First record of *Helicotylenchus varicaudatus* Yuen, 1964 (Nematoda: Hoplolaimidae) parasitizing *Ammophila arenaria* (L.) Link in Portuguese coastal sand dunes

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Summary. A spiral nematode, *Helicotylenchus varicaudatus* Yuen, 1964, parasitizing *Ammophila arenaria* (L.) Link, the dominant grass in the Portuguese coastal sand dunes, is reported from Portugal for the first time and raises to seven the number of *Helicotylenchus* species detected in Portugal. A redescription of the species, with illustrations, and light and scanning electron microscope images of both female and male specimens, is presented. The rDNA containing the internal transcribed spacer regions (ITS) of *H. varicaudatus* was analysed with ITS-RFLP using the restriction endonuclease *Hinf* I. Molecular data from the ribosomal small subunit (SSU) (18S) confirmed the identification.

Key words: marram grass, ITS-RFLP, morphobiometry, SSU (18S), taxonomy.

Introduction

The genus *Helicotylenchus* was established by Steiner (1945) and more than 200 species are now attributed to this genus (Marais, 2001). *Helicotylenchus* is cosmopolitan, occurring in both cultivated and uncultivated soils. Firoza and Maqbool (1994) reported that more than one species often occur in the same sample and that the nematodes sometimes occur in large numbers. Due to the large number of species and to the intraspecific variation

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of some characters, it is difficult to identify species of Helicotylenchus (Fortuner et al., 1981; Fortuner, 1984a, 1984b; Marais, 2001). Helicotylenchus species have been classified as ectoparasites, semi-endoparasites and even migratory endoparasites (Decraemer and Hunt, 2006). Plant damage directly attributed to *Helicotylenchus* has been reported for *H*. digonicus, H. dihystera, H. indicus, H. labiatus, H. multicinctus, H. oleae and H. pseudorobustus (Inserra et al., 1979; Mancini et al., 1983; Saeed et al., 1989; Sarah, 1989, Vovlas and Larizza, 1994; Wouts and Yeates, 1994). In most plants with which Helicotylenchus is associated, the damage is insidious rather than severe, although nematode attack may lead to secondary infections from other pathogens (Yeates and Wouts, 1992).

During an investigation of nematodes associated with marram grass, *Ammophila arenaria* (L.) Link, in Portuguese coastal sand dunes, a population of *Helicotylenchus* was found. *Helicotylenchus* is the most abundant genus of plant parasitic nematodes associated with *A. arenaria* in Portuguese sand dunes along the northern and south-western Atlantic coast (Schreck Reis *et al.*, 2005). It is most abundant in the northern part of the country during the summer months, when population numbers of more than 100 nematodes g^{-1} of dry root are found, and interestingly the nematodes are more abundant in the roots than in the soil (Schreck Reis *et al.*, 2005). According to Schreck Reis *et al.* (2008) this *Helicotylenchus* species does not cause any negative effects on A. *arenaria* above or below-ground.

The Portuguese *Helicotylenchus* population was studied and some considerable differences in some morphometric parameters of the females were found, e.g. they had a greater body length, raising the possibility that more than one species was involved. However, molecular data from ITS-RFLP analysis and the rDNA SSU (18S) partial sequence indicated that only one species occurred. The *Helicotylenchus* species infecting marram grass was identified as *Helicotylenchus varicaudatus* Yuen, 1964 and is here redescribed and illustrated. Seven *Helicotylenchus* species are now reported from Portugal (Table 1).

| Species | Associated plant | Reference |
|---|---|------------------------|
| H. digonicus | Sugar cane | Lima (1962) |
| H. dihystera (syn. of H. dihysteroides) | Begonia sp., Colocasia esculenta, Cactus sp., Mentha sp., Pelargonium sp., Poligonaceae | Macara (1962) |
| | Musa sp. | Sher (1966) |
| | Maize and beans | Siddiqi (1972b) |
| | Tomato | Siddiqi (1972a) |
| | - | Krall (1985) |
| H. erythrinae | Amaryllis sp. | Macara (1962) |
| H. paraplatyurus | - | Siddiqi (1972a) |
| | - | Krall (1985) |
| H. pseudorobustus | Sugar cane and soybean | Lima (1962) |
| | Carrot and tomato | Abrantes et al. (1978) |
| | Leek and millet | Fortuner et al. (1984) |
| H. varicaudatus | Ammophila arenaria | - |
| H. vulgaris | Olea europaea | Abrantes et al. (1987) |

Table 1. Helicotylenchus species identified in Portugal.

Materials and methods

Origin and nematode propagation

Nematodes were obtained from the roots of A. arenaria collected by the first author (C. Schreck Reis) in the coastal sand dunes of the São Jacinto Natural Reserve, Aveiro (40° 41′ N, 8° 44′ W), a well preserved sand dune system in the northern Portuguese coast. Roots were cut into c. 1 cm pieces and nematode specimens were recovered using the modified Baermann funnel method (Abrantes et al., 1976). Nematodes were also propagated on A. arenaria plants. Three-weekold seedlings were transferred to 1.5 L pots containing sterilized sand (four seedlings per pot), and each seedling was inoculated with 30 nematodes recovered from A. arenaria roots. The pots were placed in a controlled-climate chamber, watered twice a week with tap water and once a month with Hoagland's nutrition solution. Every six months the cultures were transferred to new seedlings.

Morphological and morphometrical examination

The nematodes were extracted from the A. arenaria roots using the modified Baermann funnel method, killed by gentle heat and fixed in triethanolamine formalin water solution (TAF), processed with anhydrous glycerol and mounted in desiccated glycerine (Seinhorst, 1959; Hooper, 1986; Santos and Abrantes, 1988). Two male paratypes (slides RIT765 and RIT766) and two female paratypes (slides RIT767 and RIT768) were deposited with accession No. IG 31510, in the nematode collection of the National Museum of Natural History, Royal Belgian Institute of Natural Sciences, Brussels, Belgium. All remaining nematodes, 8 males (slides 53/1 to 53/8) and 38 females (slides 53/9 to 53/46) were deposited in the nematode collection of the Nematology Laboratory, Department of Life Sciences, University of Coimbra, Portugal. For scanning electron microscopy (SEM), nematodes fixed in gluteraldehyde were transferred to a 2% osmium tetroxide solution and dehydrated in increasing concentrations of ethanol. After critical point drying with carbon dioxide and gold sputter coating, the specimens were viewed and photographed in a FEI Quanta 400 FEG/EDAX Genesis X4M scanning electron microscope at 10 kV (Eisenback and Hirshmann, 1979).

Molecular studies

Molecular studies were carried out using specimens established and multiplied on *A. arenaria* plants.

DNA of the Portuguese isolate was extracted according to Williams et al. (1992) with some modifications: 10 and 15 females of larger size, 15 and 20 females of smaller size, and 15 and 20 males were individually hand-picked and transferred to 0.2 mL PCR tubes containing 2.5 μ L of lysis buffer (50 mM KCl, 10 mM Tris pH 9, 1.5 mM MgCl₂, 60 mg mL⁻¹ proteinase K). The tubes were incubated at -70°C for one hour and then transferred to 60°C for 60 min followed by 15 min at 95°C in a thermal cycler. The ITS region was amplified by adapting the methods of Cherry et al. (1997), Powers and Harris (1993) and Berry et al. (2007) using the forward primer rDNA2 (5'-TTGATTACGTCCCT-GCCCTTT-3[^]) and the reverse primer rDNA1.58S (5'-ACGAGCCGAGTGATCCACCG-3') (Vrain et al., 1992; Cherry et al., 1997). A PCR mixture $(22.5 \ \mu L)$ containing 0.3 μM of each primer, 1 U Tag polymerase (Q-Biogene), 50 mM KCl, 10 mM Tris pH 9, 1.5 mM MgCl₂ and 200 *u*M dNTPs was added to the tubes. Amplification was done in a GeneAmp PCR System 2700 (Applied BioSystems, Darmstadt, Germany) thermal cycler using an initial denaturation at 94°C for 5 min, 30 reaction cycles of 94°C for 1 min, 57°C for 1 min, 72°C for 2 min and a final extension at 72°C for 5 min. Ten μL of the reaction mixture was resolved by electrophoresis in a 1% agarose gel stained with ethidium bromide. The amplified ITS region (10 *u*L) was digested for four hours at 37°C using 2.5 U of Hinf I (Amersham BioSciences, Little Chalfont, UK). Evaluation was performed in a 2% agarose gel stained with ethidium bromide.

For SSU (18S) amplification and sequencing, DNA was extracted from three samples containing 100 males, 100 females and a mixture of 100 males and females. Nematodes were lysed by thermal shock by immersing them in liquid nitrogen for 5 minutes after which they were incubated in a water bath at 100°C for 5 minutes. The lysate was then purified with the DNeasy Blood and tissue kit (Qiagen, Cologne, Germany) according to the manufacturer's instructions. The rDNA SSU (18S) was amplified using the universal primer 988F (5'-CTCAAAGATTAAGC-CATGC-3') and a nematode-specific primer 1912R (5'-TTTACGGTCAGAACTAGGG-3') (Holterman *et* al., 2006). PCR was performed in a final volume of 25 μ L and contained 2 μ L of DNA, 0.2 μ M of each PCR primer, 0.2 mM dNTPs 1.8 mM MgCl₂, 1× buffer and 2.5 U FideliTaq DNA polymerase (USB). The following PCR program was used: 94°C for 5 min.: 35× (94°C, 40 sec.; 50°C, 45 sec.; 68°C, 90 sec.) followed by 68°C, 10 min. The purified amplification products (High Pure PCR Product purification kit, Roche Diagnostics, Indianapolis, IN, USA) were sequenced using standard procedures at Eurofins MWG Operon (Ebersberg, Germany). Sequences were then manually reviewed to confirm and correct automatic base calling. Sequences from males, females and mixed samples were aligned by Clustal W (default parameters) to check for sequence similarity. Sequences of closely related species were identified by searching the GenBank nucleotide database (National Center of Biotechnology Information, NCBI, www.ncbi.nlm. nih.gov) and used to generate a Clustal W alignment (Thompson et al., 1994), with the mixed sample sequence from the Portuguese isolate, and Globodera pallida (U855119) and G. rostochiensis (AY593877) as outgroup. The sequences used are listed in Table 2. Maximum likelihood was performed using PAUP* 4b10 (Swofford, 2002). The robustness of the inferred tree was tested using nonparametric bootstrapping (with 1000 pseudo-replicates).

The sequence data from the 18S ribosomal RNA gene partial sequence reported in this study were deposited in the GenBank database (NCBI) under accession number HM237044.

Results and discussion

Helicotylenchus varicaudatus Yuen, 1964

Female

Habitus C-shape (12.5%) or spiral (87.5%) (Figures 1A, E and 2A). Body length with large ampli-

tude, 692.5±82.5 (510-890) um long (Table 3). Lip region hemispherical, not offset, with two to five lip annules, occasional anastomosis (Figures 1A, B, 2E and 3B). Prestoma rectangular, centrally located on the labial disc, and surrounded by six pore-like openings of the inner labial sensilla (Figure 3A). Labial disc rounded in frontal view (Figure 3A). First lip annule with six longitudinal incisions, corresponding to two lateral lips and four medial lips (two sub-dorsal and two sub-ventral) (Figure 3A). Amphidial openings oval shaped, located between the labial disc and the lateral lips (Figure 3A). Cephalic framework well developed. Cephalids not seen. Stylet slender with anterior faces of stylet knobs rounded (57.5%) or flattened (42.5%) (Figures 1A, B and 2E). Medium bulb elongated, oval shaped, 9.1±0.7 (8–11) µm wide and 12.3±1 (9–12.5) μ m long (Table 3). Hemizonid two annules long, located two to three annules anterior to the excretory pore (n=9). Hemizonion not seen. Excretory pore located anterior to level of esophago-intestinal valve at 16±1.6 (12.5–21.4) % of body length (Table 3). Oesophageal glands forming a wrap-around over anterior end of intestine, longest overlap being ventral, 52.1 \pm 9.8 (31–74) μ m long (Table 3, Figures 1A and 2B). Lateral field with four lines, areolated opposite the oesophageal region. The inner two lines end in a v- or u-shaped tail (Figures 1C–D and 3C). Fasciculi not seen. Reproductive system with two functional genital branches, without regression of the posterior branch (Figures 1A and 2A). Anterior genital branch 20±3.5 (15.4-26.7) and posterior genital branch 19.1 ± 3.7 (13.2–26) as a percentage of body length (n=15) (Table 3). Spermatheca offset, rounded, filled with sperm. Epiptygma folded into vagina. Phasmids pore-like, smaller than the corresponding ventral tail annule, located posterior to anus (Figures 1C, D and 2D). Tail 13.4±1.9

Table 2. GenBank accession numbers of the closely related species sequences used for alignment.

| Species | Accession number (GenBank) |
|--|----------------------------|
| Helicotylenchus pseudorobustus isolate HeliPse | AY284606 |
| H. multicinctus strain HeliMul1 | FJ969124 |
| H. canadensis isolate HeliCan | AY284605 |
| H. vulgaris isolate HeliVul | AY284607 |
| H. varicaudatus isolate wb14 | EU306354 |
| H. dihystera | AJ966486 |

 $(9.5-17.5) \mu m \log (Table 3)$, with four to eight ventral tail annules; shape variable, asymmetrically rounded (35%) having a slight ventral indentation (Figures 1C, D, 2D and 3D,E).

Male

Habitus straight (10%) or arcuate (90%) (Figures

1H and 2F). Heads of males slightly higher than heads of females. Lip region (Figures 1F, 2G and 3F,G), prestoma (Figure 3G), labial disc (Figure 3G), first lip annule (Figure 3G), amphidial openings and cephalic framework (Figure 3G) similar to those of the females. Stylet slender with anterior face of stylet knobs posteriorly rounded (40%)

Table 3. Morphometric data of *Helicotylenchus varicaudatus* Yuen, 1964. All measurements are in μm and in the form: mean \pm SD (range).

| Character | Portugal | | Belgium, New Zealand, Poland, Russia, The Netherlands, Turkey, UK ^a |
|--|--------------------------------|------------------------------|--|
| | Females $(n = 40)$ | Males (n= 10) | Females |
| L | $692.5\pm82.5\ (510-890)$ | $631 \pm 52.6 (530 - 700)$ | 520–910 |
| a | $29.9 \pm 2.4 \ (23.5 - 35.8)$ | $33.9{\pm}2.4~(30.3{-}37.4)$ | 17.4-29 |
| b | $7.6\pm0.8(5.8-8.7)$ | $7.5 \pm 0.6 (6.6 - 8.5)$ | 4.3–7.7 |
| b' | $4.8 \pm 0.6 (3.6 - 6.3)$ | $4.4{\pm}0.3$ (3.9–4.7) | 3.4–6 |
| с | $52.2 \pm 7.5 (39.4 - 70.7)$ | $34\pm2.6(34-37.3)$ | 32.5–77 |
| c' | $1\pm0.1\ (0.7-1.3)$ | $1.9{\pm}0.2~(1.6{-}2.2)$ | 0.5–1.2 |
| m (5) | 46.3 ± 2.6 (40.9–52.1) | $47.2 \pm 2.5 (42.9 - 50)$ | 44–57 |
| 0 (%) | $23\pm5(15-31)$ | $24.5{\pm}6.1~(18.2{-}34.1)$ | 10-39.5 |
| Excretory pore as a percentage of total length | 16±1.6 (12.5–21.4) | $15.7 \pm 0.9 (14 - 16.6)$ | - |
| V (%) | $64{\pm}1.5~(61{-}67)$ | _ | 57.2–67 |
| OV ₁ (%) | $20\pm3.5~(15.4-26.7)$ | _ | 18–32 |
| $\mathrm{OV}_{2}\left(\% ight)$ | $19.1 \pm 3.7 (13.2 - 26)$ | _ | 17.5–30 |
| Head region height | $3.6\pm0.6(3-5.5)$ | $3.6 \pm 0.5 (2.5 - 4.5)$ | _ |
| Head region width | 6.5±0.8 (5–8) | $6.4 \pm 0.6 (5.5 - 7.5)$ | _ |
| Stylet length | $23.7 \pm 1.1 (22 - 26)$ | $21.2 \pm 1.2 (20 - 23)$ | 23.8-33.6 |
| Stylet cone length | $10.9 \pm 1 \ (9 - 12.5)$ | $10{\pm}0.9~(8.5{-}11)$ | _ |
| Stylet knobs height | $2.9{\pm}0.4~(2.5{-}4)$ | $2.2 \pm 0.3 (2 - 2.5)$ | _ |
| Stylet knobs width | 5±0.8 (3.5–7) | $3.6 \pm 0.7 \ (2.5 - 4.5)$ | 5–6 |
| Stylet base to dorsal gland opening (DGO) | $5.4 \pm 1.1 (3.5 - 7)$ | 5.1±1.1 (4–6.5) | 3–13 |

continued on the next page

| Character | Portugal | | Belgium, New Zealand, Poland, Russia, The Netherlands, Turkey, UK ^a |
|--|-------------------------------|------------------------------|--|
| - | Females $(n = 40)$ | Males (n= 10) | Females |
| Medium bulb length | $12.3\pm1(9-12.5)$ | $11.2 \pm 1.5 (9 - 13)$ | _ |
| Medium bulb width | $9.1 \pm 0.7 (8 - 11)$ | 7.8 ± 0.9 (7–10) | - |
| Medium bulb valve length | $3.4\pm0.4(2.5-4)$ | 2.8 ± 0.3 (2.5-3) | - |
| Medium bulb valve width | 2.5±0.3 (2-3) | $2.1\pm0.2(2-2.5)$ | _ |
| Head to esophagus- intestine junction | 91.6±6.1 (80–107) | 84.7±5.7 (76.5–93) | 104–133 |
| Head to excretory pore | $109.7 \pm 7 (94 - 121)$ | 98.9 ± 6.3 (86–108) | 112–137 |
| Head to posterior end of esophageal gland | $144{\pm}10.9~(120{-}167)$ | $145.1{\pm}16.6~(126{-}172)$ | 140–183 |
| Head to vulva | $440.1 \pm 48.7 (335 - 550)$ | _ | 365–500 |
| Body width at stylet knobs | $14.4 \pm 1.5 (12.5 - 18.5)$ | $11.4\pm0.8(10-12)$ | _ |
| Body width at excretory pore | 18.1±1.3 (16–22) | $15.6\pm1.1\ (13.5-17.5)$ | - |
| Greatest body width at mid-body | 23.3±2.9 (15–28.5) | 18.6±1 (17–20) | 22–34 |
| Body width at vulva | $21.1\pm2.9(14-26)$ | _ | _ |
| Body width at anus | $13.6 \pm 1.5 (10 - 17)$ | $9.9{\pm}0.6(9{-}11)$ | _ |
| Width of one body annule at mid body | $1.9\pm0.3(1-2.5)$ | 1.9±0.2 (1.5–2) | 1.3–1.9 |
| Spicule length | _ | $22.4{\pm}1.8(20{-}25)$ | _ |
| Gubernaculum length | _ | $5.9{\pm}0.9$ (4.5–7) | _ |
| Number of annules from phasmids to anus/cloaca | One to four posterior | Two to three posterior | Seven anterior to four posterior |
| Distance of phasmids to tail terminus | $10.8 \pm 1.9 (7 - 14)$ | $14.2\pm1.5(12-16)$ | - |
| Tail length | $13.4 \pm 1.9 \ (9.5 - 17.5)$ | $18.6\pm1(17-20)$ | 8–19 |
| Number of ventral tail annules | 6.1±1.2 (4–8) | 9.3±0.9 (8–11) | 5–11 |

$Table\ 3\ continued$

^a Yuen (1964); Sher (1966); Volkova (1987); Bongers (1988); Eroshenko and Volkova (1988); Yeates and Wouts (1992), Brzeski (1998), Kepenekci and Ökten (1996); Bert and Geraert (2000).



Figure 1. *Helicotylenchus varicaudatus*. Females (A–E). Whole female (A), head, lateral view (B), tails (C,D) and habitus (E). Males (F–H). Head, lateral view (F), tail, lateral view (G) and habitus (H). (Drawings by Fernando Correia).



Figure 2. *Helicotylenchus varicaudatus*. Females (A–E). Habitus (A), anterior region, lateral (B), vulva region (C), tail (D) and head (E). Males (F–H). Habitus (F), anterior region (G) and tail (H). v, vulva; ep, excretory pore; a, anus; ph, phasmid. Scale bars: A, B, F, G=50 μ m; C, D, E, H=25 μ m.



Figure 3. *Helicotylenchus varicaudatus*. Females (A–E). Lip region, face view (A), lip region, lateral view (B), lateral fields (C) and tails (D,E). Males (F–H). Lip region, lateral view (F), lip region, face view (G) and tail (H). Scale bars: A, G=1 μ m; B, C, D, E, F, H=5 μ m.

or flattened (60%) (Figures 1F and 2G). Hemizonid two annules long, located two to three annules anterior to excretory pore (n=2). Oesophageal glands forming a wrap-around over the anterior end of the intestine, with a 61.7±16.1 (38.5–90) μ m long ventral overlap (Table 3 and Figure 2G). Lateral field areolated opposite the oesophageal region and the bursa. Phasmids one to two annules posterior to the cloaca level (Figure 1G). Spicule length exceeds tail length (Figures 1G and 2H). Bursa extends to end of tail (Figures 1G, 2H and 3H). Tail with rounded projection curved ventrally (Figures 1G and 2H).

Remarks

The description of the Portuguese H. varicaudatus population agrees with previous descriptions of H. varicaudatus from various locations. The specimens of this study ranged widely in body length, 510–890 μ m, but they conformed to the body length reported in the literature, 520–910 μ m (Kepenekci and Ökten, 1996; Brzeski, 1998). The V value showed the least variation with a coefficient of variation (CV) of 2% and a range of 61–67%, which agreed with V values previously reported for H. varicaudatus, 56.9-68 % (Volkova, 1987; Bert and Geraert, 2000). The stylet length of the current specimens, 22–26 μ m, was equal to the lower end of the range reported in the literature, 23.8–33.6 μ m (Eroshenko and Volkova, 1998; Bert and Geraert, 2000). The coefficient of variation for stylet length was 5%. Stylet length usually has the smallest CV among the quantitative characters, 1.7% in the progeny of a single *H. dihystera* female, and 1.6 to 4% in field populations of a single species (Fortuner, 1979; Fortuner et al., 1981). The character of a subdivided first lip annule is reported only for a few species, H. varicaudatus, H. silvicola Van den Berg and Marais, 1995, H. curatus Marais, Van den Berg, Swart and Tiedt, 2004 and to an Italian population of H. multicinctus (Cobb, 1893) Golden, 1956 (Vovlas, 1983). No other Helicotylenchus species has been reported as having a division of the first lip annule (Sher and Bell, 1975; Loof, 1984; Abrantes et al., 1987; Marais and Buckley, 1992; Geraert, 1997; Marais, 1998; Marais and Quénéhervé, 1999; Orion et al., 1999; Bert and Geraert, 2000; Marais et al., 2000; Van den Berg and Marais, 1995; Van den Berg et al., 2003; Marais et al., 2004) and the only H. multicinctus population reported as having a subdivided first lip annule is the Italian population. The Italian H. multicinctus population was not available for study, but according to the published data it may be an Italian population of H. varicaudatus. Yuen (1964) stressed the variability of the tail shape in his description of H. varicaudatus. The specimens examined in this study showed less variation than the original description, and mostly showed only two tail shapes. The Portuguese population differed from most other populations in that it contained male nematodes. Males were found at all locations, although usually only in small numbers. Males were not usually found in the other populations; they have only been reported in populations from The Netherlands (Loof, 1984; Bongers, 1988) and Poland (Brzeski, 1998).

Helicotylenchus varicaudatus has been reported from various countries: Austria, Belgium, Bulgaria, the Czech Republic, England, France, Germany, India, Italy, New Zealand, Poland, Russia, Slovakia, Spain, The Netherlands, Turkey, and the United States (Yuen, 1964; Sher, 1966; Krall, 1985; Yeates and Wouts, 1992; Brzeski, 1998; Bert and Geraert, 2000; Stollarova, 2001; Lehman, 2002; Talavera and Navas, 2002; Háněl, 2007). Only Brzeski (1998) reported *H. varicaudatus* from sand dunes on the Baltic coast, without however specifying the host plant.

Molecular studies

Amplification of the ITS region of rDNA produced a 980-bp product. Restriction digestion with *Hinf* I produced a pattern having a strong band with 400 bp, and a fainter band with ca. 160 bp for all samples regardless of the specimen used (bigger females, smaller females or males) (Figure 4).

Amplification of DNA 18S produced a 1100-bp product for the three samples: males, females and a mixture of males and females. The sequences used are listed in Table 3. All the sequences were identical when aligned by Clustal W, showing that the same species occurred in all three samples (misalignments were found only with the homopolymers, and these were sequencing artefacts). Only the sequence from the mixture of males and females was therefore used for further analysis.

The smallest differences were in the 18s rDNA sequence of H. varicaudatus accession number EU306354. The Portuguese H. varicaudatus isolate differed from the Belgian isolate in 10 SSU rDNA nucleotides (1%) with a 912 bp sequence overlap.





Figure 4. (A) ITS-PCR amplified products on 1.5% agarose gels. 1. *Helicotylenchus varicaudatus* bigger females (10 and 15 nematodes), 2. *H. varicaudatus* smaller females (15 and 20 nematodes) and 3. *H. varicaudatus* males (15 and 20 nematodes). (B) *Hinf*I-digested PCR-RFLP patterns on 2% agarose gels. 1. *Helicotylenchus varicaudatus* bigger females (15 nematodes), 2. *H. varicaudatus* smaller females (20 nematodes) and 3. *H. varicaudatus* males (20 nematodes). SF=DNA marker, Smart Ladder SF (100 bp ladder, Eurogentec, Belgium).

However, phylogenetic analysis placed these isolates together with high support (bootstrap=98%) and placed it as sisters to a clade of *H. canadensis* and *H. vulgaris* with maximal support (Figure 5). Phylogenetic analysis with *H. varicaudatus* accession number EU306354 (Bert and Geraert, 2000; Bert *et al.*, 2008) therefore supported the identification of the Portuguese isolate as *H. varicaudatus*.

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Figure 5. Maximum likelihood (ML) tree of *Helicotylenchus* species retrieved from the GenBank database and from the Portuguese isolate aligned with Clustal W (Thompson *et al.*, 1994) with *Globodera pallida* and *G. rostochiensis* as outgroup. ML was performed using PAUP* 4.0b10 (Swofford, 2002). Robustness of the inferred tree was tested using nonparametric bootstrapping (with 1000 pseudoreplicates). GenBank accession codes are shown in parentheses. Bootstrap support values are indicated at nodes.

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