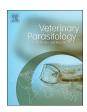
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#### Regional report

# *Dracunculus* infections in domestic dogs and cats in North America; an under-recognized parasite?



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#### ABSTRACT

We reviewed 62 new cases and 18 published reports of Dracunculus infections in domestic dogs and cats to describe the epidemiology of this parasite in dogs and cats in North America. We collected host and parasite data when available, including age, sex, and breed of dog, nematode location in the host, and any clinical signs at presentation and/or description of the apparent lesion. For dogs, infections were noted in six of the AKC breed groups, but none was reported from the toy group or the miscellaneous breed class. Age of infected dogs ranged from 7 months to 19 years (median 4 years; average 5.3 years), and infection rates were similar in male and female dogs. Most nematodes were associated with the distal extremities, but worms were also found in the chest/thorax, abdomen, head, and flank. Although most infected dogs had a single worm, three dogs had two or more worms that were collected from multiple lesions. Three new cat cases, with similar lesions, presentations and seasonality, were detected in Alabama, North Carolina and Texas. Cases were reported from a wide geographic range throughout eastern North America, during every month of the year, but 72% of infections were diagnosed in the late winter to early spring (December to May). All collected worms were larvigerous females which cannot be identified to species based on morphologic characters. Thus, we attempted to amplify and sequence a portion of the cytochrome c oxidase subunit I (COI) gene for specific identification. Although 13 worms from 12 cases were available, sequences were obtained for only eight worms from seven cases. These eight worms were D. insignis, a common parasite of raccoons (Procyon lotor) and other primarily carnivorous mammals. Female worms are the most likely to be detected in dogs and cats because male worms do not emerge, parasites should be preserved in ethanol for molecular identification. Although this study used convenience sampling of available data, we found that the parasite is widespread throughout the eastern US and Canada and that Dracunculus infections in dogs are more common than is revealed in published literature. However, more research is needed to understand the epidemiology, including transmission route(s), prevalence, and distribution of this parasite.

#### 1. Introduction

Nematodes in the genus *Dracunculus* (Spirurida; Dracunculoidea) are large subcutaneous parasites of mammals and reptiles (snakes and turtles). Currently, there are 12 recognized species, primarily from snakes, but little is known about the diversity and host-specificity of these *Dracunculus* species (Moravec, 2012). Most data on this group of parasites resulted from research on the medically important human Guinea worm (*Dracunculus medinensis*). Historically, *D. medinensis* has been reported rarely from domestic dogs, but in recent years the number of reported canine infections in the few remaining endemic African countries has increased dramatically (Eberhard et al., 2014; Eberhard et al., 2016a; Molyneux and Sankara, 2017).

In North America, *D. insignis* is commonly reported in several species of wildlife, including carnivores within the families Procyonidae and Mustelidae. This parasite was first reported in raccoons (*Procyon lotor*) in the late 1800s and reports are now widespread in the eastern United States and Canada (Chandler, 1942a,b; Cheatum and Cook, 1948; Crichton and Beverley-Burton, 1973a, 1977). Another parasite, *D. lutrae*, has been described from North American river otters (*Lontra canadensis*) from Canada (Crichton and Beverley-Burton, 1973b). Unfortunately, females of most *Dracunculus* spp. cannot be definitively identified to species morphologically and most previous reports in wildlife are based on detection of the large subcutaneous larvigerous females. Although males can be identified based on morphological characteristics, they are rarely detected in infected animals because they do not attain an easily detectable size (1–3 cm) nor do they emerge from the body (Crichton and Beverley-Burton, 1973a).

and herein review their epidemiology. Furthermore, when possible, we obtained COI gene sequences to confirm *Dracunculus* species identification.

#### 2. Methods

We obtained information on *Dracunculus* cases in dogs and cats throughout North America from academics, commercial and state veterinary diagnostic laboratories, research parasitologists, and through direct contact with veterinarians who had diagnosed cases. When possible, we collected the following information for each dog or cat: month/year of diagnosis; county and state (or province) of residence; age, sex, and breed; nematode location in host; and any associated clinical signs at presentation and/or description of the apparent lesion. When available, we classified dogs into their respective American Kennel Club (AKC) breed groups. For some factors (i.e., geographic distribution, month of diagnosis) we included data from 16 previously published cases in dogs and 2 cases in cats (Supplemental Table).

Specimens preserved in ethanol were shipped to the Southeastern Cooperative Wildlife Disease Study (SCWDS) for molecular characterization. Material from one case was fixed in formalin and submitted for routine histologic examination. We extracted DNA from ethanol-fixed worms using the Qiagen DNeasy DNA Purification Kit (Germantown, MD) following the manufacturer's protocol for tissue extraction. A portion of the COI gene was amplified using a cocktail of M13-labeled primers for nematodes (Prosser et al., 2013). When the COI gene would not amplify, amplification of a portion of the 18S rRNA gene was attempted (Bimi et al., 2005). Amplicons were visualized on 0.8% agarose gels stained with Gel Red Nucleic Acid Gel Stain 10,000× in DMSO (Biotium, Hayward, CA), extracted from the gel and purified using the QIAquick gel extraction kit (Qiagen), then bidirectionally sequenced at the Georgia Genomics Facility (Athens, GA). Consensus sequences for each sample were compared with related available sequences using the nucleotide BLAST function available through the National Center for Biotechnology Information (NCBI) (https://blast.ncbi.nlm.nih.gov/ Blast.cgi).

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