18-29)	24	–	–
Tail	22	23.6±4.9 (15.5-33.0)	19.3±2.1 (15-21)	19.7±3.7 (14-23)	21	23	23
Tail diam.	15	13.4±3.1 (9-19)	13.1±1.9 (11-16)	11.5±2.1 (7.5-13.0)	17	–	–
Hyaline tail zone	8	8.3±1.8 (4-11)	7.7±0.8 (7.0-9.5)	4.0±0.8 (2.5-4.5)	4.5	–	–
Annuli (width of 10 annuli at mid-body)	10	10±2 (7-15)	9±2 (7-13)	8±2 (7-10)	13	7	7
Tail ventral annuli	10	11.7±1.0 (10-14)	–	11±1 (10-12)	11	–	–
Spicules (arc)	–	–	15.8±0.6 (15-17)	–	–	–	14.5
Gubernaculum	–	–	7.1±1.3 (5.5-9.0)	–	–	–	4

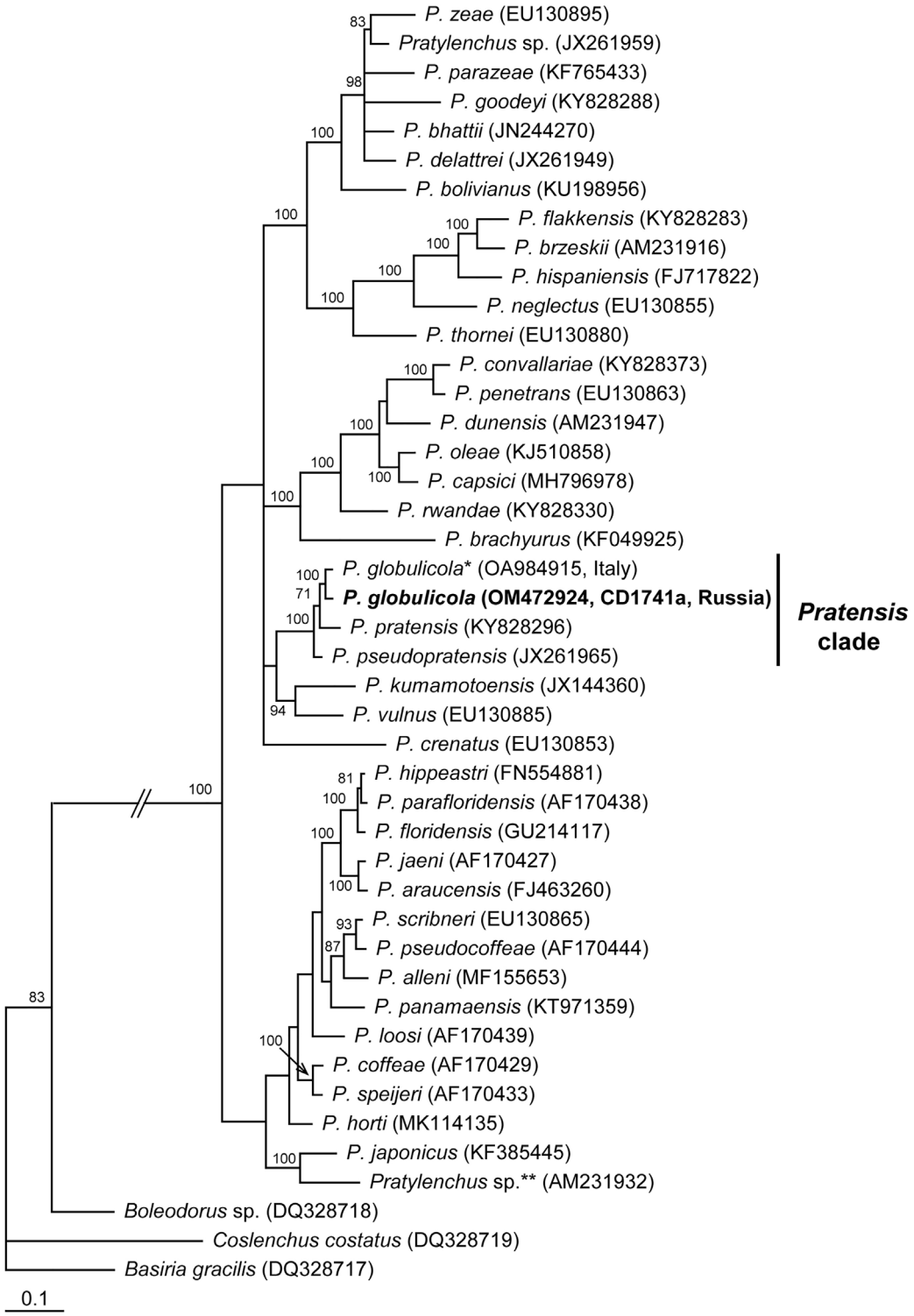

Fig. 3. Phylogenetic relationships of *Pratylenchus globulicola* with other *Pratylenchus* species as inferred from Bayesian analysis using the D2-D3 expansion segments of the 28S rRNA gene sequences under the GTR + I + G model. Posterior probabilities greater than 70% are given for appropriate clades. New sequence is indicated in bold. * – originally identified as *P. vovlasi* syn. n. by Troccoli *et al.* (2021); ** – originally identified as *P. pratensis* by de la Peña *et al.* (2007) and corrected by Janssen *et al.* (2017).

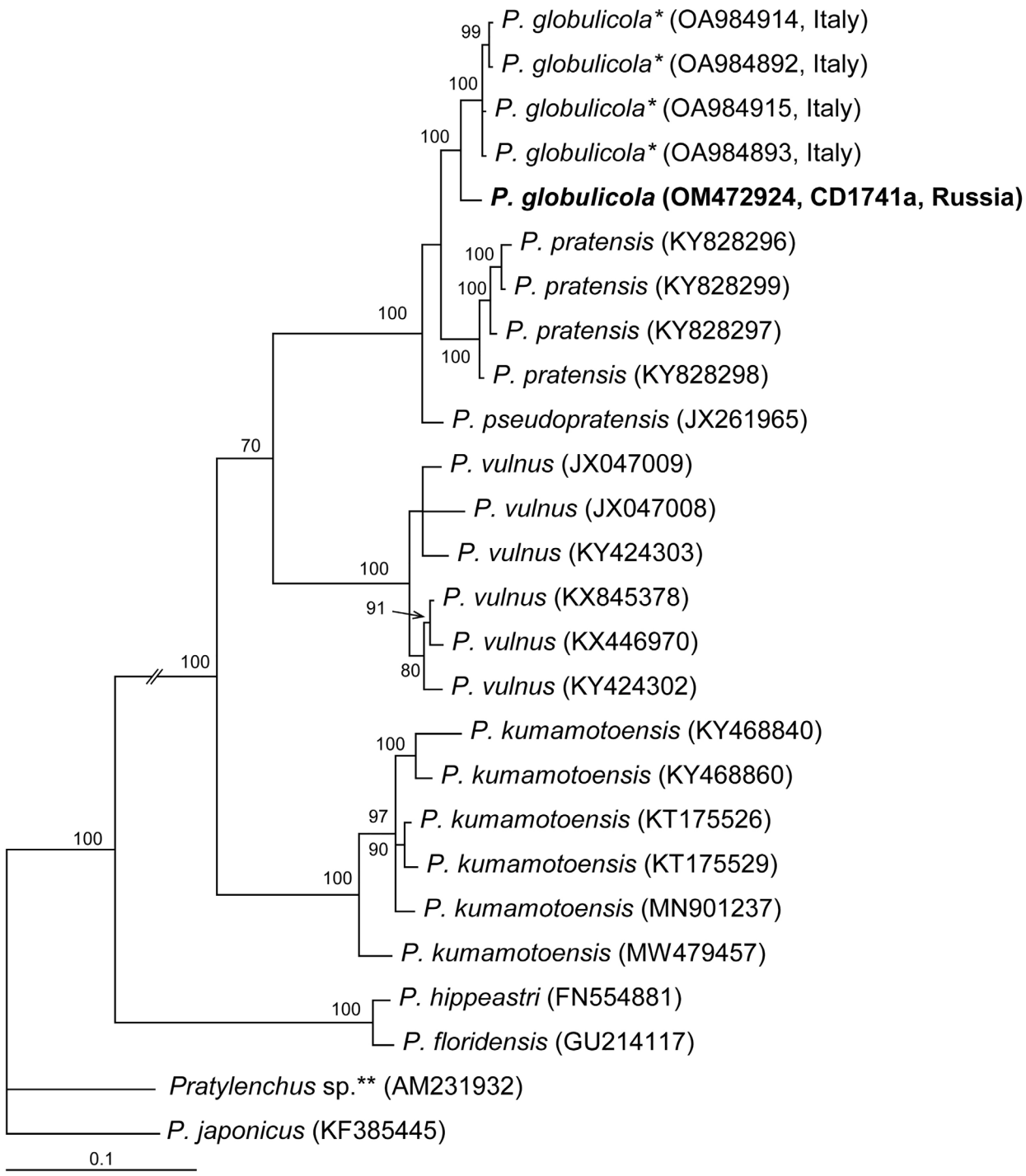

Fig. 4. Phylogenetic relationships of *Pratylenchus globulicola* with some populations of the *Pratensis* clade and other related species as inferred from Bayesian analysis using the D2-D3 expansion segments of the 28S rRNA gene sequences under the GTR + I + G model. Posterior probabilities greater than 70% are given for appropriate clades. New sequence is indicated in bold. * – originally described as *P. vovlasi* syn. n. by Troccoli *et al*. (2021); ** – originally identified as *P. pratensis* by de la Peña *et al*. (2007) and corrected by Janssen *et al.* (2017).

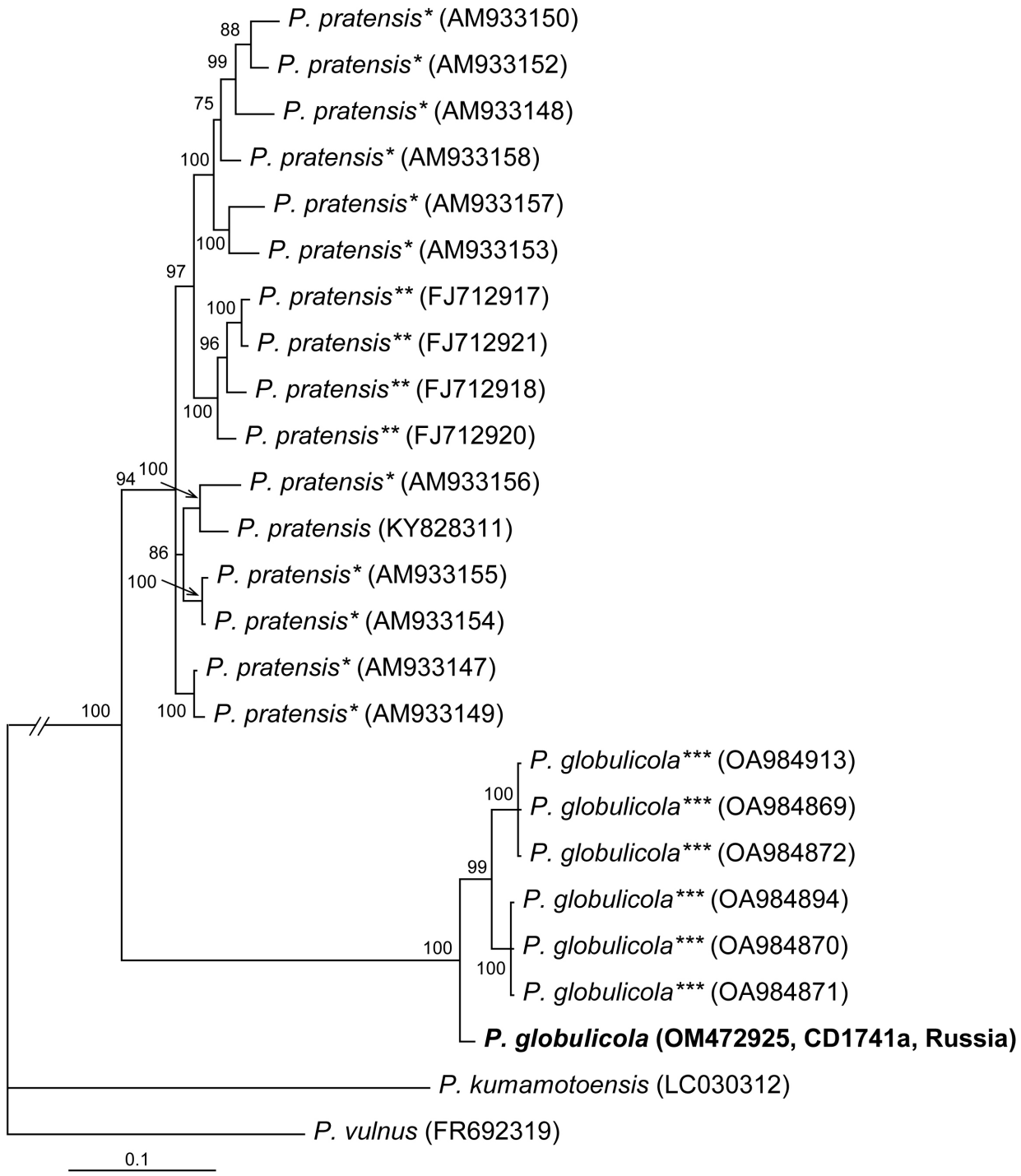

Fig. 5. Phylogenetic relationships of *Pratylenchus globulicola* with some populations of *P. pratensis* as inferred from Bayesian analysis using the ITS rRNA gene sequences under the GTR + I + G model. Posterior probabilities greater than 70% are given for appropriate clades. New sequence is indicated in bold. * – originally described as *P. lentis* by Troccoli *et al.* (2008) and corrected by Janssen *et al.* (2017); ** – originally identified as *P. fallax* by Waeyenberge *et al*. (2009); *** – originally described as *P. vovlasi* syn. n. by Troccoli *et al*. (2021).

P. globulicola. The observed differences between presently recovered population of *P. globulicola* and the Italian population *P. vovlasi* syn. n. were in number of lip annuli (four at one side and three at the other side *vs* three annuli at both sides in lateral view), a higher and strongly sclerotised cephalic region with mean height 3.9 *vs* 2.5 µm and moderately sclerotised in *P. vovlasi* syn. n., and number of ventral tail annuli 12 (10-14) *vs* 16 (14-20). All these differences could be considered as intraspecific variations. The sequence variations in both rRNA gene fragments (1.8% in 28S and 3.4% in ITS rRNA genes) between populations of *P. globulicola* from Russia and Italy are also in the range of intraspecific variations observed in related species like *P. pratensis*, *P. vulnus* and *P. kumamotoensis*. Host of *P. vovlasi* syn. n. was raspberry, *Rubus* sp. (Rosaceae) and the hosts of *P. globulicola* included *Pisum sativum* (Fabaceae) and *Ribes nigrum* (Rosaceae).

Pratylenchus globulicola differs from *P. pseudopratensis* in lateral field structure (four equidistant incisures *vs* central band between inner two incisures wider that outer ones and containing additional one or two coarsely running incisures), number of ventral tail annuli (10-14 *vs* 16-26) (Seinhorst, 1968; Castillo & Vovlas, 2007). Additionaly, *P. pseudopratensis* was found in herbaceous crops and fruit trees (Ryss, 1988; Castillo & Vovlas, 2007), but not in the Fabaceae as reported for *P. globulicola*.

Pratylenchus globulicola differs from *P. pratensis* in tail tip shape (smooth and truncate *vs* annulated and conical), spermatheca shape (spherical *vs* oval), number of tail annuli (10-14 *vs* 20-28), mean c' value (1.5-2.1 *vs* 2.2-2.7), position of phasmids (in posterior part of female tail *vs* at mid-tail) (Ryss, 1988).

Pratylenchus globulicola differs from *P. vulnus* in tail tip shape (truncate smooth *vs* narrowly conical smooth), spermatheca shape (spherical *vs* oval), lateral field with equidistant incisures *vs* central band distinctly narrower than outer bands, median bulb spherical *vs* elongated oval, posterior genital branch with two to three rudimentary oocytes *vs* distinctly rudimentary ovary, stylet length in females (14-15 *vs* 15-18 µm), c' mean value (1.8 *vs* 2.7), and PUS/BW mean value (1.5 *vs* 2.0) (Ryss, 1988).

Pratylenchus globulicola differs from *P. kumamotoensis* in number of lip annuli (four at one side and three at another side *vs* two annuli on both sides or rarely with three annuli on one side), posterior genital branch with three to four distal cellular elements *vs* distinctly rudimentary ovary, tail annuli (10-14 *vs* 20-22), PUS/BW mean value (1.5 *vs* 2.3-2.5), and mean c' value (1.5-2.1 *vs* 2.3-2.8) (Mizukubo *et al.*, 2007; Kim *et al.*, 2016). Furthermore, the host plants of *P. globulicola* belong to Rosaceae and Fabaceae *vs Chrysanthemum* spp., Asteraceae for *P. kumamotoensis*.

DISCUSSION

The present study showed that *P. globulicula* is a valid species and its synonymisation with *P. penetrans* proposed by several authors (Loof, 1978, 1991; Luc, 1987; Ryss, 1988; Andrássy, 2007; Castillo & Vovlas, 2007; Geraert, 2013) was not supported.

Some observed differences in the body length of *P. globulicula* in the present study and those from the original description can be explained by errors in the scale used by V.I. Romaniko. Measurements of the original slide materials made by the first author confirmed this statement.

The positions of both anterior genital tube and PUS to right from intestine are considered here as presumably important diagnostic characters for *P. globulicula*. Such positions are quite different from those for *Bursaphelenchus* spp. (Aphelenchoididae) and Diplogastridae. In the latter taxa the anterior genital tube is located to the right of the intestine and the posterior genital branch placed to the left (Ryss *et al.*, 2021a, b). However, in *Bursaphelenchus irokophilus*, both anterior female gonad and PUS are located to the right of the intestine (Torrini *et al.*, 2019). It is possible that the location of PUS to the intestine and the anterior genital tube may be used as the good taxonomic character, which was neglected earlier.

Pratylenchus globulicula belongs to the *Pratensis* group. The cryptic species diversity and correctness of species identification within this group should be studied more thoroughly. For example, there are some reports of *P. pseudopratensis* from distant points in the world (Ryss, 1988; Castillo & Vovlas, 2007); however, the exact identification of these findings still needs to be confirmed using molecular tools.

ACKNOWLEDGEMENTS

The authors thank Dr J.J. Chitambar (CDFA, CA, USA) for critical reading and correction of the manuscript draft. The study was supported by the Russian Foundation for Basic Research (project no. 20-04-00569-a). The sampling of material and maintenance of the Nematode Collection was funded by Government Contract 122031100260-0

for A.Yu. Ryss. The authors used the collection slides from the Nematode Collection of the Zoological Institute of the RAS (UFK ZIN RAS).

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А.Ю. Рысс, М.В. Приданников и С.А. Субботин. Переописание вида корневой нематоды *Pratylenchus globulicola* Romaniko, 1960 (Tylenchida: Pratylenchidae) из Уральского Федерального округа России.

Резюме. В статье дано переописание корневой нематоды *Pratylenchus globulicola* Romaniko, 1960. Вид *Pratylenchus globulicola* первоначально был описан как паразит бобовых в Уральском Федеральном округе, Россия, но позже сведен в синоним с *P. penetrans* несколькими таксономистами. В 2010 и 2011 годах были собраны новые образцы с пратиленхами в типовом местонахождении, из типового хозяина и иных местных хозяев; выделенные самки и самцы нематод были морфологически идентифицированы как *P. globulicola*. В результате исследования обозначены неотип (самка) и неопаратипы (самки и самцы) этого вида. Нематоды имеют 4 губных кольца на одной стороне и 3 на другой стороне плоской головной области; сильно склеротизированный головной скелет и мощный 14-15 мкм стилет с уплощенными спереди базальными головками; DGO = 2.5-3. 5 мкм; лопасть желез глотки = 41 (29-54) мкм; боковое поле с 4 равноудаленными, не ареолированными инцизурами; монодельфная женская половая система справа от кишечника и PUS (задний мешок матки), расположенный также справа от кишечника; сперматека сферическая или овальная, в среднем 14 × 13 мкм, заполнена сферическими или овальными сперматозоидами диаметром 3 мкм и ядром, занимающим почти весь объем сперматозоида; расстояние от сперматеки до вагины 41.9 (19-60) мкм; V = 78 (72-82)%; PUS с 3-4 рудиментарными ооцитами, расположен справа от кишки 24.4 (17-33) мкм; PUS в 1.2 (0.8-1.5) раза больше диаметра тела на уровне вульвы и составляет 36 (23-49)% от расстояния вульва-анус; хвост субцилиндрический, тупо усеченный, c = 11.7 (10-14) кольцами на вентральной стороне. Фазмиды расположены немного позади середины хвоста. Кончик хвоста гладкий и плоский. Молекулярный анализ ITS рРНК и D2-D3 сегментов расширения 28S рРНК генов *P. globulicola* показал, что эти гены наиболее схожи с таковыми у *P. vovlasi* syn. n. Вид *P. vovlasi* syn. n. был предложен здесь в качестве младшего синонима *P. globulicola* на основе анализа морфологических и молекулярных данных. Последовательности генов *P. globulicola* кластеризовались с генами *P. pratensis* и *P. pseudopratensis*, образуя высоко поддерживаемую кладу *Pratensis*.