Short Note

Characterisation of *Coomansus parvus* (de Man, 1880) from Russia with the first report of males

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De Man (1880) originally described *Mononchus parvus* from soil samples collected from dunes in The Netherlands. Jairajpuri (1970) proposed a new genus *Clarkus* and transferred this species to it. Later, Jairajpuri & Khan (1977) subdivided the genus *Clarkus* into *Clarkus* (*sensu stricto*) and *Coomansus* and designated *C. parvus* as the type species of this newly-established genus.

Coomansus parvus was found on all continents except Australia (Andrássy, 2009). According to our research, this species is widespread throughout the European part of Russia, but usually its population densities are low. Recently, a large number of females and also three males of this species were found in the Fili Park, Moscow, Russia. This is the first report on males of this species.

Table 1. Measurements and ratios of 15 females and 3 males of *Coomansus parvus* from Moscow, Russia. If not otherwise stated, measurements are in µm.

Morphological characters	Females	Males
L	823.25 ± 59.58 (736-944)	931 ± 54.77 (880-989)
a	17.5 ± 1.19 (16-19)	19.8 ± 2.0 (17.7-21.7)
b	3.35 ± 0.18 (3.1-3.7)	3.36 ± 0.03 (3.34-3.4)
c	14.5 ± 1.12 (12-16)	20.5 ± 1.93 (18.3-21.7)
c'	2.18 ± 0.05 (2.1-2.3)	1.36 ± 0.14 (1.24-1.52)
V, %	63 ± 2.33 (59.5-67.9)	–
G1, %	12.1 ± 1.52 (9.6-14.8)	–
G2, %	12.6 ± 0.85 (11.5-13.8)	–
Lip width	22.1 ± 1.27 (20-23.7)	22.6 ± 0.28 (22.5-23.0)
Apex of dorsal tooth, %	60 ± 1.85 (56-62)	61 ± 1 (60-62)
Buccal cavity length	24.8 ± 0.4 (24-25)	25.3 ± 0.58 (25-26)
Buccal cavity width	11.7 ± 0.85 (10-12.5)	12.16 ± 0.29 (12-12.5)
Oesophagus	268.6 ± 19.78 (218-274)	276.93 ± 16.25 (263.5-295)
Tail	56.8 ± 3.6 (55-69)	46.4 ± 8.4 (40.4-56)
Spicule	–	56.6 ± 7.37 (51-65)
Gubernaculum	–	15.7 ± 0.26 (15.5-16)
Number of supplements	–	15.3 ± 1.15 (14-16)
Lateral guiding pieces	–	19.6 ± 2.52 (17-22)

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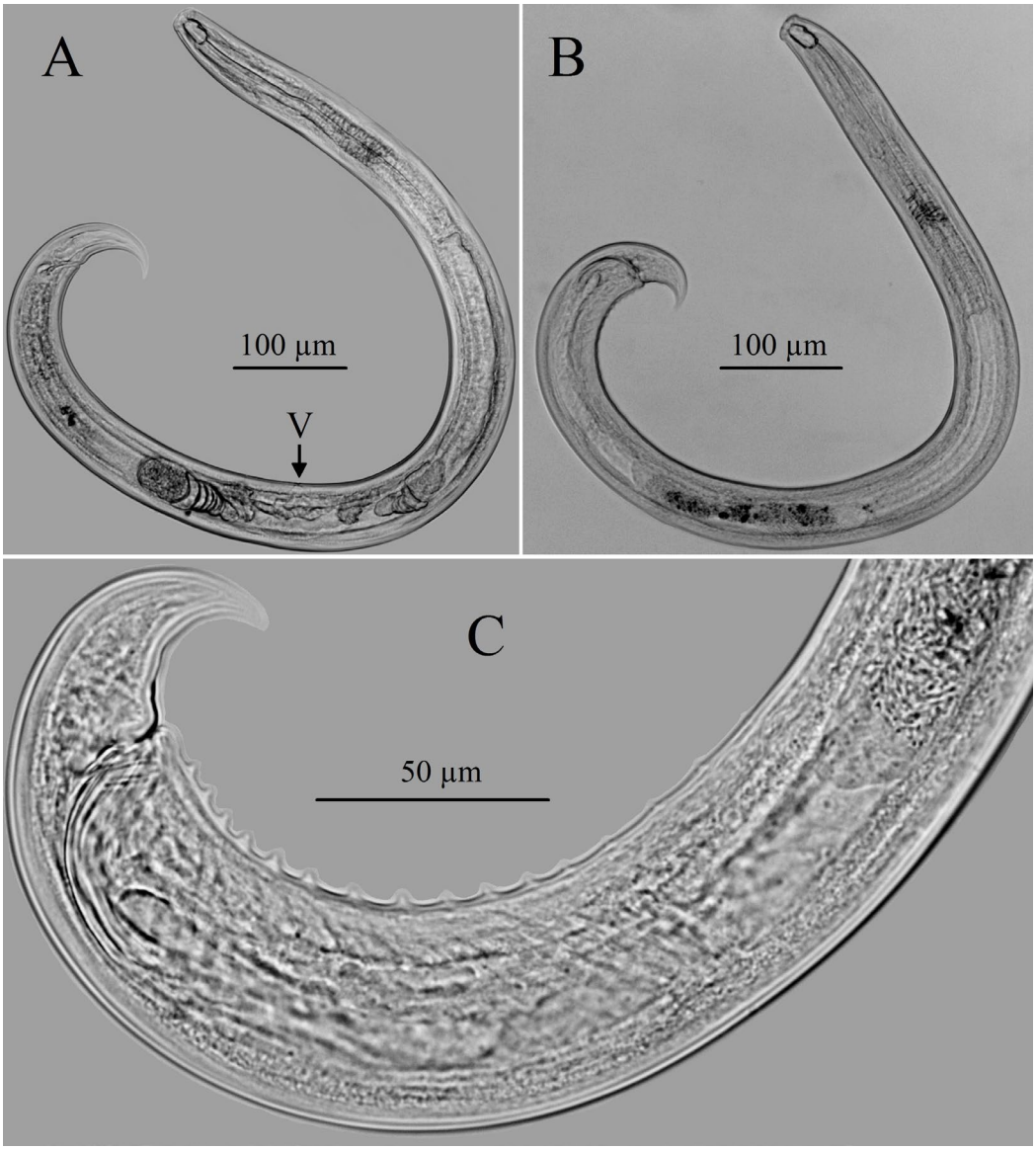

Fig. 1. Light micrographs of *Coomansus parvus*. A: Entire female, B: Entire male, C: Posterior end of male.

Soil samples were collected from the rhizosphere of wild red raspberries (*Rubus idaeus* L.). The geographical location of the sampling site is 55°45'3.06" N; 37°28'36.084" E. Nematodes were extracted using a modification of the decanting and sieving method (Flegg, 1967). For morphological studies, the nematodes were killed with hot water, fixed in a 5% formalin solution, and mounted in glycerin on slides using the Seinhorst technique (Seinhorst, 1959). Molecular studies were performed using the scientific equipment of Core Research Facility of the 'Bioengineering' Centre (Moscow, Russia). For this work, nematodes frozen in distilled water were used. There were three replicates. Each replicate was a test tube with several specimens of *C. parvus*. Their total DNA was extracted using the Wizard kit (Promega, USA) according to the manufacturer's instructions. The forward Nem_18S_F (5'-CGC GAA TRG CTC ATT ACA ACA GC-3') and the reverse Nem_18S_R (5'-GGG CGG TAT CTG ATC GCC-3') primers (Floyd *et al.*, 2005) were used for the amplification of the fragment of the 18S rRNA gene. The D2-D3 expansion segments of the 28S rRNA gene were amplified using the forward D2A (5'-CAA GTA CCG TGA GGG AAA GTT G-3') and the reverse D3B (5'-TCG GAA GGA ACC AGC TAC TA-3') primers (Nunn, 1992). The amplifications were performed in a Tetrad thermal cycler (Bio-Rad, USA). PCR products were purified using the Wizard PCR Preps kit (Promega, USA). The sequencing of the PCR products was carried out

with the same primers using the genetic analyser ABI 3730 (Applied Biosystems, USA). Low-quality segments of sequences at the 5' and 3' ends were removed. Then, the newly obtained sequences were submitted to the GenBank database under accession numbers MT703902 and MT705327.

Description. Female (Fig. 1A). Body C-shaped upon fixation. Cuticle about 2.5 µm thick at anterior part, 3 µm at mid body and up to 5 µm at tail terminus. Lip region offset; papillae distinct. Buccal cavity tapering at the base. Amphid about 4 µm long, cup-shaped, with a slit-like aperture, situated anterior to apex of the dorsal tooth. Tooth slightly anteriorly directed. Reproductive apparatus amphidelphic with short, symmetrical, and reflexed ovaries. Vulva transverse, without vulval papillae. *Pars distalis vaginae* short, lacking any differentiation. *Pars refringens vaginae* oval sclerotised pieces, about 3 × 3.5 µm each. *Pars proximalis vaginae* 6-10 µm long. Uterine eggs one or two at the same time, 80-100 × 32.5-40 µm. Rectum 0.7-0.9 times as long as the anal body width. Tail conoid, ventrally curved, with a finely rounded tip. Caudal glands and spinneret absent.

Remarks. Females of this population do not differ significantly from the original description (De Man, 1880) and some other descriptions of this species (Mulvey, 1967; Choi & Choi, 1987; Farahmand *et al.*, 2009; Iliev & Ilieva, 2016). Females of some populations from India (Rawat *et al.*, 1999), Costa Rica (Zullini *et al.*, 2002) and Vietnam (Nguyen Vu Thanh, 2005) have a longer tail (up to 80 µm long) and a greater value of c' (up to 3.8). Females from a population collected in Spain (Jiménez-Guirado *et al.*, 2007) differ by having a longer body (up to 1.4 mm) and tail (up to 105 µm).

Male (Fig. 1B). General morphology is similar to that of a female. Genital system diorchic; its total length is 36-39% of the body length. Each testis is about 95 µm long, opposed with elongate, spindle-shaped spermatozoa. Spicules rather thick, ventrally curved, 1.7-1.8 times as long as the anal body diameter, measured along the axis (Fig. 1C). Gubernaculum well developed, extending laterally to spicules. Lateral guiding pieces with fine bifurcated tip near cloaca aperture. The distance between the ventromedian supplements gradually decreases from anterior to posterior. Tail shorter than that of females, conoid, ventrally curved, with a finely rounded tip. Caudal glands and spinneret absent. Males are rare. Sex ratio in the studied population was 1:25.

Molecular characterisation. Despite the wide geographical range of the studied nematode species, as it is known from the literature (Andrássy, 2009), there are only two sequences of *C. parvus* deposited in the GenBank. They are the sequences of the 18S rRNA gene of the specimens collected in The Netherlands. The sequences obtained from different individuals in this study were identical to the sequence of *C. parvus* from The Netherlands (AY284767).

The sequences of the D2-D3 expansion segments of the 28S rRNA gene were most similar to the *Prionchulus* sp. sequence from Central Mexico, with 88.84% similarity (KY750805). Other sequences of this segment of mononchid nematodes deposited in GenBank had a similarity lower than 88%.

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