

Redescription of *Haemonchus longistipes* (Nematoda: Strongylida) Parasitizing The Camel, *Camelus dromedarius* by Light Microscopy in Egypt

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Abstract: *Haemonchus longistipes*, known as the barber's pole worm, is a very common parasite and one of the most pathogenic nematodes of ruminants. Adult worms attach to abomasal mucosa and feed on the blood. This parasite is responsible for anemia, oedema and death of infected sheep and goats, mainly during summer in warm, humid climates. The present study introduced a morphological description for the adult male and female worms isolated from five out of ten gastrointestinal tracts of the dromedary *Camelus dromedaries* collected from the main slaughter house at Cairo, Egypt. By light microscopy, it was observed that the body length of the isolated male worms was 11.4-15.3 (14.9±3.0) mm with a lobbed terminal bursa supported by long, slender rays. The dorsal lobe was asymmetrical with Y-shaped dorsal ray. Spicules long with a length of 0.41–0.68 (0.52±0.04) mm, each provided with a small barb and pore near its extremity. Body of female worms measured 14.6-16.5 (15.5±0.3) mm long. The length from anterior end to the cervical papillae was 0.21-0.53 (0.45±0.05) mm. The vulva of the female had a linguiform process or flap. Tail without a spine and the anal pore at the posterior end of the body had a visible dorsal rim and a muscular ventral rim not documented before in the paste description. Also, the presence of a knob type of female worms as well as eggs morphology were not previously seen. The parasite isolated was compared morphologically with the most similar previous species of the same genus. It was concluded that *Haemonchus* species infecting camels in Egypt need a massive study with using molecular techniques to detect and record the exact taxonomy and type species of this genus.

Key words: *Haemonchus* Spp. • Nematoda • *Camelus dromedaries* • Light Microscopy

INTRODUCTION

The most important nematodes of domestic animals and wildlife are those with adults infecting the gastrointestinal system causing severe economic losses and population decrease worldwide [1-3]. *Haemonchus longistipes*, *Nematodirus mauritanicus*, or *N. dromedarii* are the nematodes which are specific to the dromedary while other camel nematodes such as *Trichostrongylus prolohlurus*, *T. vitrinus*, *Ostertagia mongolica*, *Marshallagia mentulata*, *N. spathiger*, or *Oesophagostomum venulosum* may infect sheep and goats [4, 5]. *Haemonchus* spp. (order *Strongylida*) is the stomach nematode worm infecting the abomasum of ruminant hosts and causes significant economic losses worldwide [5, 6], they reduce the productivity and performance of camels and predispose them to other infectious diseases [7]. Haemonchosis is a disease caused by the most prevalent and pathogenic parasite

Haemonchus species, which also known as the red stomach worm, wire worm or barber's pole worm, they are common parasites of domesticated ruminants and have achieved a worldwide distribution in part due to the movement of their economically important hosts. Adult worms are attached to abomasal mucosa and feed on the blood, the adult female is easily recognized by its trademark "barber pole" coloration. The red and white appearance is because *Haemonchus* species is a blood feeder and the white ovaries that coil around the intestines are filled with blood. The male adult worm is much smaller and displays the distinct feature of a well developed copulatory bursa, containing an asymmetrical dorsal lobe and a Y-shaped dorsal ray. Many species of *Haemonchus* are found in domestic ruminants: *H. contortus* [8], primarily a parasite of the domestic sheep *Ovis aries*, also it infects numerous other domestic and wild ruminants; *H longistipes* [9]; a parasite of the camel (*Camelus dromedarius*); *H. placei*, is primarily a parasite

of domestic cattle (*Bos taurus*) but it has been found also in the domestic sheep, white-tail deer (*Odocoileus virginianus*) and pronghorn antelope (*Antilocapra americana*). *H. mitchelli*; *H. okapiae* and *H. similis*; infecting domestic cattle in a few southern states of the U.S.A., Central and South America, Asia and several Atlantic and Pacific islands [10-13], in *Bos indicus* in Tanzania and Uganda, domestic sheep in Brazil, white-tail deer in Florida and in numerous other ruminants and localities [14, 15].

The present study aimed to redescribe morphologically and morphometrically the pathogenic nematode isolated from the camel *Camelus dromedarius* by light microscopy in Egypt.

MATERIALS AND METHODS

Ten gastrointestinal tracts of the camel *Camelus dromedarius* (Family: Camelidae) were collected during the year of 2018 from the main slaughter house of Cairo, Egypt and transported to the Parasitology laboratory, Zoology Department, Faculty of Science, Cairo University. Organs were separated from each other, placed in shallow plastic jars containing saline solution (0.85%) and then examined for helminth parasites. After their recovery from the hosts, nematode worms were washed in normal saline to free them from mucus and then fixed in hot 70% ethyl alcohol, then preserved in glycerin alcohol and mounted in glycerin and glycerin jelly. Photomicrographs were taken with the help of Zeiss research photomicroscope supplied with Canon Digital Camera. Female worms were examined for its type of cuticular process and vulvar morphology in the region of vulva as described by Rose [16]. Adult male worms were used for species identification; the tails of male worms were cut before the bursa and mounted in lactophenol for clear examination of the spicules under a microscope.

RESULTS

From the ten gastrointestinal tracts examined, only five were found infected with adult male and female nematode worms mainly in the abomasa of camels. In general, worms were yellow with filliform body tapered anteriorly only in male worms and towards both ends in females (Fig. a). No buccal capsule, small buccal cavity was observed with a dorsal lancet (Fig. b). Prominent cervical papillae, spine-like (Fig. c). Transverse striations were present along the worm body (Fig. d). The linguiform vulvar flap was encountered as the most predominant

morph type with two subtypes, the subtype A (Fig. e) which was the predominant form in the study area and subtype B (Fig. f).

Female: Body length of female worms measured 14.6-16.5 (15.5±0.3) mm. Esophagus length was 1.42-1.86 (1.72±0.2) mm. The distance between anterior end to the cervical papillae was 0.21-0.53 (0.45±0.05) mm. Ovejector well developed posteriorly and anteriorly, consisted of distinct parts. Vagina was 0.15-0.19 (0.17±0.03) mm long. The vulva of the female had a linguiform process or flap. Tail without a spine and the anal pore at the posterior end of the body had a simple dorsal rim and a muscular ventral rim (Fig. g).

Male: Body length was 11.4-15.3 (14.9±3.0) mm. Esophagus was 1.23-1.68 (1.41±0.02) mm long. The distance from the anterior end to cervical papillae was 2.83-4.85 (3.26±0.2) mm. Bursa with elongated lobes supported by long, slender rays (Fig. I). Dorsal lobe was asymmetrical with Y-shaped dorsal ray (Fig. J). Spicules long with a length of 0.41-0.68 (0.52±0.04) mm, each provided with a small barb and pore near its extremity. Synlophe was bilaterally symmetrical, consisted of a maximum of 40-45 ridges (Fig. K).

DISCUSSION

Parasitic controls as well as management of camel husbandry represent a huge problem worldwide where camels become susceptible to viral and parasitic infections from pasture during feed intake [17, 18]. *Haemonchus* has become the most serious parasite affecting small ruminants throughout the world [19, 20]. The present study introduced morphological description of *H. longistipis* from the dromedary, *C. dromedarius* in Egypt. The variations in morphology depend mainly on the total body length, cervical papillae, spicules length and the distribution and arrangement of synlophe. Among *Haemonchus* spp., a 42-ridge synlophe has been observed only in *H. mitchelli*, *H. okapiae*, *H. longistipes* [19]. The synlophes of the first three species consist of 42 ridges distributed over the anterior half of the body. These species can be separated by unique structural characteristics of their synlophes, spicules and copulatory bursa. The distal tip of the left spicule of *H. mitchelli* bears a barb that is almost twice as long as the short barb and about half as long as the long barb on the right spicule. In contrast the barb on the left spicule of *H. okapiae* is similar in size to the short barb and is

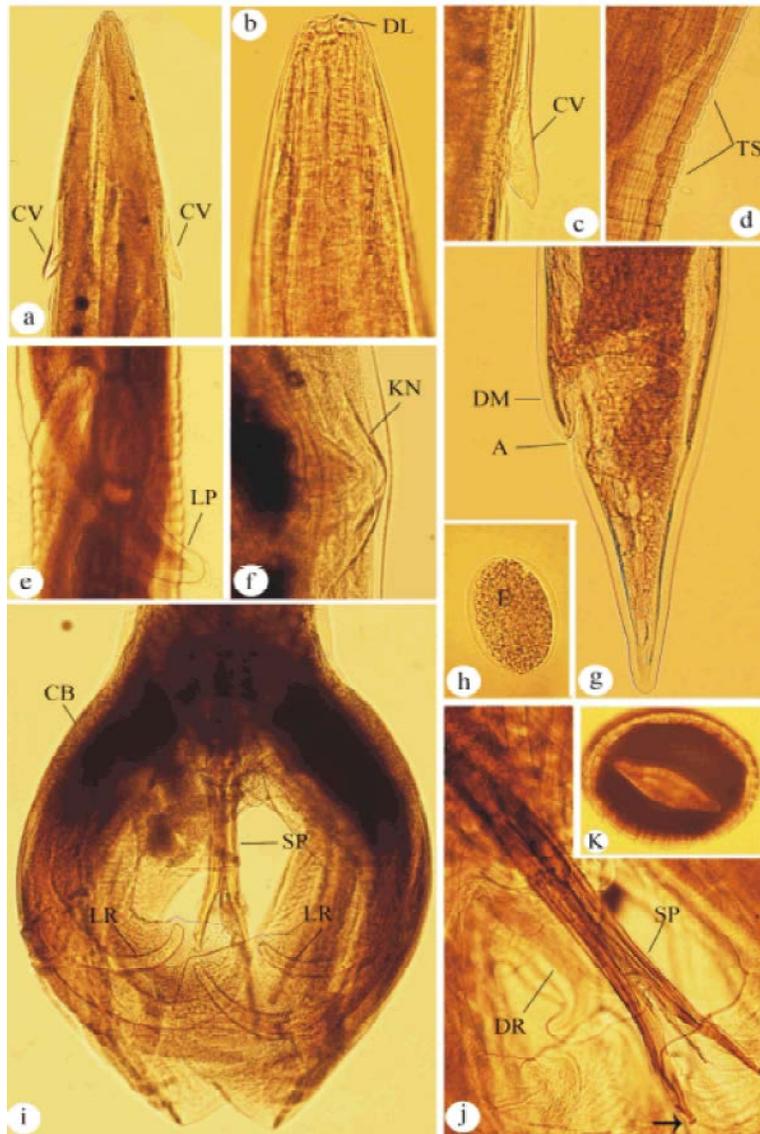


Fig. 1(a-k): Photomicrographs of *Haemonchus longistipes* showing: (a, b) the anterior part with two cervical papillae (CV) and a dorsal lancet (DL); (c) cervical papillae (CV); (d) transverse cuticle striations (TS); (e) linguiform valvular female with linguiform process (LP); (f) knobbed valvular type with knob (KN); (g) the posterior region of female; A anus; covered by dorsal rim (DM); (h) egg (E); (i) copulatory bursa (CB) of male, asymmetrical spicules (SP), lateral (LR) and dorsal rays (DR); (j) spicules (SP), with two small barbs (arrow); (k) section through the mid-esophagus showing cuticle ridges

about 25% as long as the long barb of the right spicule. Also, the present study showed widespread and common polymorphism of vulvar morphology of the female *Haemonchus* worms. The A subtype linguiform was observed to be the dominant contributor of the linguiform morphotype composition. This finding is in contrast to the previous findings [21-24] reported that the predominance of the same morph type in small ruminants

of Hawassa. He claimed that this is probably attributed to the differences in the climates of the study sites or to the smaller size per abomasum in some of the studies specimens. Many investigators indicated that vulvar polymorphism has advantages such as increasing the ability to use a wider range of available habitats so it may be a marker of ecological adaptation, it has a great taxonomic significance and is important to understand the

biology of these parasites [25, 30]. Finally, it was concluded that *Haemonchus* species infecting camels in Egypt need a massive study with using molecular techniques to detect and record the exact taxonomy and type species of this genus.

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