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First report of four dagger nematode species of the genus *Xiphinema* (Nematoda: Longidoridae) from banana in Syria using an integrative approach

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Abstract A nematological survey was conducted between 2021 and 2022 in banana fields distributed in two major banana-producing regions in the western coast of Syria. As a result, six populations of *Xiphinema* spp. identified as *X. diffusum, X. pachtaicum, X. simile, X. vuittenezi* and *X. zagrosense* were isolated from the rhizosphere of banana plants (*Musa* sp.) and characterized using morphological and molecular data based on two rRNA genes (D2–D3 expansion segments of the 28S, and ITS fragments) and partial region of the cytochrome oxidase I gene (*COI* mtDNA) sequences. Moreover, the molecular identification of the endosymbionts of these populations was also performed using the complete 16S rDNA gene. The phylogenetic relationships of the recovered species of nematodes and respective endosymbionts were reconstructed. *Candidatus* Xiphinematobacter sp.

(OR196969; OR196971) and *Ca.* Xiphinematobacter sp. (OR196970) were detected in *X. diffusum* and *X. simile*, respectively, and clustered together with other *Ca.* Xiphinematobacter sp.A and sp.I respectively. To our knowledge, this is the first report of *X. diffusum, X. simile, X. vuittenezi* and *X. zagrosense* parasitizing banana in Syria, extending the geographical distribution of these species within the Mediterranean Basin.

Introduction

Dorylaimida Pearse, 1942 is one of the most abundant and diverse orders within the phylum Nematoda Potts, 1932 (Potts, 1932; Pearse, 1942; Ahmed & Holovachov, 2021). The genus *Xiphinema* Cobb, 1913, commonly known as dagger nematode, belongs to the family Longidoridae Thorne, 1935 and to the suborder Dorylaimina Pearse, 1936 (Ahmed & Holovachov, 2021; Gutiérrez-Gutiérrez et al., 2016; Pearse, 1936). According to morphological and biological features, members of *Xiphinema* are currently divided into two sub-groups: (*i*) *Xiphinema* non-*americanum* group, comprising around 237 species (172 species listed in original key by Loof & Luc, 1990, 11 species in the first and 31 species in the second supplement

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by Loof and Luc (1993) and Loof et al. (1996); till 2019, 60 species added to the genus or revalidated as listed by Mirzaie Fouladvand et al., 2019, and five species added to the genus since 2019 by Jahanshahi Afshar et al., 2019; Vazifeh et al., 2019; Archidona-Yuste et al., 2020a, b; Cai et al., 2020; Poureskandarian et al., 2023), mainly characterized by a wide morphological diversity: having a body J- to C-shaped after heat relaxation, a relatively long body (usually among 3.0 and 8.5 mm long) and odontostyle, female with high variation in the reproductive system, with or without any type of uterine differentiations (i.e. Z or pseudo-Z organ, crystal-like and/or spine-like structures in the tubular part of the uterus) and a wide diversity of tail shapes (Coomans et al., 2001; Loof & Luc, 1990; Taylor & Brown, 1997); and (*ii*) *Xiphinema americanum* group, accounted with 60 valid species (49 species listed by Lamberti et al., 2000, 11 extra species listed by Mobasseri et al., 2019a, b; three species added by Jahanshahi Afshar et al., 2021; Naghavi et al., 2022a; Gu et al., 2022), characterized by a spiral body after heat relaxation, a relatively small body (usually among 1.2 and 3.0 mm long), a female reproductive system with two equally developed genital branches, short uteri without uterine differentiations, endosymbiotic bacteria in intestinal cells and in the reproductive system in some species, and a conical tail with sharp to broadly rounded tip (Coomans et al., 2001; Lamberti et al., 2000; Palomares-Rius et al., 2016, 2021). *Xiphinema* species cause severe damage to plants by their direct feeding on root cells (Jones et al., 2013; Taylor & Brown, 1997). However, some of them retain/transmit economically important nepoviruses (genus Nepovirus, family Comoviridae) (Taylor & Brown, 1997; Trudgill et al., 1983). Furthermore, some of these *Xiphinema* species are included in the list of quarantine organisms of the European and Mediterranean Plant Protection Organization (EPPO) (OEPP/EPPO, 2022) which emphasizes the need for an accurate nematode identification at the species level.

An integrative taxonomic approach is the most efficient and accurate strategy to overcome practical issues with dagger nematodes (Gutiérrez-Gutiérrez et al., 2010, 2011b; 2013; Archidona-Yuste et al., 2016a, b; 2020b; Palomares-Rius et al., 2017; Cai et al., 2019, 2020; Mobasseri et al., 2019a, b). Untill recently, *Xiphinema* spp. populations were usually only identified at the species-level using polytomous

diagnostic keys (Lamberti et al., 2000, 2004; Loof & Luc, 1990; Loof et al., 1996). Nowadays, sequencing RNA-based markers represents a powerful approach for species-level taxonomic identification within the genus *Xiphinema* and understanding of the evolutionary relationships within this genus (Gutiérrez-Gutiérrez et al., 2010, 2011b; 2013; Archidona-Yuste et al., 2016a, b; 2019; Cai et al., 2018, 2019; Mobasseri et al., 2019a, b; Naghavi et al., 2022a).

Members of the *X. americanum* group harbour bacterial endosymbionts belonging to '*Candidatus* Xiphinematobacter' and '*Candidatus* Xiphinematincola pachtaicus*' species (Palomares-Rius et al., 2016, 2021; Brown, 2018; Mobasseri et al., 2019a, b). These endosymbionts are vertically transmitted from mother to offspring (Brown, 2018; Palomares-Rius et al., 2016, 2021). The 16S rRNA gene is useful for studying the taxonomy and genetic diversity of bacterial endosymbionts and resolving the nematode-endosymbiont bacteria coevolution (Lazarova et al., 2016a; Mobasseri et al., 2019a, b; Orlando et al., 2016; Palomares-Rius et al., 2016, 2021).

Previous studies have reported the occurrence and geographical distribution of dagger nematodes in Syria and to date a total of six *Xiphinema* species have been described, namely *X. americanum* sensu lato (s.l.) Cobb, 1913, *X. diversicaudatum* (Micoletzky, 1927) Thorne, 1939, *X. elongatum* Schuurmans Stekhoven & Teunissen, 1939, *X. index* Thorne & Allen, 1950, *X. italiae* Meyl, 1953, and *X. pachtaicum* (Tulaganov, 1938) Kirjanova, 1951 (Abdine et al., 2007; Al-Halabi & Al-Assas, 2021; Ali, 2023; Allouf, 2013; Greco et al., 1984, 1992; Kawas & Al-Assas, 2011; Khaleel et al., 2010; Lamberti, 1984; Lamberti et al., 1999a).

A precise and accurate diagnosis of dagger nematode species in Syria is a crucial requisite for the selection of effective control methods. However, updated information on the biological diversity including DNA data, geographical occurrence, and distribution of dagger nematodes in banana (*Musa* sp.) plantations and their associated endosymbiont bacteria is lacking. Thus, the objectives of this work were the following: (1) to characterize and describe *Xiphinema* populations obtained from nematode surveys from two major banana-growing regions of the West Coast of Syria using integrative taxonomy; (2) to update information on the diversity of *Xiphinema* spp. recorded from Syria; (3) to establish

phylogenetic relationships of the identified *Xiphinema* species with available sequenced species; and (4) to characterise the diversity and phylogeny of *Candidatus* Xiphinematobacter associated with populations of the *X. americanum*-group obtained from present survey.

Material and methods

Soil sampling and morphological studies

During two consecutive years (2021–2022) on the west coast of Syria, soil samples were collected from the rhizosphere of banana plants (*Musa* sp.) in 95 fields located in two of the main banana-growing regions (Latakia and Tartous). All sampling areas were arbitrarily chosen. Longidorid specimens were extracted from 500 cm^3 soil samples using the modified Cobb washing, sieving and flotation technique (Flegg, 1967). As a result, 18 populations of *Xiphinema* were isolated from soil samples from which six populations were considered for further characterization (Table 1). The other populations showed low density (less than two juveniles were recovered).

After observation under a stereoscope, adult specimens of each morphotypes (or putative species) were hand-picked, and kept in both TAF fixative solution (Triethanolamine) and ethanol 70% (v/v) for morphological and molecular analyses, respectively.

Subsequently, specimens maintained in TAF were processed to glycerol using Seinhorst's method (Seinhorst, 1959) as modified by De Grisse (1969). The light micrographs and measurements of the nematode population, including the main diagnostic key characteristics [i.e., De Man indices (de Man, 1880), Loof-Coomans indices (Loof & Coomans, 1968), and other measurements and morphological features (Coomans et al., 2001; Lamberti et al., 2000, 2004; Loof & Luc, 1990)] were performed using an Olympus BX50 light microscope equipped with an Olympus DP70 digital camera (Olympus BX50, Hamburg, Germany) and Cell software (Olympus Software Imaging for Life Sciences). All measurements were expressed in micrometers (μm). All abbreviations are as defined in Jairajpuri and Ahmad (1992). Etymology used to describe the female genital branches is accodace with Coomans et al. (2001).

DNA sequencing and molecular methods

Total DNA isolation was performed using a thermodynamic and chemical approach according to Gutiérrez-Gutiérrez et al. (2020). DNA was extracted from a single individual adult specimen. Each individual nematode was placed in a 2 μL drop of sterile water on the flat cap of a PCR tube containing 20 μL of lysis buffer solution compounded by 10 μL ddH$_2$O, 6 μL 10×PCR buffer, 2 μL Mg^{2+} and 2 μL of proteinase K (20 mg/mL) (Nalgene®). Each specimen was cut into

Table 1 Five species of *Xiphinema* Cobb, 1913 recovered from the West Coast of Syria, their species names, locality, related plants, sequenced loci and GenBank accession numbers

Species	Sample code	Locality	Host	GenBank accession			
				D2-D3	ITS1	*COI* mtDNA	16S
Xiphinema diffusum	M64	Hraisson, Baniyas, Tartous	banana trees (*Musa* sp.)	OR196832, OR196837	OR197584	OR196695	OR196969, OR196971
Xiphinema pachtaicum	M54	Siyannu, Jableh, Latakia	banana trees (*Musa* sp.)	-	OR197587	OR196696	-
Xiphinema simile	M69	Hraisson, Baniyas, Tartous	banana trees (*Musa* sp.)	OR196834	OR264513	-	OR196970
Xiphinema vuittenezi	M78	Hraisson, Baniyas, Tartous	banana trees (*Musa* sp.)	OR196836, OR428495	OR197585	-	-
Xiphinema vuittenezi	M79	Hraisson, Baniyas, Tartous	banana trees (*Musa* sp.)	OR196835, OR428496	OR197586	OR196697	-
Xiphinema zagrosense	M74	Hraisson, Baniyas, Tartous	banana trees (*Musa* sp.)	OR196833	-	-	-

(-) Not obtained

several very small pieces, usually between three and five pieces, with surface-sterilized and pointed pins. Next, tubes were centrifuged at 12,000 rpm for 30 s to 1 min and frozen at −75 °C (for 60 min). Samples were mixed for 10 s, centrifuged at 12,000 rpm for 30 s to 1 min, and incubated at 57 °C (2 h), 65 °C (2 h) and 95 °C (15 min). PCR amplification was performed in a final volume of 25 μL containing: 1 μL of DNA template, 12.5 μL NZYTaq 2× Green Master Mix (1.25 mM MgCl2, 200 mM dNTPs, 0.2 U/μL DNA Polymerase) (NZYTech, Lisbon, Portugal), 0.6 μL of each primer (10 mM), and 10.3 μL of ddH$_2$O. Each rDNA (D2–D3 of 28S rRNA gene, the internal transcribed spacer 1 (ITS1) region, and 16S rRNA gene) and mtDNA (the partial portion of *COI* gene) fragment was amplified using one or several primer pairs (Table S1). All PCR assays were conducted as described by Gutiérrez-Gutiérrez et al. (2018, 2020). These PCR assays were conducted using DNA positive controls and a negative control containing sterile water. The PCR cycle conditions were followed as described by Gutiérrez-Gutiérrez et al. (2018, 2020) and Palomares-Rius et al. (2016, 2021). For a complete amplification of the 16S rRNA gene from the bacterial endosymbionts, specific PCR cycle conditions were used: initial denaturation at 95 °C for 3 min; followed by 30 amplification cycles of 94 °C for 30 s; an annealing temperature of 50 °C (27F/1492R; 27F/920R; 27F/800R) or 55 °C (360F/920R; 360F/1492R) for 30 s, 72 °C for 30–60 s; and final extension of 72 °C for 10 min. Each PCR product was purified and sequenced by STABV-IDA (Caparica, Portugal). Additionally, 360R, 800R, 920R and 1100R primers (Table S1) were used to guarantee a robust and complete sequence. All new sequences of the Syrian populations of dagger nematode species were deposited into the GenBank database under the accession numbers indicated on the Table 1.

Molecular phylogenetic analyses

The newly obtained rDNA sequences (D2–D3 expansion segments of 28S rRNA gene and partial ITS1) and mtDNA sequences (partial *COI* mtDNA gene) from all known dagger nematode species and complete 16S rRNA from all endosymbiotic bacteria found in this survey (Table 1), together with other available selected sequences from the National Center

for Biotechnology Information (NCBI) were used for phylogenetic analyses. Outgroup taxa for each studied gene was chosen according to previously published data by Archidona-Yuste et al. (2016a, b), Mobasseri et al. (2019a, b) and Palomares-Rius et al. (2016). MAFFT v. 7 (Katoh et al., 2019) and ClustalX2 (Larkin et al., 2007) with default parameters used for aligning. After sequence alignment, ambiguous regions were removed with Gblocks v. 0.91b (Castresana, 2000) using less stringent parameters (www. phylogeny.fr). Homogeneities of base frequencies and optional substitution models for 28S rRNA, ITS1, 16S rRNA, and COI mtRNA datasets were tested with Kakusan4 (Tanabe, 2011). Bayesian inference (BI) was performed using the software MrBayes v. 3.2.1 (Ronquist et al., 2012). For BI, the substitution model was selected by the Bayesian information criterion (BIC) and five different models were selected for our study. Convergence of the MCMC chains and burn-in length were assessed and checked in Tracer 1.7.1 (Rambaut et al., 2018). A number of 5,000,000 generations was performed for each BI analysis, sampling every 100th tree and discarding 25% of samples as 'burn-in'. Finally, the final consensus trees were visualized using FigTree v. 1.4.3 (Rambaut, 2009).

Results

Morphology and morphometrics of dagger nematode species of the genus Xiphinema recovered from the West Coast of Syria

Syrian population of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979 (Fig. 1; Table 2).

Distribution

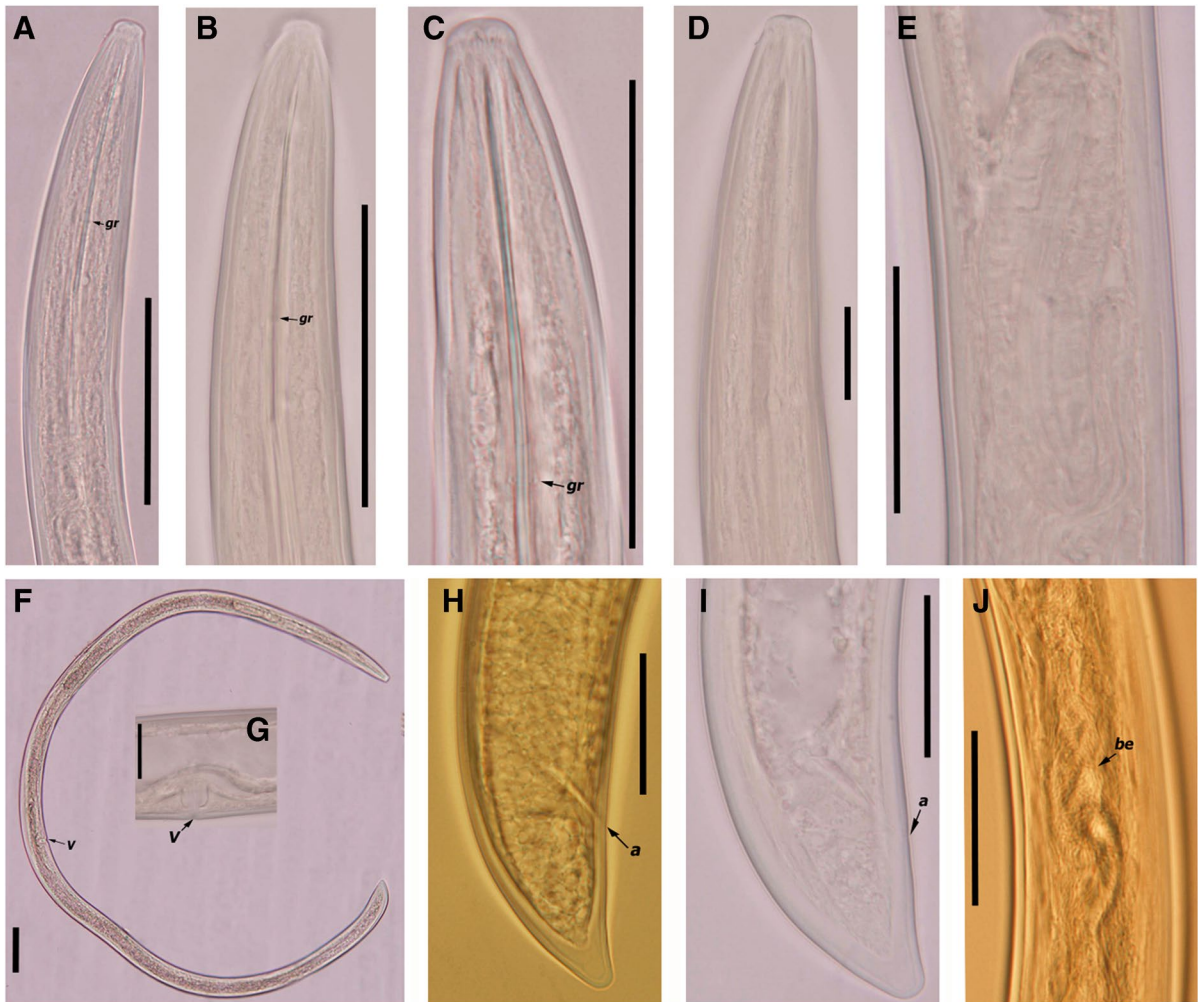Collected from the rhizosphere of banana (*Musa* sp.) trees at Hraisson, Baniyas district, Tartous, Syria (Table 1).

Brief description

The Syrian population of this species was characterised by a robust body, forming a close C-to open spiral when killed by heat. Cuticle appearing smooth, 2.5 (2.4–2.6) μm thick along body but thicker at the tail tip. Lip region expanded, rounded laterally and

Fig. 1 Light micrographs of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979 females from the rhizosphere of banana (*Musa* sp.) from Hraisson (Baniyas, Tartous), Syria (**A-J**). A-B: Female anterior body region; **C-D**: Lip region; **E**: Basal bulb; **F**: Entire female specimen; **G**: Vulva region; **H**: J4 tail region; **I**: Female tail region; **J**: Bacterial endosymbionts. Abbreviations: a = anus; be = bacterial endosymbionts; gr = guiding ring; v = vulva. (Scale bars: A-C = 75 μm; D, H = 25 μm; E, I = 30 μm; F = 85 μm; G = 20 μm; J = 43 μm)

slightly flattened frontally, separated from the rest of the body by a shallow constriction. Odontostyle robust 1.7 (1.6–1.8) times longer than the odontophore, the latter with well-developed flanges (Fig. 1). Guiding sheath typical of the genus with the guiding ring at about 75.8 (71.4–79.1) μm distance from anterior end. Basal bulb cylindrical, 4.0 (3.5–4.7) times longer than wide. Glandularium 3.6 (3.4–3.8) times longer than basal bulb width. Cardia with hemispherical shape, 4.3 (3.9–4.5) μm long. Prerectum often indistinct. Rectum clearly visible 27 (24.4–29.1) μm long. Reproductive system didelphic-amphidelphic with equally developed branches, anterior branch 229 (213.2–246.5) μm long and posterior branch 258 (251.4–267.0) μm long, opposed, ovaries reflexed, and uteri short, without any differentiations. Ovaries showing bacterial endosymbionts (Fig. 1J). Vulva slightly post-equatorial, a transverse slit; vagina occupying two-third of the corresponding body width. Tail short, dorsally convex, slightly concave ventrally with rounded terminus. Males were not fround for this species. Only fourth (J4) juvenile stages were found and they were distinguished from other stages according to Robbins et al. (1996) (Table 2). Fourth

Table 2 Morphometrics of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979, *Xiphinema simile* Lamberti et al., 1983, *X. pachtaicum* (Tulaganov, 1938) Kirjanova, 1951, *X. vuittenezi* Luc et al., 1964, and *X. zagrosense* Ghaemi, Pourjam, Pedram, Robbins, Ye, & Decraemer, 2012 from the rhizosphere of banana (*Musa* sp.) from Latakia and Tartous, Syria. All measurements in µm and in the format: mean ± s.d. (range)*

Species	X. diffusum		X. simile	X. pachtaicum	X. vuittenezi			X. zagrosense
Character	M64		M69	M54	M79			M74
Character	Females	J4	Females	Females	Females	J4	J3	Female
n	7	2	4	4	4	5	1	1
L	1564.8 ± 132.3 (1383.5–1702.8)	(1376.0, 1386.3)	1746.6 ± 43.3 (1703.5–1790.0)	2038.8 ± 61.7 (1989.7–2108.0)	2626.0 ± 172.0 (2369.0–2739.0)	1725.0 ± 112.4 (1836.0–2118.4)	1616.2	4131.6
a	37.1 ± 3.5 (32.5–40.7)	(33.9, 35.3)	62.6 ± 1.7 (60.9–64.4)	60.8 ± 1.0 (59.8–61.8)	45.9 ± 1.7 (44.1–48.0)	46.4 ± 1.3 (45.2–48.4)	40.4	59.3
b	6.1 ± 0.4 (5.6–6.5)	(4.4, 5.4)	6.9 ± 0.4 (6.5–7.4)	8.2 ± 0.0 (8.1–8.2)	5.6 ± 1.1 (4.0–6.5)	4.8 ± 8.3 (4.4–5.3)	4.9	6.7
c	58.0 ± 2.0 (56.4–60.3)	(44.4, 45.2)	61.4 ± 3.4 (57.7–64.4)	74.4 ± 2.1 (72.3–76.5)	75.8 ± 7.1 (68.3–82.2)	53.8 ± 4.9 (49.1–61.4)	38.9	107.4
c′	1.0 ± 0.0 (0.9–1.0)	(1.2, 1.2)	1.7 ± 0.0 (1.6–1.7)	1.4 ± 0.0 (1.4–1.4)	0.9 ± 0.1 (0.8–0.9)	1.1 ± 0.1 (1.0–1.2)	1.4	0.8
V (%)	54.3 ± 0.4 (53.9–54.9)	-	59.9 ± 0.7 (59.1–60.4)	56.4 ± 0.4 (56.1–56.9)	50.9 ± 0.8 (51.1–52.0)	-	-	48.5
G$_1$ (%)	14.3 ± 1.8 (12.5–16.1)	-	9.5 ± 1.1 (8.9–10.8)	9.8 ± 0.6 (9.3–10.2)	12.6 ± 0.3 (12.4–12.9)	-	-	11.6
G$_2$ (%)	16.1 ± 1.4 (14.8–17.4)	-	8.9 ± 0.3 (8.7–9.3)	8.5 ± 0.7 (8.0–9.0)	12.2 ± 0.2 (12.0–12.3)	-	-	12.2
Odontostyle length	90.9 ± 0.9 (89.8–92.2)	(74.0, 74.8)	72.6 ± 1.4 (71.5–74.2)	90.9 ± 0.4 (90.5–91.3)	138.3 ± 3.9 (133.0–141.5)	109.0 ± 3.0 (106.0–113.8)	91.8	155.0
Replacement odontostyle length	-	(85.9, 93.2)	-	-	-	132.7 ± 3.4 (127.8–135.5)	109.7	-
Odontophore length	52.7 ± 2.9 (49.6–55.8)	(45.7, 46.5)	40.3 ± 0.8 (39.4–41.0)	50.1 ± 0.3 (49.8–50.4)	67.8 ± 2.2 (65.4–70.5)	62.0 ± 3.7 (56.0–65.9)	56.9	102.5
Lip region width	12.2 ± 0.5 (11.5–12.7)	(10.2, 11.2)	9.2 ± 0.3 (8.9–9.4)	9. 2 ± 0.2 (9.0–9.4)	13.5 ± 0.6 (12.9–14.2)	11.6 ± 0.3 (11.2–12.1)	10.5	13.6
Lip region height	4.4 ± 0.6 (3.7–4.9)	(3.7, 4.4)	3.7 ± 0.3 (3.3–4.0)	3.6 ± 0.4 (3.2–3.9)	5.2 ± 0.5 (4.6–5.5)	3.4 ± 0.3 (3.2–3.8)	3.0	4.6
Oral aperture-guiding ring	75.0 ± 3.8 (71.4–79.1)	(60.1, 60.4)	62.7 ± 0.7 (61.9–63.4)	75.1 ± 0.8 (74.3–75.9)	126.7 ± 10.2 (114.9–133.0)	99.9 ± 3.6 (94.5–103.4)	79.3	157.2
Pharynx length	258.9 ± 19.3 (225.0–273.6)	(257.1, 313.2)	254.2 ± 20.4 (230.6–267.4)	251.8 ± 11.6 (244.3–265.1)	478.0 ± 77.2 (419.0–591.5)	412.5 ± 12.5 (399.7–431.0)	332.0	612.9
Pharyngeal basal bulb length	71.6 ± 3.1 (69.1–75.4)	(64.4, 66.1)	71.8 ± 2.1 (69.8–74.0)	76.5 ± 1.3 (75.0–77.3)	98.4 ± 1.4 (97.4–100.0)	87.0 ± 8.4 (77.3–99.6)	65.7	169.8
Pharyngeal basal bulb width	18.2 ± 1.6 (16.0–19.9)	(17.0, 18.6)	11.3 ± 1.3 (10.0–12.5)	13.2 ± 0.6 (12.7–13.9)	20.9 ± 3.7 (17.0–24.3)	19.5 ± 2.8 (15.6–23.3)	20.1	21.35

Table 2 (continued)

Species	X. diffusum		X. simile	X. pachtaicum	X. vuittenezi			X. zagrosense
Character	M64		M69	M54	M79			M74
Character	Females	J4	Females	Females	Females	J4	J3	Female
Gladu-larium length	63.1 ± 2.3 (60.9–65.0)	(50.2, 55.0)	60.3 ± 3.3 (56.5–62.7)	66.8 ± 0.2 (66.6–67.0)	86.0 ± 1.8 (84.0–87.4)	74.6 ± 4.0 (71.6–81.4)	-	148.2
Cardia length	4.3 ± 0.3 (3.9–4.5)	(3.3, 3.7)	3.2 ± 0.4 (2.8–3.6)	4.2 ± 1.1 (3.0–5.0)	6.2 ± 0.5 (5.8–6.5)	4.6 ± 1.3 (3.5–6.0)	-	7.08
Body width at mid-body	42.4 ± 4.7 (37.4–47.9)	(39.0, 40.6)	27.9 ± 0.1 (27.8–28.0)	33.2 ± 0.5 (32.7–33.6)	57.3 ± 5.6 (49–3–62.1)	42.2 ± 2.2 (39.0–44.6)	39.9	69.7
Body width at anus	27.68 ± 2.1 (24.8–30.2)	(24.6, 25.2)	17.1 ± 0.5 (16.6–17.6)	19.2 ± 0.5 (18.7–19.8)	39.9 ± 4.0 (33.9–42.3)	33.6 ± 1.9 (30.7–36.0)	29.1	48.1
Body width at guiding ring	30.5 ± 2.5 (27.6–33.6)	(26.1, 28.9)	18.7 ± 0.3 (18.4–18.9)	22.9 ± 0.2 (22.6–23.1)	43.3 ± 4.7 (37.2–48.8)	37.3 ± 1.4 (35.6–39.4)	31.5	47.8
Tail length	27.0 ± 2.6 (23.0–29.9)	(30.7, 31.0)	28.5 ± 0.9 (27.8–29.5)	26.7 ± 0.7 (26.2–27.5)	34.9 ± 4.7 (29.0–39.6)	36.6 ± 2.3 (33.7–38.8)	41.6	38.5
Vagina total	21.3 ± 1.5 (20.2 –23.9)	-	15.8 ± 0.9 (15.3–16.6)	18.9 ± 0.8 (18.1–19.7)	29.8 ± 1.3 (28.7–31.6)	-	-	44.4
Cuticle wide at mid-body	2.5 ± 0.1 (2.4 –2.6)	(1.9, 2.3)	1.4 ± 0.1 (1.3 –1.5)	1.7 ± 0.2 (1.5 –1.9)	3.3 ± 0.5 (2.6 –3.8)	3.0 ± 0.3 (2.5 –3.2)	2.1	3.57
Rectum length	25.4 ± 4.0 (19.3–29.1)	(18.0, 18.2)	16.7 ± 1.9 (14.5–18.0)	19.6 ± 1.2 (18.7–21.0)	41.4 ± 1.1 (40.6–42.1)	31.7 ± 1.5 (29.2–32.8)	24.0	49.9
J	9.3 ± 1.1 (7.5–10.3)	(8.2, 10.1)	5.7 ± 0.6 (5.3–6.4)	10.6 ± 1.2 (9.3 –11.5)	13.4 ± 1.9 (12.2 –16.2)	8.6 ± 0.6 (7.9 –9.3)	6.9	13.4
Peg	-	-	-	-	4.8 ± 1.6 (3.0–5.9)	7.7 ± 1.7 (4.9–9.2)	12.2	-

*Abbreviations are defined inJairajpuri and Ahmad (1992)

(-) Not obtained

(J4) juvenile stages were similar to adult specimens, except for their smaller size, longer tail, higher index c´, and absence of sexual characteristics (Fig. 1H).

Remarks

This species was found in a soil sample of banana (*Musa* sp.) trees (sample code: M64) at Hraisson, Baniyas district, Tartous, Syria (Table 1). The population presented low numbers of individuals in soil (20 individuals/500 cm³ of soil). The morphological and morphometric traits of this population closely agree with those of the type population (Lamberti & Bleve-Zacheo, 1979) and other subsequent records of this species (Chen et al., 2005; Heyns & Coomans, 1994; Lamberti et al., 1991, 2002; Lazarova et al., 2006; Luc et al., 1998; Shokoohi et al., 2021; Wang et al., 1996), except for minor intraspecific variations in the a and c ratios (e.g. 46–51 μm and 63–84 μm in the type population *vs* 33–41 μm and 56–60 μm), which may be because of geographical intraspecific variability. Apparently, our population of this species is almost indistinguishable from other species belonging to the *X. brevicolle* species complex (Lazarova et al., 2019), except by minor differences in morphological data, morphometric measures, but conspicuous differences in DNA sequences at level of the nematode and its associated bacterial endosymbionts. This species was originally described infecting *Pelargonium* plants in Réunion Island, Africa (Lamberti & Bleve-Zacheo, 1979) and later was reported from

cultivated and wild ecosystems worldwide (Lamberti et al., 2000, 2002; Chen et al., 2005; Oliveira et al., 2005; Lazarova et al., 2006, 2019; Gutiérrez-Gutiérrez et al., 2016; Shokoohi et al., 2021). To our knowledge, these findings represent the first record for this species associated with banana plants in Syria, extending its geographical distribution in Asia.

The Syrian population of *Xiphinema pachtaicum* (Tulaganov, 1938) Kirjanova, 1951 (Fig. 2; Table 2).
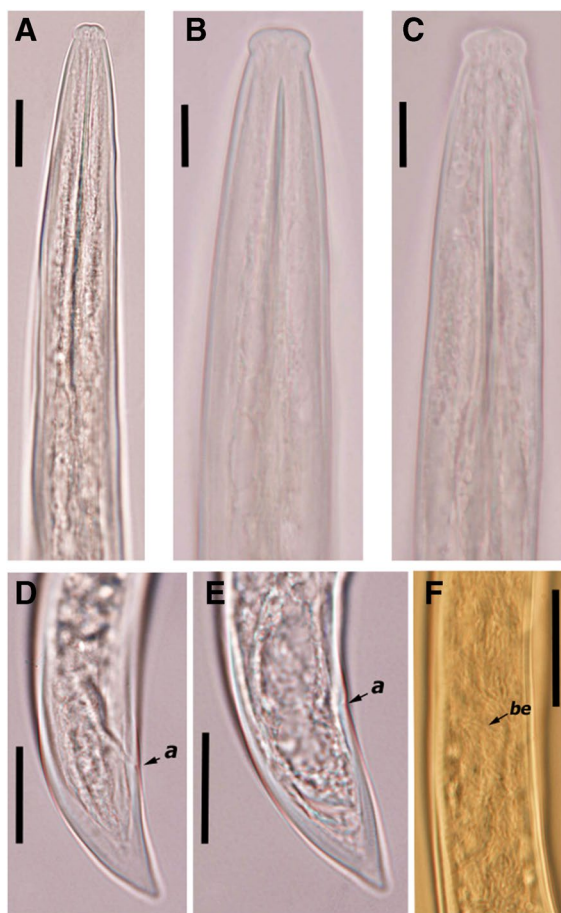
Fig. 2 Light micrographs of *X. simile* Lamberti et al., 1983 (**A-B, D, F**) and *X. pachtaicum* (Tulaganov, 1938) Kirjanova, 1951 (**C, E**) from the rhizosphere of banana (*Musa* sp.) from Hraisson (Baniyas, Tartous), and Siyannu (Jableh, Latakia), Syria (**A-F**). **A**: Female anterior body region; **B-C**: Lip region; **D-E**: Female tail region; **F**: Bacterial endosymbionts. Abbreviations: a = anus; be = bacterial endosymbionts. (Scale bars: A, E = 18 μm; B-C = 9 μm; D = 17 μm; F = 28 μm)

Distribution

Collected from the rhizosphere of banana (*Musa* sp.) trees at Siyannu, Jableh district, Latakia, Syria (Table 1).

Brief description

The Syrian population of this species was characterised by a slender body, forming a close C to coiled spiral, when killed by heat. Cuticle appearing smooth, 1.7 (1.5–1.9) μm thick along body but thicker at tail tip. Lip region expanded and distinctly offset from the rest of the body. Odontostyle long, 1.8 times longer than the odontophore with weak flanges. Guiding sheath typical of the genus with the guiding ring near the base of the odontostyle. Basal bulb cylindrical, 5.8 (5.5–6.0) times longer than wide. Glandularium 5.0 (4.8–5.2) times longer than basal bulb width. Cardia conoid-rounded, 4.2 (3.0–5.0) μm long. Prerectum indistinct. Rectum visible, 19.6 (18.7–21.0) μm long. Reproductive system didelphic-amphidelphic with two short and equally developed genital branches, anterior branch 196.1 (188.6–203.9) μm long and posterior branch 170.6 (162.0–179.7) μm long, ovaries opposed and reflexed, and uteri without any differentiations. Ovaries darkened in fixed specimen, endosymbionts apparently absent under light microscope. Vulva, posterior to mid-body, a transverse slit; vagina occupying two-third of the corresponding body width. Tail conoid with pointed terminus. Males and juveniles were not found for this species.

Remarks

This species was found in a soil sample of banana (*Musa* sp.) tree (sample code: M54) at Siyannu, Jableh district, Latakia, Syria (Table 1). This population presented low specimens densitiy (14 individuals/500 cm^3 of soil). The morphological traits and morphometric data of females closely agree with those of the described population by Lamberti and Siddiqi (1977) and with other populations already reported (Barsi & Lamberti, 2002; Fadaei et al., 2003; Getaneh et al., 2015; Gutiérrez-Gutiérrez et al., 2011a, b; Kumari et al., 2005; Lamberti & Bleve-Zacheo, 1979; Lamberti et al., 1993; Mobasseri et al., 2019a, b; Vazifeh et al., 2019). Our population of this species is almost indistinguishable from other *X.*

pachtaicum-subgroup species (Gutiérrez-Gutiérrez et al., 2012; Archidona-Yuste et al., 2016b), except by some indiscernible morpho-anatomical differences, but notable differences in DNA sequences. Although this species has already been reported from Syria by Lamberti (1984) and Greco et al. (1992), no molecular and morphometric data were formerly provided for those populations. This species is widespread in the countries bordering the Mediterranean Sea, central and Eastern Europe, Africa and Asia (Gutiérrez-Gutiérrez et al., 2016; Lamberti et al., 2000, 2002; Taylor & Brown, 1997). To our knowledge, this is the first record of this species associated with banana plants in Syria. Furthermore, these findings confirm that it is widely distributed in the Middle Eastern.

The Syrian population of *Xiphinema simile* Lamberti et al., 1983 (Fig. 2; Table 2).

Distribution

Collected from the rhizosphere of banana (*Musa* sp.) trees at Hraisson, Baniyas district, Tartous, Syria (Table 1).

Brief description

The Syrian population of this species was characterised by a slender body, forming a close C to spiral shape when killed by heat. Cuticle smooth under light microscope, 1.4 (1.3–1.5) µm thick along body but thicker at tail tip. Lip region expanded, flat, rounded in corners, and offset from the rest of the body. Odontostyle 1.8 (1.8–1.9) times longer than the odontophore, the latter with weak flanges. Guiding ring 62.7 (61.9–63.4) µm from the anterior end. Basal bulb cylindrical, 6.4 (5.6–7.4) times longer than wide. Glandularium 5.4 (5.0–5.7) times longer than basal bulb width. Cardia conoid-rounded shape, 3.2 (2.8–3.6) µm long. Prerectum indistinct. Rectum 16.7 (14.5–18.0) µm long. Reproductive system didelphic-amphidelphic with two equally developed branches, anterior branch 165.3 (153.0–188.1) µm long and posterior branch 154.6 (150.1–160.2) µm long, opposed and reflexed ovaries with bacterial symbionts, and short uteri without any differentiation, vulva, posterior to mid-body, a transverse slit; vagina occupying 55–59% of the corresponding body diameter. Tail conical, dorsally convex, with finely rounded

terminus. Males and juveniles were not found for this species.

Remarks

This species was found in a soil sample of banana (*Musa* sp.) tree (sample code: M69) at Hraisson, Baniyas district, Tartous, Syria (Table 1) in low density (18 individuals/500 cm³ of soil). The morphological features and morphometric measurements of females closely agree with those of the type population (Lamberti et al., 1983) and with other populations from Europe (Barsi & De Luca, 2008; Barsi & Lamberti, 2002, 2004; Barsi, 1994a; Kumari, 2006; Lamberti et al., 1999b; Lazarova et al., 2008; Lišková, 1995; Lišková & Brown, 1996; Lišková et al., 1993; Peneva & Choleva, 1992; Repasi et al., 2008) and outside Europe (Coomans & Heyns, 1997; Naghavi et al., 2022a). It is morphologically close to other members of *X. simile*-subgroup species (Lazarova et al., 2016a, b), except by some minor morphological and morphometric differences, but remarkable differences in DNA sequences. *Xiphinema simile* is widespread in the European countries in association with agricultural crops, and landscape trees and grasslands (Barsi & De Luca, 2008; Barsi & Lamberti, 2002, 2004; Barsi, 1994a; Kumari, 2006; Lamberti et al., 1999b, 2000; Lazarova et al., 2008; Lišková, 1995; Lišková & Brown, 1996; Lišková et al., 1993; Peneva & Choleva, 1992; Repasi et al., 2008; Taylor & Brown, 1997). Outside Europe, this species has been only reported from Kenya (Coomans & Heyns, 1997) and Iran (Naghavi et al., 2022a). To our knowledge this is the first record of this species infesting soils around banana trees in Syria, extending its geographical distribution in the Middle Eastern.

The Syrian populations of *Xiphinema vuittenezi* Luc, Lima, Weischer, Flegg, 1964 (Fig. 3; Table 2).

Distribution

It was recovered from two soil samples collected from the rhizosphere of banana (*Musa* sp.) trees at Hraisson, Baniyas district, Tartous, Syria (Table 1).

Brief description

The Syrian population of this species was characterised by a cylindrical body, forming a close C, when
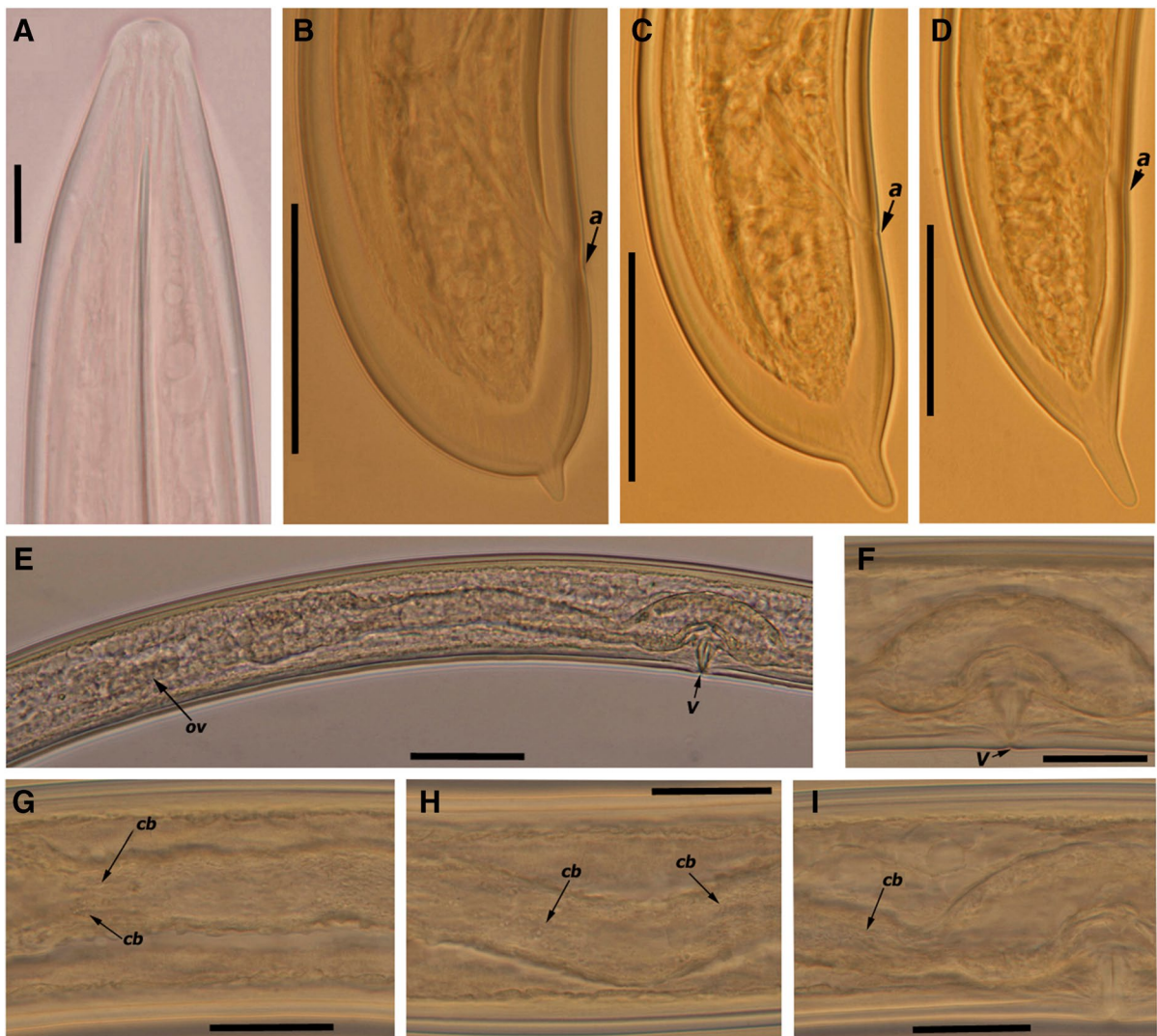
Fig. 3 Light micrographs of *Xiphinema vuittenezi* Luc, Lima, Weischer, Flegg, 1964 females from the rhizosphere of banana (*Musa* sp.) from Hraisson (Baniyas, Tartous), and Siyannu (Jableh, Lattakia), Syria (**A-I**). **A**: Lip region; **B**: Female tail region; **C**: J4 tail; **D**: J3 tail; **E**: Posterior reproductive branch; F: Vulva region; G-I: detail of female genital track showing crystalloid bodies. Abbreviations: a = anus; cb = crystal bodies; gr = guiding ring; ov = ovary; v = vulva. (Scale bars: A = 13 μm; B = 41 μm; C-D = 30 μm; E = 58 μm; F-I = 29 μm)

killed by heat. Cuticle smooth under light microscope, 3.3 (2.6–3.8) μm thick along body but thicker at tail tip. Lip region rounded, offset from the rest of the body by depression. Odontostyle robust, two times longer than the odontophore, the later with well-developed flanges. Guiding ring 126.7 (114.9–133.0) μm from the anterior end. Basal bulb cylindrical, 4.8 (4.0–5.9) times longer than wide. Glandularium 4.2 (3.6–4.9) times longer than basal bulb width. Cardia conoid-rounded, 6.2 (5.8–6.5) μm long. Prerectum

579.5 (573.7–585.3) μm long. Rectum as long as the anal body diameter. Reproductive system didelphic-amphidelphic with branches about equally developed without any Z-differentiation but containing crystalloid bodies distributed over the entire length (Fig. 3). Vulva a transverse slit, situated at mid-body; vagina usually occupying half of the corresponding body diameter. Tail short, broadly round, with a peg (Fig. 3). Males were not found for this species. Third (J3) and fourth (J4) juvenile stages were found and

they were similar to adult specimens, except for their smaller size, higher index c´, and absence of sexual characteristics (Fig. 3). All stages are distinguishable by relative body lengths, functional, and replacement odontostyle (Robbins et al., 1996) (Table 2). J3 characterized by a conical tail with a rounded end subdigitate extension (Fig. 3). J4 characterized by a tail bluntly rounded, slightly dorsally convex-conoid with a terminal peg (Fig. 3).

Remarks

This species was found in two soil samples collected from the rhizosphere of banana (*Musa* sp.) trees (sample codes: M78 and M79) at Hraisson, Baniyas district, Tartous, Syria (Table 1). The only one adult specimen that was detected in the sample M78 was checked under light microscope before sequencing it. Then, this population (M78) was only molecularly characterized. The code 79 showed low nematode density (14 individuals/500 cm³ of soil). The morphological features and morphometric measurements of the fixed females closely agree with those of the type population (Luc et al., 1964), in which their authors did not consider the presence of crystalloids in this species (Coomans et al., 2001). It matches well with other populations from Europe and Middle East (i.e. Mojtahedi et al., 1980; Barsi, 1989, 1994b; Roca et al., 1989, 1991; Coiro et al., 1989, 1992; Barsi & Lamberti, 2000; Kumari et al., 2005; Groza et al., 2013; Gutiérrez-Gutiérrez et al., 2016; Vazifeh et al., 2019; Naghavi et al., 2022b), except for minor differences in the body length and b ratio (e.g. 2800–3400 μm and 6.7–7.0; 3008–4109 μm and 6.0–8.7; 3250 –3760 μm and 7.3–7.9 *vs* 2369–2739 μm, 4.0–6.5) (Kumari et al., 2005; Roca et al., 1989; Vazifeh et al., 2019) which may be because of geographical intraspecific variability. This species is widespread in the European countries, especially Central Europe (Mojtahedi et al., 1980; Lamberti et al., 1983; Barsi, 1989, 1994b; Roca et al., 1989, 1991; Taylor & Brown, 1997; Coiro et al., 1989, 1992; Barsi & Lamberti, 2000; Coomans et al., 2001; Walker, 2004; Kumari et al., 2005; Groza et al., 2013; Vazifeh et al., 2019; Naghavi et al., 2022b). To our knowledge this is the first record of this species associated with banana plants. Furthermore, these findings represent the first detection of this species in Syria.

The Syrian population of *Xiphinema zagrosense* Ghaemi, Pourjam, Pedram, Robbins, Ye & Decraemer, 2012 (Fig. 4; Table 2).

Distribution

Collected from the rhizosphere of banana (*Musa* sp.) trees at Hraisson, Baniyas district, Tartous, Syria (Table 1).

Brief description

The Syrian population of this species is characterised by a cylindrical body, forming an open C shape when killed by heat. Cuticle smooth under light microscope, 3.57 μm thick at mid-body. Lip region rounded, separate from the rest of the body by a slight depression. Odontostyle robust, 1.5 times longer than the odontophore, the later with well-developed flanges. Guiding ring 157.2 μm from the anterior end. Basal bulb cylindrical, eight times longer than wide. Glandularium seven times longer than basal bulb width. Cardia semi-circular, 7.1 μm long. Prerectum 11 times the anal body diameter and rectum as long as the anal body diameter. Reproductive system didelphic-amphidelphic with branches about equally developed without Z-differentiation, uterus bipartite which is composed of *pars dilatata uteri* and tubular portion with crystalloids (Fig. 4). Vulva a transverse slit, situated at mid-body; vagina occupying more than half of the corresponding body diameter. Tail convex conoid with a broadly rounded terminus (Fig. 4). Male and juveniles were not found for this species.

Remarks

This dagger nematode species was found in a soil sample of banana (*Musa* sp.) tree (sample codes: M74) at Hraisson, Baniyas district, Tartous, Syria (Table 1). It showed a low density (2 individuals/500 cm³ of soil). The morphological and morphometric features of females closely agree with those of the type population (Ghaemi et al., 2012), except for minor differences in the lip region diameter and height (15.0–18.0 μm and 7.0–9.0 μm *vs* 13.6 μm and 4.6 μm), which should be considered as an intraspecific variability. This species is morphologically close to members of *X. pyrenaicum* complex (Gutiérrez-Gutiérrez et al., 2010; Lamberti et al., 1992; Pedram

Fig. 4 Light micrographs of *Xiphinema zagrosense* Ghaemi, Pourjam, Pedram, Robbins, Ye & Decraemer, 2012 female from the rhizosphere of banana (*Musa* sp.) from Hraisson (Baniyas, Tartous), Syria (A-H). **A-B**: Lip regions; **C**: Vulva region; **D**: detail of female genital track showing crystalloid bodies; **E–F**: Female tail region; **G**: Detail of basal bulb; **H**: posterior uterine branch. Abbreviations: a = anus; cb = crystalloid bodies; ov = ovary; v = vulva. (Scale bars: A-B = 22 μm; C-D = 35 μm; E–F: 48 μm; G = 42 μm; H: 70 μm)
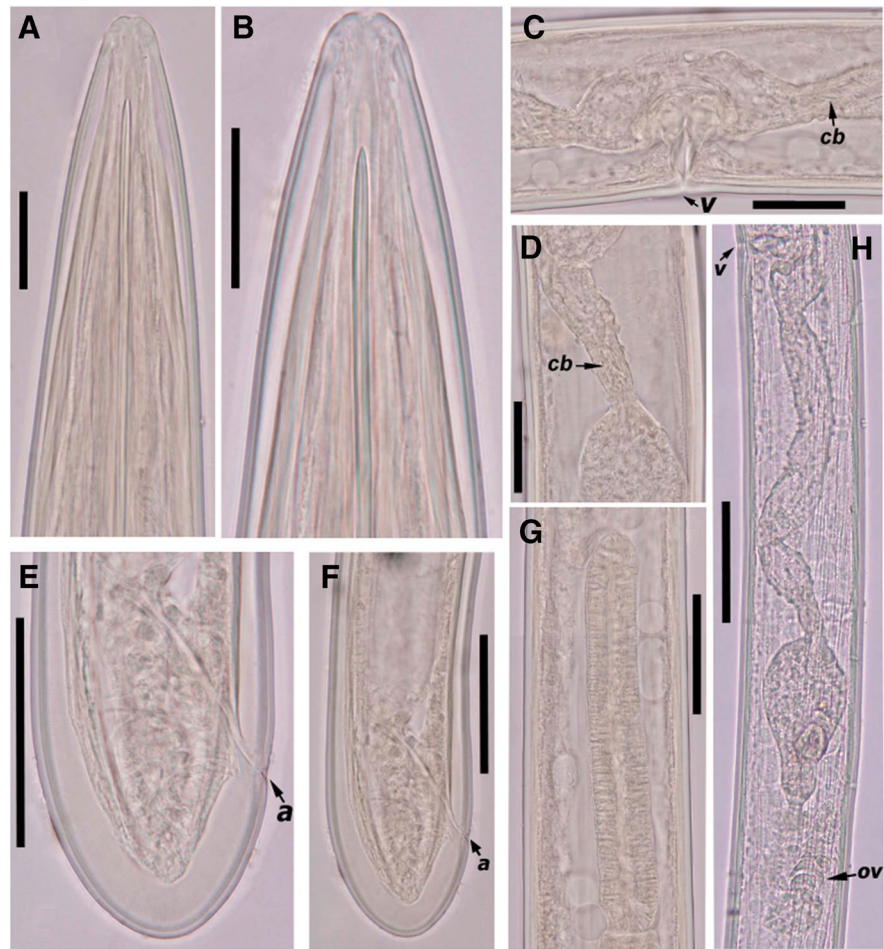

et al., 2009, 2012), except by some indiscernible morpho-anatomical differences, but notable differences in DNA sequences. This species was described in association with grasses in natural environments from Iran (Ghaemi et al., 2012). To our knowledge, this is the first record of this species outside its type locality, extending its distribution in the world, and first report of its association with banana plants.

Sequence analysis and phylogeny of 28S rRNA gene

Xiphinema americanum-group spp.
The two 28S sequences of the Syrian isolate of *X. diffusum* (OR196832, OR196837) obtained showed high homology (99–100%) with *X. brevicolle* complex, such as *X. diffusum* (e.g., AY601600, MK050001, and MK050002) and *X. brevicolle* Lordello & Da Costa 1961 (e.g., KY512785– KY512787 and AY601601),

but presented less than 98% homology with the topotype population of *X. brevicolle* (MH248813). The 28S sequence of *X. simile* (OR196834) showed a high homology (99–100%) with sequences of the same species, namely *X. simile* (AY601609, JQ780368–JQ780370, KJ802889–KJ802890, ON500623, MK957227–MK957228). For these species, the respective Bayesian phylogenetic tree (Fig. 5) showed that *X. diffusum* and *X. brevicolle* were grouped together within the well-supported clade of these same species and clearly separated from the topotype population of *X. brevicolle* (MH248813). These results could be due to a possible misidentification of the species in GenBank. Although the Syrian isolate of *X. simile* was phylogenetically closest to European and Asian populations of the same species (e.g. AY601609, JQ780368–JQ780370, KJ802889– KJ802890), the
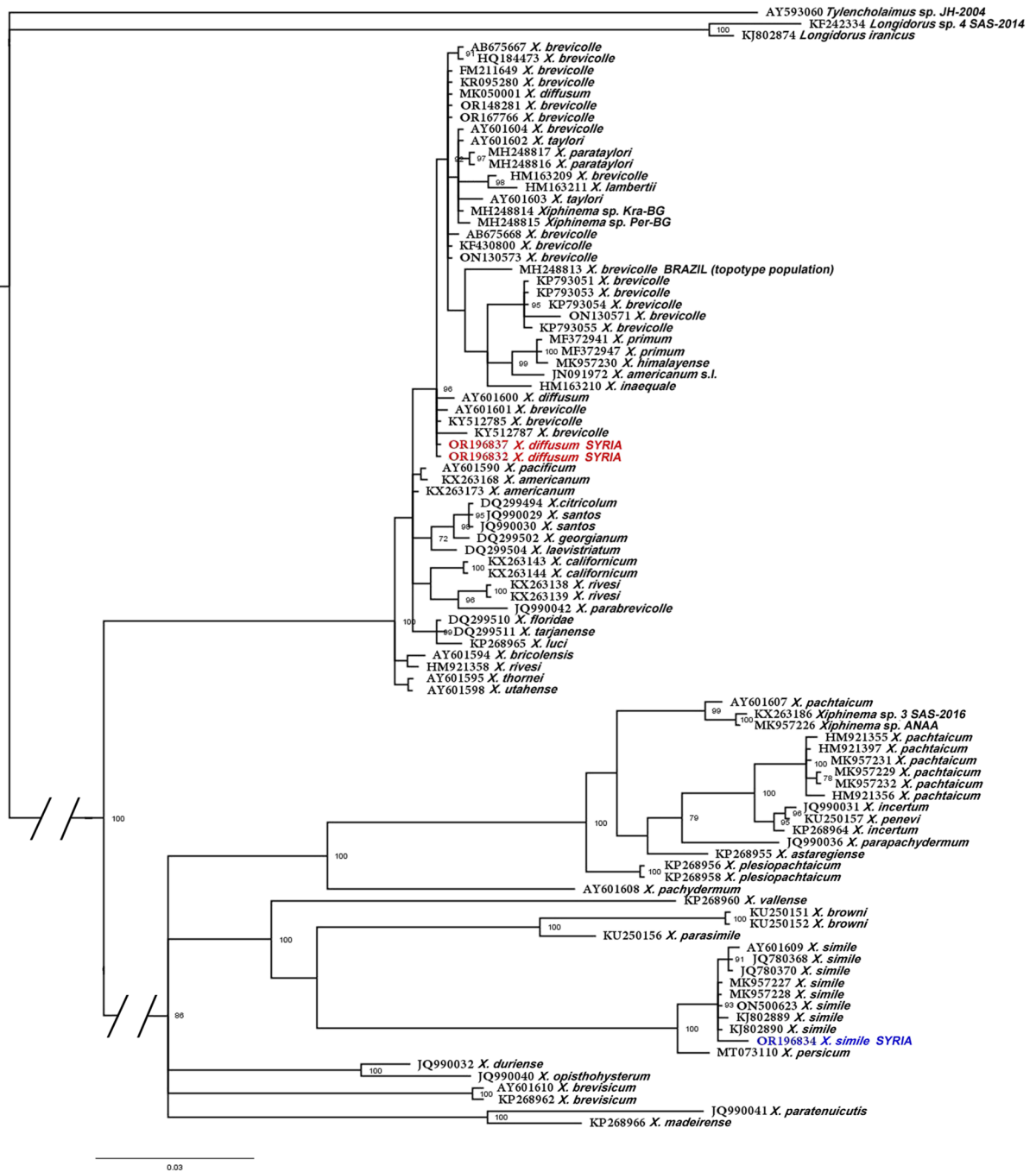
Fig. 5 Phylogenetic relationships of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979 and *X. simile* Lamberti et al., 1983. Bayesian 50% majority rule consensus trees was inferred from 96 sequences of D2-D3 expansion segments (713 bp) of 28S rRNA sequences aligned under the SYM + G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in red and navy blue. Scale bar = expected changes per site
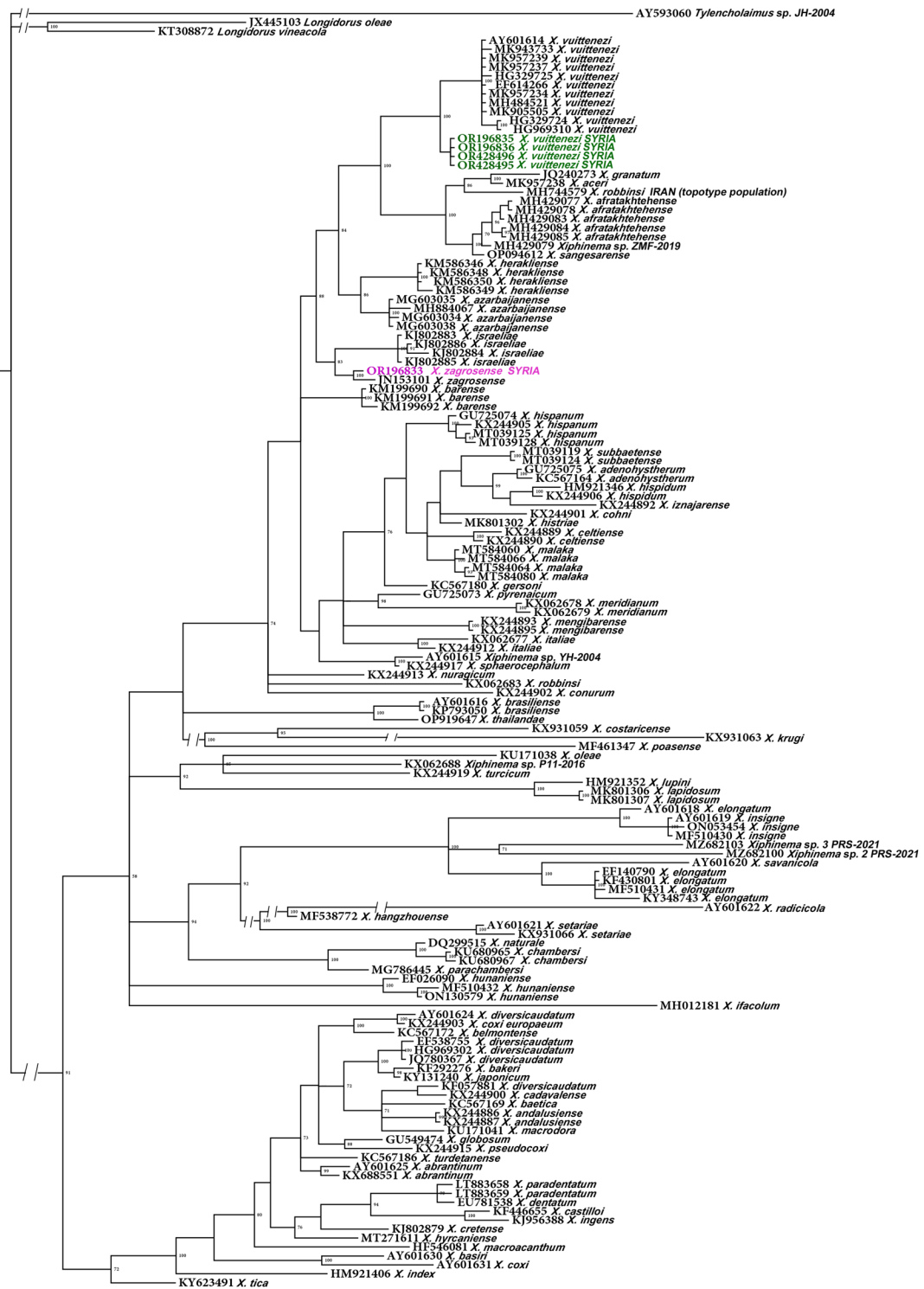
◀ **Fig. 6** Phylogenetic relationships of *Xiphinema vuittenezi* Luc et al., 1964*, and *X. zagrosense* Ghaemi, Pourjam, Pedram, Robbins, Ye, & Decraemer, 2012. Bayesian 50% majority rule consensus trees was inferred for 143 sequences of D2-D3 expansion segments (673 bp) of 28S rRNA sequences aligned under the GTR + G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in green and pink. Scale bar = expected changes per site

length of all these sequences were different, yielding intraspecies cladogenesis and varied branch lengths inside this species clade.

Xiphinema non americanum-group spp.

The 28S sequences from Syrian populations of *X. vuittenezi* (OR196835–OR196836, OR428495–OR428496) matched closely (more than 99% of similarity) to an Iran popuation of the same species (MK905505), varying in 4–13 nucleotides and 0–5 indels. Our sequences matched also with other world isolates with 98–99% similarity (e.g. HG329724–HG329724, HG969310, AY601614, MK943733, MK957234, EF614266, MK957237, MK957239). Little intra-specific variation between the 28S sequences from the two Syrian populations of *X. vuittenezi* from Hraisson (M78 and M79, banana) was recorded (0–2 nucleotides and 0–1 indel) (Table 1). The 28S sequence of *X. zagrosense* (OR196833) showed high homology (99–100%) with *X. zagrosense* (JN153101, Iran population) with low sequence variations (only 4 nucleotides with no indels). The Bayesian phylogenetic tree of *X. vuittenezi* and *X. zagrosense* is presented in Fig. 6. The Syrian isolates of *X. vuittenezi* were closest to isolates of the same species from different world populations but not within the same clade (Fig. 6), mostly due to the intraspecific variations of the 28S sequences from isolates that distinguished Hungarian, Iranian, Romanian, Czech and Russian populations from the Syrian, yielding intraspecies cladogenesis with two subclades inside this species clade. In relation to *X. zagrosense*, the Iranian (JN153101) and Syrian (OR196833) populations clustered in a well-supported sub-clade.

Sequence analysis and phylogeny of ITS rRNA

*Xiphinema americanum-group spp.*

Concerning the ITS region, the Syrian population of *X. diffusum* (OR197584) presented 95–96% sequence

similarity with other *X. brevicolle* complex sequences, such as *X. diffusum* (e.g., AY359858, MK050006) and *X. brevicolle* (e.g., FM211423, FM211420, FM211426, HQ184474, KY512780), with a considerable intra-species variability recording 21–48 nucleotide differences and 8–13 indels. For *X. pachtaicum*, the Syrian ITS sequence (OR197587) showed more than 99% match with other sequences from the same species (e.g. AY430178, KU250149), presenting little sequence polymorphisms (0–5 nucleotides and 0–3 indels). The ITS sequence of *X. simile* (OR264513) showed 95% sequence similarity with the Spanish *X. simile* isolates (KX263242– KX263243), followed by Iranian isolates of *X. persicum* Jahanshahi Afshar et al. (2021) (94% of similarity) (MT073075, MT073077– MT073078). Our ITS sequences of *X. simile* showed an intraspecific variability with 30–29 nucleotides and 10–11 indels. As for their phylogenetic inference (Fig. 7), the Syrian populations of *X. diffusum* (OR197584) were closely related with several isolates of the *X. brevicolle* complex from different countries and clearly separated from the topotype population of *X. brevicolle* (MH248804). All ITS sequences of *X. diffusum* clustered together within the same clade; however, Korean and Syrian isolates (e.i. OR197584, MK050006) were separated from the South African isolate (AY359858). This could be dues to *X. diffusum* has variation among some isolates for this marker. The ITS sequences of *X. pachtaicum* and *X. incertum* Lamberti et al., 1983 were clustered in the same clade, mostly because the sequences were shorter and poor quality in the database. The ITS sequences of *X. simile* and *X. persicum* were also grouped in the same clade, probably due to the high intraspecific variation among some populations.

Xiphinema non americanum-group spp.

The two ITS sequences from Syrian populations of *X. vuittenezi* (OR197585– OR197586), that shared in-between 99% similarity, showed 89–91% sequence similarity with several isolates of *X. vuittenezi* (e.g. HG329722–HG329723, HG969308–HG969308; MK909917; AJ437028) and 89% similarity with *X. iranicum* Pedram et al., 2009 (EU477386); presenting a intraspecific variation of 3–46 nucleotide mismatches and 0–15 indels. The corresponding Bayesian phylogenetic tree is represented in Fig. 8. The Syrian ITS sequences of *X. vuittenezi* clustered
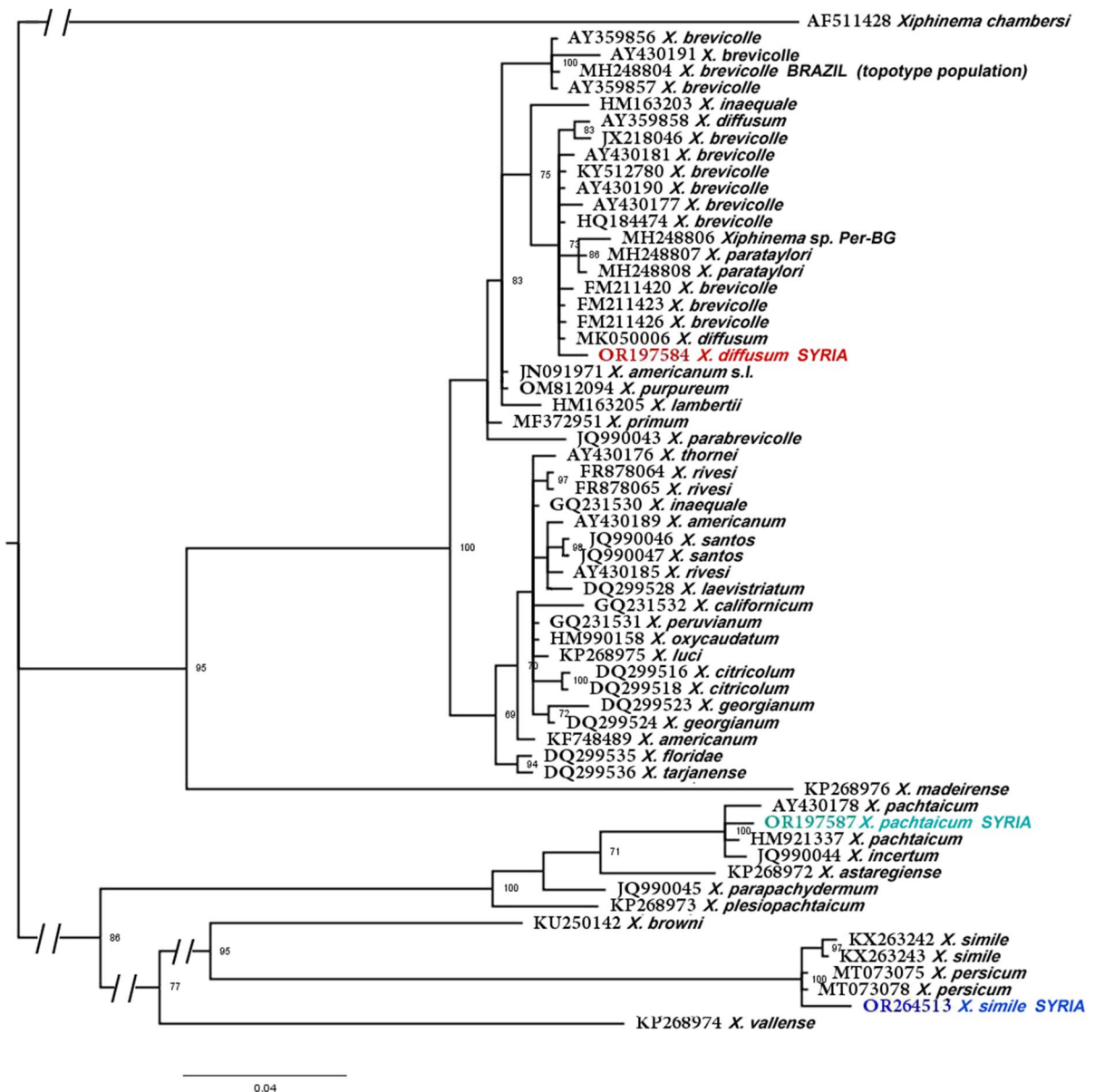
Fig. 7 Phylogenetic relationships of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979, *X. simile* Lamberti et al., 1983, and *X. pachtaicum* (Tulaganov, 1938) Kirjanova, 1951. Bayesian 50% majority rule consensus trees was inferred from 61 sequences of ITS1 rRNA (381 bp) aligned under the K80+G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in red, navy blue, and sky blue. Scale bar = expected changes per site

together in a well-supported subclade within the clade of *X. vuittenezi* (e.i. OR197585– OR197585, AY359858, HG969308– HG969309, MK909917, HG329722–HG329723, AJ437028) and *X. iranicum* (EU477386), probably due to *X. vuittenezi* shows a high intraspecific variation for this marker as well as the shorter and poor quality in some sequences deposited in the database.

Fig. 8 Phylogenetic relationships of *Xiphinema vuittenezi* Luc et al., 1964. Bayesian 50% majority rule consensus trees was inferred from 61 sequences of ITS1 rRNA (260 bp) aligned under the K80+G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in green. Scale bar = expected changes per site

Sequence analysis and phylogeny of COI mtDNA

Xiphinema americanum-group spp.

The Syrian COI sequences of *X. diffusum* (OR196695) showed a sequence similarity of 97–100% to sequences from the *X. brevicolle* complex, such as *X. diffusum* (e.g., AM086698– AM086701) and *X. brevicolle* (e.g., ON107524, ON107526– ON107529), with intraspecific variation of 1–9 nucleotides. For *X. pachtaicum*, our COI sequence (OR196696) showed high homology (98–100% of similarity) with other sequences of this species (e.g. KX263112–KX263113, HM921378), with 0–8 nucleotides mismatches. Regarding the phylogenetic tree

(Fig. 9), the Syrian COI sequences of *X. diffusum* and *X. brevicolle* grouped together in the well-supported clade and clearly separated from the topotype population of *X. brevicolle* (AM086707, MH248818). This could be dues to a plausible misidentification of these species for some sequences available in GenBank. Moreover, all COI sequences of *X. pachtaicum* also clustered in a well-supported sub-clade, however, the length of some sequences was different, yielding different branch lengths inside this species clade.

Xiphinema non americanum-group spp.

The COI sequence from Syrian population of *X. vuittenezi* (OR196697) showed 83% similarity to the Russian isolate of this species (OQ699231) and less than 79% similarity with other *Xiphinema* species. Regarding the phylogenetic inference (Fig. 10) showed that our *X. vuittenezi* COI sequence was clustered, with good support, in-between *X. afratakhtehense* (MH429098) and the cluster of the Russian and Czech isolates of *X. vuittenezi* (OQ699231 and EF614265). This could be dues to a poor quality of these sequences and overlapping peaks, yielding intraspecies cladogenesis.

Phylogenetic analysis of the bacterial endosymbionts 'Candidatus Xiphinematobacter' and correlation with host phylogeny

The complete 16S rRNA gene of the bacterial endosymbionts 'Candidatus Xiphinematobacter' were successfully amplified from *X. diffusum* (OR196969, OR196971) and *X. simile* (OR196970), with an approximate size of 1400 bp. Both sequences from *X. diffusum* were 100% identical and matched closely (99–100% identity) with several sequences of Chinese, Brazilian, and Australian Xiphinematobacter species reported from *X. diffusum* populations (KJ614450–KJ614453). A sequence of South African population of Xiphinematobacter from *X. brevicolle* complex (AF217462) also grouped in this cluster. When compared with Xiphinematobacter species detected in topotype population of *X. brevicolle* (KJ614447), the latter sequence had only 96% identity. The other endosymbiont from *X. simile* (OR196970) matched closely (99–100% identity) with two sequences of a Greek population of this same species (KT735097–KT735098) from *X.*
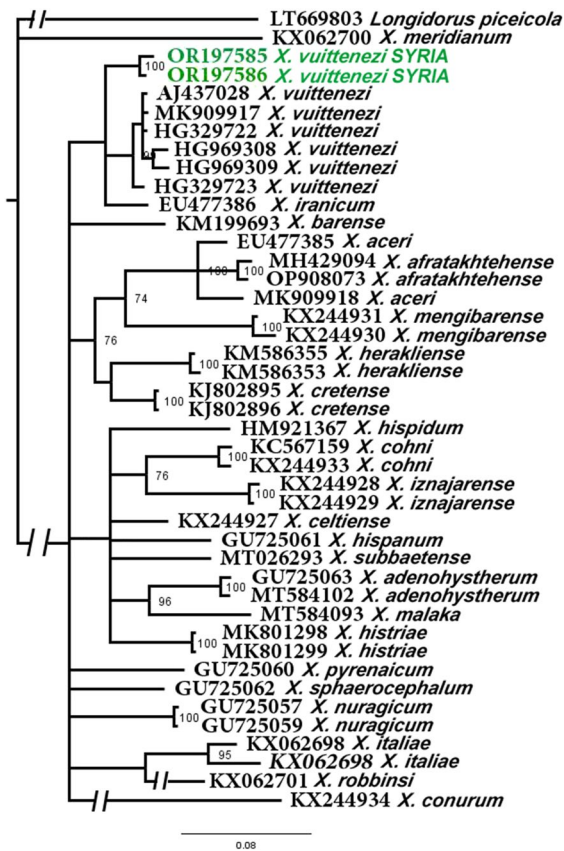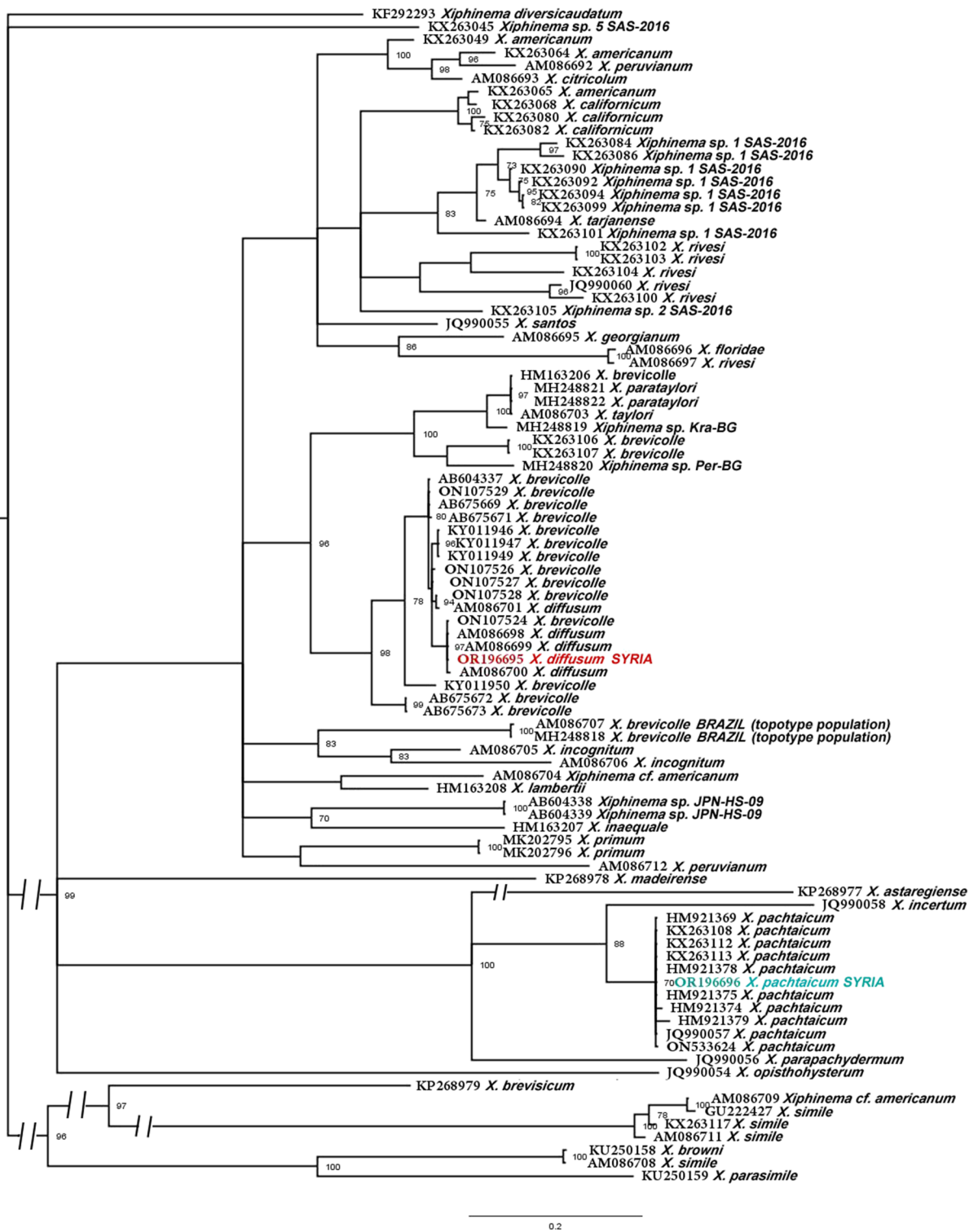
◄**Fig. 9** Phylogenetic relationships of *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979 and *X. simile* Lamberti et al., 1983 and *X. pachtaicum* (Tulaganov, 1938) Kirjanova, 1951. Bayesian 50% majority rule consensus trees was inferred from 91 sequences of *COI* mtDNA (341 bp) aligned under the HKY85+G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in red and sky blue. Scale bar=expected changes per site

simile. Figure 11 presents the BI tree (50% majority rule consensus tree) of 70 sequences of 16S rRNA for '*Ca.* Xiphinematobacter' and three outgroup species [Uncultured *Eubacterium* spp. WCHD3-88 (AF050561), *Spartobacteria bacterium* (AB245341) and *Terrimicrobium sacchariphilum* (GU129926)]. The phylogenetic analysis within the genus '*Candidatus* Xiphinematobacter' differentiated 18 well-supported clades corresponding to the 18 species denoted as species A through species R (Fig. 11). In exception of '*Candidatus* Xiphinematobacter' sp. A, which was isolated from two *X. americanum* s.s., *X. pachtaicum*, and *X. simile* from Europe (KT735098, KJ614457, KJ614458) and Asia (MT568602, OR196970, KX263187), and '*Candidatus* Xiphinematobacter' sp. R, which was isolated from *X. americanum* s. str., *X. americanum* s. s., *X. rivesi* Dalmaso, 1969, *X. peruvianum* Lamberti & Bleve-Zacheo, 1979, *X. georgianum* Lamberti & Bleve-Zacheo, 1979, the other '*Candidatus* Xiphinematobacter' species were all isolated from one or two host nematode species. '*Candidatus* Xiphinematobacter' sp. I included two sequences of one population of *X. diffusum* from Syria, which grouped in the well-supported clade with other populations from Asia, Australia, Africa, and South America, and one population of *X. brevicolle* complex from South Africa, with high clade support (0.95 BPP), clearly separated of the sequence of '*Candidatus* Xiphinematobacter' sp. G of the topotype population of *X. brevicolle*. '*Candidatus* Xiphinematobacter' from *X. simile* from Syria clustered in the sub-clade of '*Candidatus* Xiphinematobacter' sp. A, jointly with other sequences of the bacterium from populations of *X. simile* from other origins.

Discussion

In this study, six *Xiphinema* populations were recovered and identified from Syria belonging to five species, namely *X. diffusum*, *X. pachtaicum*, *X. simile*, *X. vuittenezi* and *X. zagrosense* by integrating morphological and molecular data. Using an integrative approach to identify species in this specious genus has already well documented (Gutiérrez-Gutiérrez et al., 2012; Ghaemi et al., 2012; Archidona-Yuste et al., 2016b, 2020a; Lazarova et al., 2019; Mobasseri et al., 2019a, b; Vazifeh et al., 2019; Naghavi et al., 2022a; Gu et al., 2022). The endosymbiont bacterias were also sequenced for two *X. americanum*-group species, *X. diffusum* and *X. simile*. Four species including *X. diffusum*, *X. simile*, *X. vuittenezi*, and *X. zagrosense* are new records from Syria, increasing the geographical distribution points of these species.

In accordance with other taxonomic studies (Lazarova et al., 2008, 2016b; Gutiérrez-Gutiérrez et al., 2011b; 2013; Archidona-Yuste et al., 2016a, b; 2020a, b; Mobasseri et al., 2019a, b; Vazifeh et al., 2019; Naghavi et al., 2022a), our results showed that the D2–D3 of the 28S rRNA and the *COI* mtDNA regions were the most conclusive molecular markers for species-level identification within genus *Xiphinema* in exception of some species within the subgroup *X. brevicolle*. Our study corroborates other studies (Lazarova et al., 2016a; Mobasseri et al., 2019a, b; Palomares-Rius et al., 2016) emphasizhing that 16S rRNA gene is a useful molecular marker for discerning among *Candidatus* Xiphinematobacte*r* species and so, as a result of their closely related *Xiphinema* hosts. In our phylogenetic, representative sequences for some species occupied different positions. An accurate way to resolve this problem is to sequence topotype specimens. Currently, most populations of *X. brevicolle* have identified only based on molecular data without morphological and morphometric analysis, occupying distant placements from the sequences of the topotype population of the species, and possibly indicating misidentification. Furthermore, recently Jahanshahi Afshar (2019) sequenced the D2–D3 fragments of 28S rRNA gene of the topotype population of *X. robbinsi* Pedram, Niknam & Decraemer, 2008 revealing a misktake identification of a Tunisian population.

Nowadays, exploring the molecular evolution and phylogenetic relationships of '*Ca.* Xiphinematobacter' species using the 16S rRNA gene is at its peak (Brown, 2018; Lazarova et al., 2016a, b; Mobasseri et al., 2019a, b; Palomares-Rius et al., 2016, 2021).
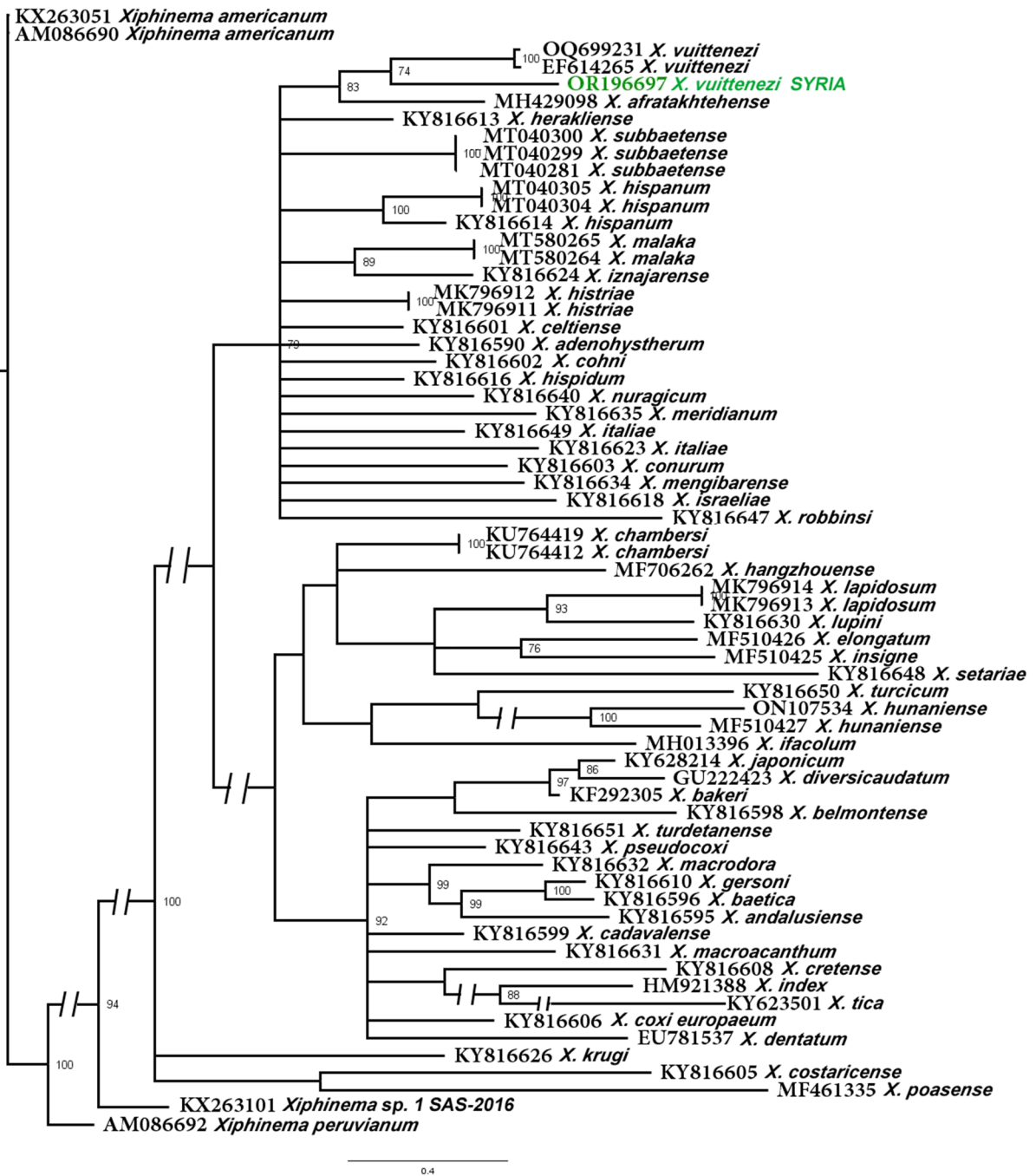
Fig. 10 Phylogenetic relationships of *Xiphinema vuittenezi* Luc et al., 1964. Bayesian 50% majority rule consensus trees was inferred from 65 sequences of *COI* mtDNA (335 bp) sequences aligned under the GTR+G+I model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are coloured in green. Scale bar=expected changes per site

Still, there is knowledge gap on the nematode-endo-symbiont bacteria co-evolution in the *X. americanum* group. Our results agree with other authors (Mobas-seri et al., 2019a, b; Palomares-Rius et al., 2016, 2021) that proposed a plausible host-endosymbiont co-speciation and suggest an adaptative role during the process of natural selection in the host *Xiphinema* species.

In conclusion, our work revealed a high biodiversity of the dagger nematode species in banana gardens of Syria. The recovered species could be regarded potential threats and monitoring of their population could prevent their outbreak.

Declarations

Research involving human participants and/or animals No specific permits were required for the described fieldwork studies. Permission for sampling the banana fields was granted by the landowner. However, the sites are not protected in any way.

Informed consent All the authors certify that this work carried out in this research followed the principles of ethical and professional conduct have been followed. The funding source had no role the design of this study and not had any role during its execution, data collection, analyses, interpretation of the data, decision to publish, or preparation of the manuscript.

Conflict of interest All authors declare no conflict of interest.

References

Abdine, M., Allak, H., Nus, B. E., Nigro, F., Catalano, L., & Digiaro, M. (2007). Phytosanitary Aspects and Nursery Production of Olive in Syria: pitfalls and perspectives. In B. Di Terlizzi, A. Dragotta, & M. Jamal (Eds.), *Syrian national strategic plan for olive oil quality. Final report, Bari: CIHEAM, Options Méditerranéennes: Série A. Séminaires Méditerranéens; n. 73* (pp. 143–151)

Ahmed, M., & Holovachov, O. (2021). Twenty years after De Ley & Blaxter – how far did we progress in understanding the phylogeny of the phylum Nematoda? *Animals, 11*(12), 3479. https://doi.org/10.3390/ani11123479

Al-Halabi, S. M., & Al-Assas, K. (2021). Survey of parasitic nematode genera associated with grapevine roots in Sweida governorate. *Syria. Arab Journal of Plant Protection, 39*(1), 14–21. https://doi.org/10.22268/AJPP-39.1.014021[inArabic]

Ali, N. (2023). Incidence and diversity of plant parasitic nematode communities associated with greenhouse ornamental plants in the coastal region of Syria. *European Journal of Plant Pathology, 166*, 491–508. https://doi.org/10.1007/s10658-023-02678-z

Allouf, N. (2013). A preliminary survey of nematodes genera associated with *Citrus* Trees in Syrian Coast. *The Jordanian Journal of Agricultural Sciences, 9*(3), 395–403. [in Arabic].

Archidona-Yuste, A., Navas-Cortes, J. A., Cantalapiedra-Navarrete, C., Palomares-Rius, J. E., & Castillo, P. (2016a). Remarkable diversity and prevalence of dagger nematodes of the genus *Xiphinema* Cobb, 1913 (Nematoda: Longidoridae) in olives revealed by integrative approaches. *PLoS ONE, 11*(11), e0165412. https://doi.org/10.1371/journal.pone.0165412

Archidona-Yuste, A., Navas-Cortes, J. A., Cantalapiedra-Navarrete, C., Palomares-Rius, J. E., & Castillo, P. (2016b). Cryptic diversity and species delimitation in the *Xiphinema americanum*-group complex (Nematoda: Longidoridae) as inferred from morphometrics and molecular markers. *Zoological Journal of the Linnean Society, 176*(2), 231–265. https://doi.org/10.1111/zoj.12316

Archidona-Yuste, A., Wiegand, T., Castillo, P., & Navas-Cortés, J. A. (2019). Dataset on the diversity of plant-parasitic nematodes in cultivated olive trees in southern Spain. *Data in Brief, 27*, 104658. https://doi.org/10.1016/j.dib.2019.104658

Archidona-Yuste, A., Wiegand, T., Castillo, P., & Navas-Cortes, J. A. (2020a). Spatial structure and soil properties shape local community structure of plant-parasitic nematodes in cultivated olive trees in southern Spain. *Agriculture, Ecosystems & Environment, 287*, 106688. https://doi.org/10.1016/j.agee.2019.106688

KJ614456 *Candidatus Xiphinematobacter sp. (X. simile)* | sp. A
KX263187 *Candidatus Xiphinematobacter sp. (X. simile)* | sp. A
100 KJ614457 *Candidatus Xiphinematobacter sp. (X. americanum s.l.)* | sp. A
KJ614458 *Candidatus Xiphinematobacter sp. (X. pachtaicum)* | sp. A
MT568602 *Candidatus Xiphinematobacter sp. (unknown)* | sp. A
95 KT735098 *Candidatus Xiphinematobacter sp. (X. simile)* | sp. A
OR196970 *Candidatus Xiphinematobacter sp. (X. simile)* SYRIA | sp. A ◀
73 KJ614455 *Candidatus Xiphinematobacter sp. (X. simile)* | sp. B
100 MF372955 *Candidatus Xiphinematobacter sp. (X. primum)* | sp. C
MF372956 *Candidatus Xiphinematobacter sp. (X. primum)* | sp. C
100
97 KJ614446 *Candidatus Xiphinematobacter sp. (X. americanum s.l.)* | sp. D
94 KT735102 *Candidatus Xiphinematobacter sp. (Xiphinema sp. Japan)* | sp. E
KT735101 *Candidatus Xiphinematobacter sp. (Xiphinema sp. Japan)* | sp. E
100 KJ614448 *Candidatus Xiphinematobacter sp. (X. incognitum)* | sp. F
100 KJ614449 *Candidatus Xiphinematobacter sp. (X. incognitum)* | sp. F
KJ614447 *Candidatus Xiphinematobacter sp. (X. brevicolle, type population)* | sp. G
100 KJ614450 *Candidatus Xiphinematobacter sp. (X. taylori)* | sp. H
KX263241 *Candidatus Xiphinematobacter sp. (X. brevicolle)* | sp. H
AF217462 *Candidatus Xiphinematobacter brevicolli (X. brevicolle)* | sp. I
KJ614452 *Candidatus Xiphinematobacter sp. (X. diffusum)* | sp. I
84 95 KJ614453 *Candidatus Xiphinematobacter sp. (X. diffusum)* | sp. I
OR196969 *Candidatus Xiphinematobacter sp. (X. diffusum)* SYRIA | sp. I ◀
OR196971 *Candidatus Xiphinematobacter sp. (X. diffusum)* SYRIA | sp. I ◀
KJ614451 *Candidatus Xiphinematobacter sp. (X. diffusum)* | sp. I
KJ614454 *Candidatus Xiphinematobacter sp. (X. peruvianum)* | sp. J
KX263240 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. K
KX263239 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. K
KX263204 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. L
KX263212 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
KX263214 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
96 KX263217 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
KX263209 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
KX263207 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
97 KX263205 *Candidatus Xiphinematobacter sp. (X. californicum)* | sp. M
KX263218 *Candidatus Xiphinematobacter sp. (Xiphinema sp. 2)* | sp. M
100 KT735064 *Candidatus Xiphinematobacter sp. (X. luci)* | sp. N
KT735065 *Candidatus Xiphinematobacter sp. (X. luci)* | sp. N
100 KJ614437 *Candidatus Xiphinematobacter sp. (X. floridae)* | sp. O
KJ614438 *Candidatus Xiphinematobacter sp. (X. tarjanense)* | sp. O
84 KX263236 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KX263235 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
AF217461 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KJ614439 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735091 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735086 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735093 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
88 KT735088 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
88 KT735089 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735092 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735095 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735094 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KT735087 *Candidatus Xiphinematobacter sp. (X. rivesi)* | sp. P
KX263222 *Candidatus Xiphinematobacter sp. (Xiphinema sp.1)* | sp. P
81 KX263227 *Candidatus Xiphinematobacter sp. (Xiphinema sp.1)* | sp. P
KX263225 *Candidatus Xiphinematobacter sp. (Xiphinema sp.1)* | sp. P
KX263230 *Candidatus Xiphinematobacter sp. (Xiphinema sp.1)* | sp. P
KT735096 *Candidatus Xiphinematobacter sp. (X. santos)* | sp. Q
AF217460 *Candidatus Xiphinematobacter americani (X. americanum s. str.)* | sp. R
KJ614443 *Candidatus Xiphinematobacter sp. (X. americanum s. str.)* | sp. R
KX263193 *Candidatus Xiphinematobacter sp. (X. americanum s. str.)* | sp. R
KX263192 *Candidatus Xiphinematobacter sp. (X. americanum s. str.)* | sp. R
78 KX263202 *Candidatus Xiphinematobacter sp. (X. americanum s. str.)* | sp. R
KJ614444 *Candidatus Xiphinematobacter sp. (X. americanum s. l.)* | sp. R
KJ614445 *Candidatus Xiphinematobacter sp. (X. americanum s. l.)* | sp. R
KJ614440 *Candidatus Xiphinematobacter sp. (X. peruvianum)* | sp. R
KJ614441 *Candidatus Xiphinematobacter sp. (X. citricolum)* | sp. R
KJ614442 *Candidatus Xiphinematobacter sp. (X. georgianum)* | sp. R
100 GU129926 *Terrimicrobium sacchariphilum*
AB245341 *Spartobacteria bacterium*
AF050561 *Uncultured Eubacterium WCHD3-88*

0,018

◄Fig. 11 Phylogenetic relationships of the endosymbiont bacterias, isolated from *Xiphinema diffusum* Lamberti & Bleve-Zacheo, 1979 and *X. simile* Lamberti et al., 1983 within 'Candidatus Xiphinematobacter'. Bayesian 50% majority rule consensus tree was inferred from 16S rRNA sequence alignment under the K80+G model. Posterior probabilities more than 70% are given for appropriate clades. Newly obtained sequences in this study are targed with a arrow. Scale bar = expected changes per site

Archidona-Yuste, A., Cai, R., Cantalapiedra-Navarrete, C., Carreira, J. A., Rey, A., Viñegla, B., Liébanas, G., Palomares-Rius, J. E., & Castillo, P. (2020b). Morphostatic speciation within the dagger nematode *Xiphinema hispanum*-Complex species (Nematoda: Longidoridae). *Plants, 9*(12), 1649. https://doi.org/10.3390/plants912164

Barsi, L. (1989). The Longidoridae (Nematoda: Dorylaimida) in Yugoslavia. I. *Nematologia Mediterranea, 17*, 97–108.

Barsi, L. (1994a). Species of the *Xiphinema americanum*-group (Nematoda: Dorylaimida) on the territory of the former Yugoslavia. *Nematologia Mediterranea, 22*(1), 25–34.

Barsi, L. (1994b). Bivulval females of *Longidorus euonymus*, *Xiphinema diversicaudatum* and *X. vuittenezi* (Nematoda: Dorylaimida). *Nematologia Mediterranea, 22*, 271–272.

Barsi, L., & De Luca, F. (2008). Morphological and molecular characterisation of two putative *Xiphinema americanum*-group species, *X. parasimile* and *X. simile* (Nematoda: Dorylaimida) from Serbia. *Nematology, 10*, 15–25. https://doi.org/10.1163/156854108783360212

Barsi, L., & Lamberti, F. (2000). Morphometric variation and juvenile stages of *Xiphinema vuittenezi* (Nematoda: Dorylaimida) in Serbia. *Nematologia Mediterranea, 28*, 3–12.

Barsi, L., & Lamberti, F. (2002). Morphometrics of three putative species of the *Xiphinema americanum*-group (Nematoda: Dorylaimida) from the territory of the former Yugoslavia. *Nematologia Mediterranea, 30*, 59–72.

Barsi, L., & Lamberti, F. (2004). *Xiphinema parasimile* sp. n. from Serbia and *X. simile*, first record from Bosnia and Herzegovina (Nematoda, Dorylaimida). *Nematologia Mediterranea, 32*(1), 101–109.

Brown, A. M. (2018). Endosymbionts of plant-parasitic nematodes. *Annual Review of Phytopathology, 56*, 225–242. https://doi.org/10.1146/annurev-phyto-080417-045824

Cai, R., Maria, M., Barsalote, E. M., Subbotin, S. A., & Zheng, J. (2018). Description of *Xiphinema hangzhouense* sp. n. (Nematoda: Longidoridae) from the rhizosphere of Magnolia grandiflora in Hangzhou, Zhejiang Province, China. *Nematology, 20*(1), 67–80. https://doi.org/10.1163/15685411-00003125

Cai, R., Archidona-Yuste, A., Cantalapiedra-Navarrete, C., Palomares-Rius, J. E., Zheng, J., & Castillo, P. (2019). Integrative taxonomy of *Xiphinema histriae* and *Xiphinema lapidosum* from Spain. *Journal of Nematology, 51*, 1–21. https://doi.org/10.21307/jofnem-2019-037

Cai, R., Archidona-Yuste, A., Cantalapiedra-Navarrete, C., Palomares-Rius, J. E., & Castillo, P. (2020). New evidence of cryptic speciation in the family Longidoridae (Nematoda: Dorylaimida). *Journal of Zoological Systematics and Evolutionary Research, 58*(4), 869–899.

Castresana, J. (2000). Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular Biology and Evolution, 17*(4), 540–552. https://doi.org/10.1093/oxfordjournals.molbev.a026334

Chen, D. Y., Ni, H. F., Yen, J. H., Cheng, Y. H., & Tsay, T. T. (2005). Differentiation of the *Xiphinema americanum*-group nematodes *X. brevicollum*, *X. incognitum*, *X. diffusum* and *X. oxycaudatum* in Taiwan by morphometrics and nuclear ribosomal DNA sequences. *Nematology, 7*(5), 713–725.

Coiro, M. I., Lamberti, F., Agostinelli, A., & Vindimian, M. E. (1989). I Longidoridae nei vigneti del Trentino. II: Il genere *Xiphinema* Cobb. *Nematologia Mediterranea, 17*, 139–148.

Coiro, M. I., Agostinelli, A., & Lamberti, F. (1992). Longidoridae (Nematoda) in the vineyards of the province of Verona. *Nematologia Mediterranea, 20*, 87–95.

Coomans, A., & Heyns, J. (1997). Three species of the *Xiphinema americanum*-group (Nematoda: Longidoridae) from Kenya. *Nematologica, 43*, 259–274.

Coomans, A., Huys, R., Heyns, J., Luc, M. (2001). Character analysis, phylogeny and biogeography of the genus *Xiphinema* Cobb, 1913 (Nematoda, Longidoridae). Vol. 287. Annales du Musée Royal de l'Afrique Centrale (Zoologie), Tervuren, Belgique, 239 pp.

De Grisse, A. T. (1969). Redescription ou modifications de quelques techniques utilisées dans l'étude de nématodes phytoparasitaires. *Mededelingen Rijksfaculteit Landbouwwetenschappen Gent, 34*, 315–359.

de Man, J. G. (1880). Die einheimischen, frei in der reinen Erde und im su ̈ssen Wasser lebende Nematoden, monographischen bearbeitet. Tijdschrift Nederlandse Dierkundige vereniging. 104 p.

Fadaei, A. A., Coomans, A., & Kheiri, A. (2003). Three species of the *Xiphinema americanum* lineage (Nematoda: Longidoridae) from Iran. *Nematology, 5*, 453–461. https://doi.org/10.1163/156854103-769224430

Flegg, J. J. M. (1967). Extraction of *Xiphinema* and *Longidorus* species from soil by a modification of Cobb's decanting and sieving technique. *Annals of Applied Biology, 60*(3), 429–437.

Fouladvand, Z. M., Pourjam, E., Castillo, P., & Pedram, M. (2019). Genetic diversity, and description of a new dagger nematode, Xiphinema afratakhtehnsis sp. nov., (Dorylaimida: Longidoridae) in natural forests of southeastern Gorgan, Northern Iran. *PloS one, 14*(5), e0214147. https://doi.org/10.1371/journal.pone.0214147

Getaneh, G., Bert, W., & Decraemer, W. (2015). First report, morphological and molecular characterization of *Xiphinema elongatum* and *X. pachtaicum* (Nematoda, Longidoridae) from Ethiopia. *Zookeys, 489*, 1–13. https://doi.org/10.3897/zookeys.489.8629

Ghaemi, E., Pourjam, E., Pedram, M., Robbins, R. T., Ye, W., & Decraemer, W. (2012). Morphological and molecular characterisation of *Xiphinema zagrosense* sp. n. (Dorylaimida: Longidoridae) from the Zagros Mountains. *Iran. Nematology, 14*(4), 445–55.

Greco, N., Di Vito, M., Reddy, M. V., & Saxena, M. C. (1984). A preliminary report of survey of plant parasitic nematodes of leguminous crops in Syria. *Nematologia Mediterranea, 12*, 87–93.

Greco, N., Di Vito, M., & Saxena, M. C. (1992). Plant parasitic nematodes of cool season food legumes in Syria. *Nematologia Mediterranea, 20*(1), 37–46.

Groza, M., Lazarova, S., Costache, C., Luca, F., Rosca, I., Fanelli, E., & Peneva, V. (2013). Morphological characterisation and diagnostics of *Xiphinema* non-*americanum* group species (Nematoda: Longidoridae) from Romania using mutiplex PCR. *Helminthologia, 50*(3), 215–231. https://doi.org/10.2478/s11687-013-0133-3

Gu, J., Ye, W., & Munawar, M. (2022). Description of *Xiphinema pupureum* n. sp. (Nematoda: Longidoridae), a new *Xiphinema americanum* group species detected from the rhizosphere of Ilex purpurea from Japan. *Nematology, 25*(1), 91–105. https://doi.org/10.1163/15685411-bja10208

Gutiérrez-Gutiérrez, C., Palomares-Rius, J. E., Cantalapiedra-Navarrete, C., Landa, B. B., Esmenjaud, D., & Castillo, P. (2010). Molecular analysis and comparative morphology to resolve a complex of cryptic *Xiphinema* species. *Zoologica Scripta, 39*(5), 483–498. https://doi.org/10.1111/j.1463-6409.2010.00437.x

Gutiérrez-Gutiérrez, C., Castillo, P., Cantalapiedra-Navarrete, C., Landa, B. B., Derycke, S., & Palomares-Rius, J. E. (2011a). Genetic structure of *Xiphinema pachtaicum* and *X. index* populations based on mitochondrial DNA variation. *Phytopathology, 101*(10), 1168–1175.

Gutiérrez-Gutiérrez, C., Palomares Rius, J. E., Cantalapiedra-Navarrete, C., Landa, B. B., Esmenjaud, D., & Castillo, P. (2011b). Prevalence, polyphasic identification, and molecular phylogeny of dagger and needle nematodes infesting vineyards in southern Spain. *European Journal of Plant Pathology, 129*, 427–453. https://doi.org/10.1007/s10658-010-9705-y

Gutiérrez-Gutiérrez, C., Cantalapiedra-Navarrete, C., Decraemer, W., Vovlas, N., Prior, T., Palomares Rius, J. E., & Castillo, P. (2012). Phylogeny, diversity, and species delimitation in some species of the *Xiphinema americanum*-group complex (Nematoda: Longidoridae), as inferred from nuclear and mitochondrial DNA sequences and morphology. *European Journal of Plant Pathology, 134*, 561–597.

Gutiérrez-Gutiérrez, C., Cantalapiedra-Navarrete, C., Remesal, E., Palomares-Rius, J. E., Navas-Cortés, J. A., & Castillo, P. (2013). New insight into the identification and molecular phylogeny of dagger nematodes of the genus *Xiphinema* (Nematoda: Longidoridae) with description of two new species. *Zoological Journal of the Linnean Society, 169*(3), 548–579. https://doi.org/10.1111/zoj.12071

Gutiérrez-Gutiérrez, C., Bravo, M. A., Santos, M. T., Vieira, P., & Mota, M. (2016). An update on the genera *Longidorus*, *Paralongidorus* and *Xiphinema* (Family Longidoridae) in Portugal. *Zootaxa, 4189*(1), 099–114. https://doi.org/10.11646/zootaxa.4189.1.4

Gutiérrez-Gutiérrez, C., Mota, M., Castillo, P., Teixeira-Santos, M., & Palomares-Rius, J. E. (2018). Description and molecular phylogeny of one new and one known needle nematode of the genus *Paralongidorus* (Nematoda: Longidoridae) from grapevine in Portugal using integrative approach. *European Journal of Plant Patholology, 151*, 155–172. https://doi.org/10.1007/s10658-017-1364-9

Gutiérrez-Gutiérrez, C., Teixeira Santos, M., Inácio, M. L., Eisenback, J. D., & Mota, M. (2020). Description of *Longidorus bordonensis* sp. nov. from Portugal, with systematics and molecular phylogeny of the genus (Nematoda, Longidoridae). *Zoosystematics and Evolution, 96*(1), 175–193. https://doi.org/10.3897/zse.96.49022

Heyns, J., & Coomans, A. (1994). Four species of the *Xiphinema americanum*-group (Nematoda: Longidoridae) from islands in the western Indian Ocean. *Nematologica, 40*(1), 12–24.

Jahanshahi Afshar, F. (2019). The first molecular phylogenetic study of Xiphinema robbinsi Pedram, Niknam & Decraemer, 2008 (Nematoda: Longidoridae) based on specimens from the type locality. *Nematology, 21*(3), 333–335. https://doi.org/10.1163/15685411-00003219

Jahanshahi Afshar, F., Shahryari, F., Gharibzadeh, F., Pourjam, E., & Pedram, M. (2019). Description of *Xiphinema azarbaijanense* n. sp. (Nematoda; Longidoridae) from West Azarbaijan province, northwestern Iran. *European Journal of Plant Patholology, 155*, 417–434. https://doi.org/10.1007/s10658-019-01776-1

Jahanshahi Afshar, F., Pedram, P., & Mobasseri, M. (2021). Description of *Xiphinema persicum* n. sp. (Nematoda: Longidoridae), a X. americanum-group species from Iran. *European Journal of Plant Pathology, 159*, 783–797. https://doi.org/10.1007/s10658-021-02201-2

Jairajpuri, M. S., & Ahmad, W. (1992). *Dorylaimida: Free-living, predaceous and plant-parasitic nematodes* (p. 458). IBH Publishing Co.

Jones, J. T., Haegeman, A., Danchin, E. G. J., Gaur, H. S., Helder, J., Jones, M. G. K., Kikuchi, T., Manzanilla-Lopez, R., Palomares-Rius, J. E., Wesemael, W. M. L., & Perry, R. N. (2013). Top 10 plant-parasitic nematodes in molecular plant pathology. *Molecular Plant Pathology, 14*, 946–961. https://doi.org/10.1111/mpp.12057

Katoh, K., Rozewicki, J., & Yamada, K. D. (2019). MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics, 20*(4), 1160–1166. https://doi.org/10.1093/bib/bbx108

Kawas, H. Z., & Al-Assas, K. M. (2011). Preliminary studies on viral diseases of olive in Damascus and Countryside and identification of accompanied nematodes. *Journal of AL-Furat University, 272*–293. [In Arabic].

Khaleel, H., Abu Al-Fadel, T., & Zeini, G. (2010). Survey and identification of parasitic nematode genera and species in the rhizosphere of apple trees at Homs governorate, Syria. *Tishreen University Journal for Research and Scientific Studies - Biological Sciences Series, 32*(4), 169–185. [In Arabic].

Kumari, S. (2006). *Xiphinema simile* (Nematoda: Longidoridae) in the Czech Republic and a note on other *Xiphinema* species. *Helminthologia, 43*, 43–50. https://doi.org/10.2478/s11687-006-0009-x

Kumari, S., Polák, J., & Choutka, R. (2005). Plant-parasitic nematodes of the genus *Xiphinema* (Nematoda: Longidoridae) in the vineyards of the Czech Republic.

Nematology, 7(1), 81–93. https://doi.org/10.1163/15685 41054192117

Lamberti, F. (1984). Nematode problems of the Mediterranean coastal stripe in the Syrian Arab Republic. *Nematologia Mediterranea, 12*, 53–64.

Lamberti, F., & Bleve-Zacheo, T. (1979). Studies on *Xiphinema americanum* sensu lato with descriptions of fifteen new species (Nematoda, Longidoridae). *Nematologia Mediterranea, 7*, 51–106.

Lamberti, F., & Siddiqi, M. R. (1977). *Xiphinema pachtaicum* [= *X. mediterraneum*]. CIH Descriptions of plant-parasitic. *Nematodes Set, 7*(94).

Lamberti, F., Choleva, B., & Agostinelli, A. (1983). Longidoridae from Bulgaria (Nematoda, Dorylaimida) with description of three new species of *Longidorus* and two new species of *Xiphinema*. *Nematologia Mediterranea, 11*, 49–72.

Lamberti, F., Ciancio, A., Agostinelli, A., & Coiro, M. I. (1991). Relationship between *Xiphinema brevicolle* and *X. diffusum*, with a redescription of Xiphinema brevicolle and description of three new species of *Xiphinema* (Nematoda, Dorylaimida). *Nematologia Meditemanea, 19*(3), 11–326.

Lamberti, F., Castillo, P., & Gómez-BarcinaAgostinelli, A. A. (1992). Descriptions of six new species of *Xiphinema* (Nematoda, Dorylaimida) from the Mediterranean region. *Nematologia Mediterranea, 20*, 125–139.

Lamberti, F., Lemos, R. M., Agostinelli, A., & D'addabo, T. (1993). The *Xiphinema americanum*-group in the vineyards of the Dao and Douro regions (Portugal) with description of two new species (Nematoda, Dorylaimida). *Nematologia Mediterranea, 21*(2), 215–225.

Lamberti, F., Molinari, S., De Luca, F., Agostinelli, A., & Di Vito, M. (1999a). Longidorids (Nematoda, Dorylaimida) from Syria with description of *Longidorus pauli* sp. n. and *Paralongidorus halepensis* sp. n. with SOD isozymes and PCR-RFLP profiles. *Nematologia Mediterranea, 27*, 63–78.

Lamberti, F., Sabova, M., De Luca, P., Molinari, S., Agostinelli, A., Coiro, M. I., & Valocka, B. (1999b). Phenotypic variations and genetic characterization of *Xiphinema* populations from Slovakia (Nematoda, Dorylaimida). *Nematologia Meditemanea, 27*(26), 1–275.

Lamberti, F., Molinari, S., Moens, M., & Brown, D. J. F. (2000). The *Xiphinema americanum*-group. I. Putative species, their geographical occurrence and distribution, and regional polytomous identification keys for the group. *Russian Journal of Nematology, 8*, 65–84.

Lamberti, F., Molinari, S., Moens, M., & Brown, D. J. F. (2002). The *Xiphinema americanum*-group. II. Morphometric relationships. *Russian Journal of Nematology, 10*, 99–112.

Lamberti, F., Hockland, S., Agostinelli, A., Moens, M., & Brown, D. J. F. (2004). The *Xiphinema americanum* group. 3. Keys to species identification. *Nematologia Mediterranea, 32*, 53–56.

Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., McGettigan, P. A., McWilliam, H., Valentin, V., Wallace, I. M., Wilm, A., Lopez, R., Thompson, J. D., Gibson, T. J., & Higgins, D. G. (2007). Clustal W and Clustal X

version 2.0. *Bioinformatics, 3*(21), 2947–2948. https://doi.org/10.1093/bioinformatics/btm404

Lazarova, S. S., Malloch, G., Oliveira, C. M., Hübschen, J., & Neilson, R. (2006). Ribosomal and mitochondrial DNA analyses of *Xiphinema americanum*-group populations. *Journal of Nematology, 38*(4), 404–410.

Lazarova, S. S., De Luca, F., & Peneva, V. K. (2008). On two closely related species of the *Xiphinema americanum* group: *X. simile* Lamberti, Choleva et Agostinelli, 1983 and *X. parasimile* Barsi et Lamberti, 2004 (Longidoridae), with a description of the male of *X. parasimile*. *ZooKeys, 3*, 29–50. https://doi.org/10.3897/zookeys.3.26

Lazarova, S. S., Brown, D. J., Oliveira, C. M., Fenton, B., MacKenzie, K., Wright, F., Malloch, G., & Neilson, R. (2016a). Diversity of endosymbiont bacteria associated with a non-filarial nematode group. *Nematology, 18*(5), 615–623. https://doi.org/10.1163/15685411-00002982

Lazarova, S., Peneva, V., & Kumari, S. (2016b). Morphological and molecular characterisation, and phylogenetic position of *X. browni* sp. n., *X. penevi* sp. n. and two known species of *Xiphinema americanum*-group (Nematoda, Longidoridae). *ZooKeys, 574*, 1–42. https://doi.org/10.3897/zookeys.574.8037

Lazarova, S., Oliveira, C. M., Prior, T., Peneva, V., & Kumari, S. (2019). An integrative approach to the study of *Xiphinema brevicolle* Lordello and Da Costa 1961, supports its limited distribution worldwide (Nematoda: Longidoridae). *European Journal of Plant Pathology, 153*(2), 441–464. https://doi.org/10.1007/s10658-018-1571-z

Lišková, M. (1995). Faunistic and ecological notes on *Xiphinema* (Nematoda: Dorylaimida) in Slovakia. *Biológia (Bratislava), 50*(2), 125–131.

Lišková, M., & Brown, D. J. F. (1996). Taxonomic validity and ecological relations of *Xiphinema pachtaicum* and *X. simile* (Nematoda: Dorylaimida), two members of the *X. americanum* group occurring in Slovakia. *Helminthologia, 33*, 137–142.

Lišková, M., Lamberti, F., Sabová, M., Valovská, B., & Agostinelli, A. (1993). First record of some species of longidorid nematodes from Slovakia. *Nematologia Mediterranea, 21*, 49–53.

Loof, P. A. A., & Coomans, A. (1968). On the development and location of the oesophageal gland nuclei in the Dorylaimina. *Nematologica, 14*, 596–597. https://doi.org/10.1163/187529268X00345

Loof, P. A. A., & Luc, M. (1990). A revised polytomous key for the identification of species of the genus *Xiphinema* Cobb, 1913 (Nematoda: Longidoridae) with exclusion of the *X. americanum*-group. *Systematic Parasitology, 16*, 35–66. https://doi.org/10.1007/BF00009600

Loof, P. A. A., & Luc, M. (1993). A revised polytomous key for the identification of species of the genus *Xiphinema* Cobb, 1913 (Nematoda: Longidoridae) with exclusion of the X. americanum-group. *Systematic parasitology, 24*, 185–189.

Loof, P. A. A., Luc, M., & Baujard, P. (1996). A revised polytomous key for the identification of species of the genus *Xiphinema* Cobb, 1913 (Nematoda: Longidoridae) with exclusion of the *X. americanum*-group: Supplement 2. *Systematic Parasitology, 33*, 23–29. https://doi.org/10.1007/BF00009717

Luc, M., Lima, M. B., Weischer, B., & Flegg, J. J. M. (1964). *Xiphinema vuittenezi* n. sp. (Nematoda: Dorylaimidae). *Nematologica, 10*, 151–163. https://doi.org/10.1163/187529264X00781

Luc, M., Coomans, A., Loof, P. A. A., & Baujard, P. (1998). The *Xiphinema americanum*-group (Nematoda: Longidoridae). 2. Observations on *Xiphinema brevicollum* Lordello & da Costa, 1961 and comments on the group. *Fundamental and Applied Nematology, 21*, 475–490.

Mobasseri, M., Hutchinson, M. C., Jahanshahi Afshar, F., & Pedram, M. (2019a). New evidence of nematode-endosymbiont bacteria coevolution based on one new and one known dagger nematode species of *Xiphinema americanum*-group (Nematoda, Longidoridae). *PLoS ONE, 14*(6), e0217506. https://doi.org/10.1371/journal.pone.0217506

Mobasseri, M., Hutchinson, M. C., Jahanshahi Afshar, F., & Pedram, M. (2019b). New evidence of nematodeendosymbiont bacteria coevolution based on one new and one known dagger nematode species of *Xiphinema americanum*-group (Nematoda, Longidoridae). *PLoS ONE, 14*(6), e0217506. https://doi.org/10.1371/journal.pone.0217506

Mojtahedi, H., Sturhan, D., Akhiani, A., & Barooti, S. (1980). Xiphinema species in Iranian vineyards. *Nematologia Mediterranea, 8*, 165–170.

Naghavi, A., Niknam, G., & Vazifeh, N. (2022a). A new species of *Xiphinema americanum* group (Nematoda: Longidoridae) from Iran, with additional data on three known species. *Systematic Parasitology, 99*(5), 545–555. https://doi.org/10.1007/s11230-022-10044-6

Naghavi, A., Niknam, G., & Fallahi, A. (2022b). Study of morphological, morphometric and molecular characteristics of two species *Xiphinema vuittenezi* Luc, Lima, Weischer &. Flegg, 1964 and *X. primum* Mobasseri, Hutchinson, Jahanshahi Afshar & Pedram, 2019. 24th Iranian Plant Protection Congress, 3rd-6th September, IRIPP, Tehran.

OEPP/EPPO. (2022). European and Mediterranean Plant Protection Organization. EPPO A1, A2 List of pests recommended for regulation as quarantine pests. (Last updated 2022/09).

Oliveira, C. M., Fenton, B., Malloch, G., Brown, D. J., & Neilson, R. (2005). Development of species-specific primers for the ectoparasitic nematode species *Xiphinema brevicolle*, *X. diffusum*, *X. elongatum*, *X. ifacolum* and *X. longicaudatum* (Nematoda: Longidoridae) based on ribosomal DNA sequences. *Annals of Applied Biology, 146*(3), 281–288. https://doi.org/10.1111/j.1744-7348.2005.040031.x

Orlando, V., Chitambar, J. J., Dong, K., Chizhov, V. N., Mollov, D., Bert, W., & Subbotin, S. A. (2016). Molecular and morphological characterisation of *Xiphinema americanum*-group species (Nematoda: Dorylaimida) from California, USA, and other regions, and co-evolution of bacteria from the genus *Candidatus* Xiphinematobacter with nematodes. *Nematology, 18*(9), 1015–1043. https://doi.org/10.1163/15685411-00003012

Palomares-Rius, J. E., Archidona-Yuste, A., Cantalapiedra-Navarrete, C., Prieto, P., & Castillo, P. (2016). Molecular diversity of bacterial endosymbionts associated with dagger nematodes of the genus *Xiphinema* (Nematoda: Longidoridae) reveals a high degree of phylogenetic congruence with their host. *Molecular Ecology, 25*(24), 6225–6247. https://doi.org/10.1111/mec.13904

Palomares-Rius, J. E., Cantalapiedra-Navarrete, C., Archidona-Yuste, A., Subbotin, S. A., & Castillo, P. (2017). The utility of mtDNA and rDNA for barcoding and phylogeny of plant-parasitic nematodes from Longidoridae (Nematoda, Enoplea). *Scientific Reports, 7*(1), 10905. https://doi.org/10.1038/s41598-017-11085-4

Palomares-Rius, J. E., Gutiérrez-Gutiérrez, C., Mota, M., Bert, W., Claeys, M., Yushin, V. V., Suzina, N. E., Ariskina, E. V., Evtushenko, L. I., Subbotin, S. A., & Castillo, P. (2021). 'Candidatus Xiphinematincola pachtaicus' gen. nov., sp. nov., an endosymbiotic bacterium associated with nematode species of the genus *Xiphinema* (Nematoda, Longidoridae). *International Journal of Systematic and Evolutionary Microbiology, 71*(7), 004888. https://doi.org/10.1099/ijsem.0.004888

Pearse, A. S. (1936). *Zoological Names. A List of Phyla, Classes, and Orders Prepared for Section F. American Association for the Advancement of Science*. Duke University Press. 24pp.

Pearse, A. S. (1942). *Introduction to parasitology* (p. 357). Springfield.

Pedram, M., Niknam, G., Robbins, R. T., Ye, W., & Karegar, A. (2009). *Xiphinema iranicum* n. sp. (Nematoda: Longidoridae) from north-western Iran. *Nematology, 11*, 11–21. https://doi.org/10.1163/156854108X398363

Pedram, M., Pourjam, E., Robbins, R. T., Ye, W., Atighi, M. R., & Decraemer, W. (2012). Morphological and molecular characterisation of *Xiphinema mazandaranense* n. sp. (Dorylaimida: Longidoridae), a new member of the *Xiphinema pyrenaicum* species complex. *Nematology, 14*, 109–119. https://doi.org/10.1163/138855411X580768

Peneva, V., & Choleva, B. (1992). Nematodes of the family Longidoridae from forest nurseries in Bulgaria. I. The genus *Longidorus* Micoletzky, 1922. *Helminthology, 32*, 35–45.

Potts, F. A. (1932). The phylum Nematoda. In L. A. Borradaile & F. A. Potts (Eds.), *The invertebrata. A manual for the use of students* (pp. 214–227). Macmillan.

Poureskandarian, M. A., Pourjam, E., & Pedram, M. (2023). New evidence on cryptic speciation in soil-inhabiting nematodes, with morphological and molecular characterisation of *Xiphinema sangesarense* n. sp. (Dorylaimida: Longidoridae) from north-central mountains of Iran. *Nematology, 25*(5), 549–563. https://doi.org/10.1163/15685411-bja10238

Rambaut, A. (2009). Figtree [Computer Software]. http://tree.bio.ed.ac.uk/software/figtree/. Accessed 01 Sep 2023.

Rambaut, A., Drummond, A. J., Xie, D., Baele, G., & Suchard, M. A. (2018). Posterior summarisation in Bayesian phylogenetics using Tracer 1.7. *Systematic Biology, 67*(5), 901–904. https://doi.org/10.1093/sysbio/syy032x

Repasi, V., Agostinelli, A., Nagy, P., Coiro, M. I., Hecker, K., & Lamberti, F. (2008). Distribution and morphometrical characterization of *Xiphinema pachtaicum*, *X. simile* and *X. brevicollum* from Hungary. *Helminthologia, 45*, 96–102. https://doi.org/10.2478/s11687-008-0018-z

Robbins, R. T., Brown, D. J. F., Halbrendt, M. J., & Vrain, T. C. (1996). Compendium of juvenile stages of *Xiphinema* species (Nematoda: Longidoridae). *Russian Journal of Nematology, 4*, 163–171.

Roca, F., Lamberti, F., & Agostinelli, A. (1989). I Longidoridae (Nematoda, Dorylaimida) delle regioni Italiane. IX. La Sicilia. *Nematologia Mediterranea, 17*, 151–165.

Roca, F., Lamberti, F., & D'errico, F. P. (1991). I Longidoridae (Nematoda, Dorylaimida) delle regioni Italiane. XI. La Campania. *Nematologia Mediterranea, 19*, 139–154.

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D. L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M. A., & Huelsenbeck, J. P. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology, 61*, 539–542. https://doi.org/10.1093/sysbio/sys029

Seinhorst, J. W. (1959). A rapid method for the transfer of nematodes from fixative to anhydrous glycerin. *Nematologica, 4*, 67–69.

Shokoohi, E., Nasira, K., Iqbal, E., Hussain, S., & Mashela, W. P. (2021). First Report of *Xiphinema diffusum* from Pakistan. *Helminthologia, 58*(1), 92–99. https://doi.org/10.2478/helm-2021-0012

Tanabe, A. S. (2011). Kakusan4 and Aminosan: Two programs for comparing nonpartitioned, proportional, and separate models for combined molecular phylogenetic analyses of multilocus sequence data. *Molecular Ecolology Resources, 11*(5), 914–921. https://doi.org/10.1111/j.1755-0998.2011.03021.x

Taylor, C. A., & Brown, D. J. F. (1997). Nematode-transmitted viruses. In F. Lamberti, C. E. Taylor, & J. W. Seinhorst (Eds.), *Nematode vectors of plant viruses* (pp. 142–143). CAB International.

Trudgill, D. L., Brown, D. J. F., & McNamara, D. G. (1983). Methods and criteria for assessing the transmission of plant viruses by longidorid nematodes. *Revue De Nématologie, 6*, 133–141.

Vazifeh, N., Niknam, G., Jabbari, H., & Naghavi, A. (2019). Description of a new dagger nematode, *Xiphinema barooghii* n. sp. (Nematoda: Longidoridae) and additional data on the three known species of the genus from northwest of Iran. *Journal of Nematology, 51*, 1–17. https://doi.org/10.21307/jofnem-2019-007

Walker, G. E. (2004). New Australian record for *Xiphinema vuittenezi* on *Vitis vinifera*. *Australasian Plant Pathology, 33*, 131–132. https://doi.org/10.1071/AP03071

Wang, S., Chiu, W. F., Yu, C., Li, C., & Robbins, R. T. (1996). The occurrence and geographical distribution of longidorid and trichodorid nematodes associated with vineyards and orchards in China. *Russian Journal of Nematology, 4*, 145–154.