

Dirofilaria immitis and *Dirofilaria striata* (Spirurida: Onchocercidae) detected in wild carnivores from Texas, United States

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ABSTRACT

Dirofilaria immitis and *Dirofilaria striata* (Spirurida: Onchocercidae) are epidemiologically important filarial nematodes detected in wild carnivores sympatric to domestic animals and humans. In this study we surveyed for *Dirofilaria* species among previous studies archived blood samples ($n = 202$) of wild carnivores sourced across Texas between the years of 2014–2016 and 2020 to 2023. In total, 117 coyotes (*Canis latrans*), 67 raccoons (*Procyon lotor*), 12 gray foxes (*Urocyon cinereoargenteus*), five bobcats (*Lynx rufus*), and one striped skunk (*Mephitis mephitis*) were tested through the amplification of the partial cytochrome oxidase c subunit 1 (*COI*) gene followed by sequencing. *Dirofilaria immitis* was detected in 11.39% (95% CI = 7.71–16.51) of the samples (21 coyotes and two raccoons), while *D. striata* was detected in a single bobcat. *Dirofilaria immitis* sequences had 99.85%–100% (99.92% \pm 0.08) similarity with other *D. immitis* sequences in GenBank. The sequence of *D. striata* from the bobcat was 100% similar to the single *COI* sequence available in GenBank. Data from this study reinforce the role of coyotes as a wild reservoir for *D. immitis* and suggest that raccoons may also play a role in the epidemiology of this parasite. This study additionally provides molecular data on *D. striata*, an understudied filarioid of felids.

1. Introduction

Filarial parasites are important vector-borne helminths in domestic and wild animals worldwide (Otranto and Deplazes, 2019; Gruntmeir et al., 2023), with those belonging to the genus *Dirofilaria* (Spirurida: Onchocercidae) considered to be of great epidemiological relevance. This genus includes 27 valid species and 15 species of which the validity is debated (Dantas-Torres and Otranto, 2013). Culicids transmit these nematodes, and microfilariae are blood-dwelling. Adult parasites are found in different anatomical locations, including the intravascular system (*Dirofilaria immitis*) (Kotani and Powers, 1982) and subcutaneous tissue (*Dirofilaria repens*, *Dirofilaria striata*) (Orihel et al., 1997; Wyatt et al., 2020).

Dirofilaria immitis is North America's most well-known filarioid species infecting companion animals (e.g., dogs, cats, ferrets) (Mosley et al., 2023). Its full life cycle has been extensively studied and involves the ingestion of blood microfilariae by culicid vectors and the

development from first-stage to infective third-stage larvae in about 14 days (McCall et al., 2008). In the vertebrate host the parasite requires at least 6 months to reach the adult stage, which is primarily found in the pulmonary arteries and right ventricle (Kotani and Powers, 1982). A variety of wild canids, such as coyotes, red foxes, and wolves, have been reported with infections (Zinck et al., 2021; Sobotyck et al., 2022). In addition, *D. immitis* infections have also been described in captive and wild felids, mustelids, ursids, and even humans (Crum et al., 1978; Papadopoulos et al., 2017; St Jean et al., 2022; Upton et al., 2023). Widely distributed across the United States, this parasite has been reported in all 50 states (Nelson et al., 2005; Little et al., 2021). While the occurrence in domestic dogs and cats is well documented, the infection in wild carnivores is less frequently reported (Kotwa et al., 2019; Sobotyck et al., 2022; Upton et al., 2022).

Dirofilaria striata is another filarioid species infecting wild carnivores in North America. This nematode has been detected in bobcats from Louisiana (Orihel and Ash 1964), in bobcats from South Carolina (Miller

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and Harkema 1968), in panthers from Florida (Forrester et al., 1985), and more recently in a domestic cat from Florida (Wyatt et al., 2020). The life cycle of *D. striata* is not entirely known but likely involves infective third-stage larvae (L3) transmitted by culicids (Orihel and Ash 1964). In contrast to *D. immitis*, *D. striata* adults are found in the hosts' subcutaneous tissues (Orihel and Ash 1964). There has been a single report of a zoonotic infection attributed to *D. striata* in the intraorbital tissue of a 9-year-old boy from North Carolina (Orihel and Isbey, 1990).

The role of wild carnivores in the epidemiology of *Dirofilaria* species has been the subject of various studies (Nelson et al., 2003; Magi et al., 2008; Aher et al., 2016). Wild canids can maintain *D. immitis* and act as a source of microfilaria to infect mosquitoes (Bowman and Atkins, 2009). Wildlife infections with *D. immitis* are of particular consideration for maintaining transmission because unlike dogs or cats, wild animals are not covered by any prophylactic program (Brown et al., 2012; Wang et al., 2014). The susceptibility of wild carnivores to *Dirofilaria* infections and the widespread distribution of these animals in North America likely makes them important in the epidemiology of these filarioids. Heartworm infections in wild canid populations, especially coyotes, likely increase the risk of *D. immitis* transmission to domestic animals and humans (Kotwa et al., 2019; Worsley-Tonks et al., 2021; Sobotytk et al., 2022).

Wild carnivores (e.g., coyotes, raccoons) can inhabit anthropized areas close to pet animals and human beings (Gates et al., 2014; Hody and Kays, 2018; Worsley-Tonks et al., 2021). Areas markedly changed by anthropic actions amplify the transmission of vector-borne pathogens, including those of zoonotic concern (Bradley and Altizer, 2007; Brearley et al., 2013; Cardozo et al., 2021). In this study, we used molecular methods to characterize *D. immitis* and *D. striata* in wild carnivores across Texas, United States.

2. Material and methods

2.1. Animals and sampling

We opportunistically tested archival DNA samples (n = 202) extracted from blood clot collected in previous research across 32 counties of Texas, US (Curtis-Robles et al., 2016; Hodo et al., 2020; Salomon et al., 2024, in press). In total, 117 coyotes (*Canis latrans*), 49 raccoons (*Procyon lotor*), 12 gray foxes (*Urocyon cinereoargenteus*), three bobcats (*Lynx rufus*) and one striped skunk (*Mephitis mephitis*) were initially included in this study. Additional raccoon (n = 18) and bobcat (n = 2) blood samples were collected during nuisance predator trapping efforts on a private ranch in Atascosa County, Texas in March 2021 and tested as well. Blood samples were collected from the heart or thoracic cavity in the field within 8 h of death. Few of these blood samples were taken from live-capture and released wildlife (IACUC, 2021-0124 D C). From all samples, eight blood samples from Walker County were collected from raccoons each month between May 2021 and May 2022 (Salomon et al., 2024, in press). Three raccoons, one skunk, and one bobcat were sampled through teaching courses in Brazos and Matagorda counties between 2020 and 2023.

2.2. PCR and sequencing

DNA was extracted from blood clots using the Omega E.N.Z.A. Tissue DNA kit (Omega, Biotek, Norcross, GA). The partial cytochrome oxidase c subunit 1 (*COI*) gene (635 bp) of filarial nematodes was amplified using the primers COIintF: 5'-TGA TTG GTG GTT TIG GTA A-3' and COIintR: 5'-ATA AGT ACG AGT ATC AAT ATC- 3'. These primers generated products of the expected size for eleven species of filarial nematodes (Casiraghi et al., 2001). The cycling conditions included an initial denaturation step at 95 °C for 2 min, followed by 40 cycles at 95 °C for 45 s, 52 °C at 45 s, and 72 °C for 90 s, and a final extension step at 72 °C for 5 min. We used nuclease-free water as a negative control and DNA of *D. immitis* as a positive control. The amplifications were viewed

after 1.5% agarose gel electrophoresis in UV transilluminator.

All amplified bands were purified using the E.Z.N.A.® Cycle Pure Kit (OMEGA Bio-Tek Inc., Norcross, GA, USA) according to the manufacturer's instructions and sequenced in both directions using the Sanger method in an ABI-3130 automatic sequencer (Applied Biosystems) at Eurofins Genomics LLC (Houston, TX). Sequences were aligned and compared to homologous sequences of *Dirofilaria* spp. available in the nucleotide sequence database at the National Center of Biotechnology Information (NCBI) (Available online: <https://www.ncbi.nlm.nih.gov/genbank/>) using ClustalW in MEGA 11 (Clark et al., 2016; Tamura et al., 2021). Phylogenetic analyses for the partial *COI* gene were performed using the Maximum Likelihood Method and a General time Reversible best-fit model with gamma distribution (2000 bootstrap replicates) in MEGA 11 (Tamura et al., 2021). A sequence of *Brugia pahangi* was used as outgroup.

2.3. Data analysis and map creation

The prevalence (%) was calculated for filarial infection along with 95% confidence intervals (95% CI) by the modified Wilson method (<https://epitools.ausvet.com.au/ciproportion>). Fisher's exact test was used to compare the *D. immitis* positivity between coyotes and raccoons. A 5% significance level was considered. The BioEstat software version 5.3 was used for statistical evaluation (Ayres et al., 2007).

For map creation, cartographic bases in shapefile format were accessed on the United States Census Bureau website. Then, these files were inserted in the QGIS version 3.28.15 software, and the raster layer was generated.

3. Results

Dirofilaria immitis DNA was detected in 11.39% (n = 23/202, 95% CI = 7.71–16.51) of the samples. In particular, 17.95% (n = 21/117, 95% CI = 12.05–25.89) of coyotes and 2.99% (n = 2/67, 95% CI = 0.82–10.95) of raccoons were positive. DNA of *D. striata* was detected in one bobcat (20%; 95% CI = 3.62–62.45). Coyotes had a higher prevalence of *D. immitis* than raccoons (p = 0.0066). All 12 gray foxes and one striped skunk tested negative. Positive animals were distributed in 34.27% (11/32) of counties in which animals were sampled (Fig. 1).

All amplified bands produced a single sequence. In particular, the molecular analyses generated 23 *D. immitis* sequences with a nucleotide identity ranging from 99.85%–100% (99.92% ± 0.08) with other *D. immitis* sequences (ON062406; LC107816). A total of six different *D. immitis* sequences were identified, two of which were shared between coyote and raccoon. Our *D. striata* sequence (PP572465) was 100% similar to the only *COI* sequence available in the GenBank database (MN635457, collected from a domestic cat from Florida) (Wyatt et al., 2020). Our sequences formed a well-supported clade (100% bootstrap support) with other *D. immitis* sequences (Fig. 2). One representative of each unique sequence was deposited in the GenBank database under accession numbers PP566947 – 52.

4. Discussion

This study revealed the presence of two zoonotic species of *Dirofilaria* in three species of wild carnivores. The positivity for *D. immitis* infection in coyotes (17.95%; 21/117) is higher than recently reported in Texas (9.83%; 12/122) (Sobotyk et al., 2022). Overall, a significant variation in prevalence rates has been observed in coyotes from North America, with reports in the last decade varying from 6.5% (Paras et al., 2012) to 37.2% (Aher et al., 2016). Regardless of the factors (e.g., geographic location, climate, population sampled, and animal age) influencing the occurrence of *D. immitis* in coyotes (Brown et al., 2012), reports of this infection in the southern United States where temperature is more suitable for mosquito development have increased over the last years (Gates et al., 2014; Aher et al., 2016; Sobotyk et al., 2022).

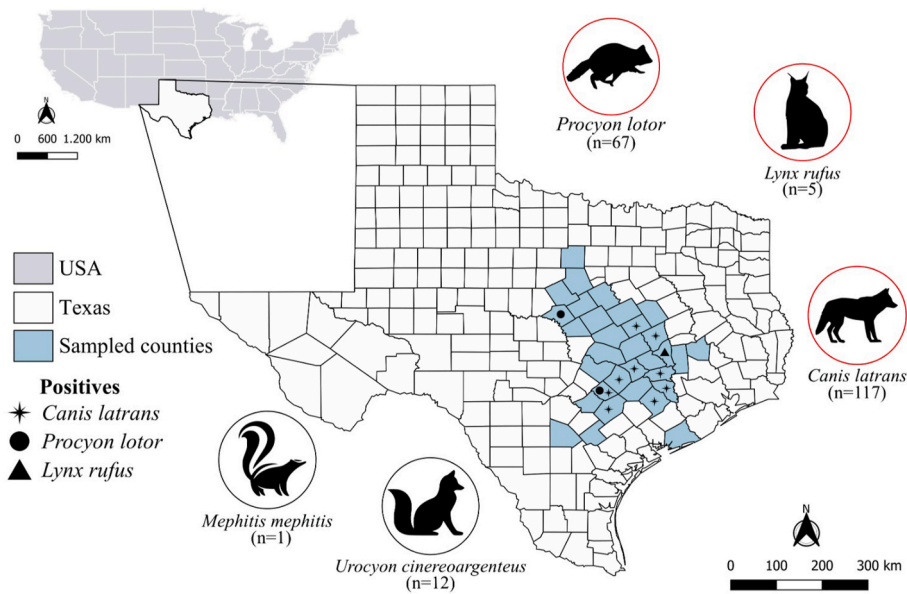


Fig. 1. Map of Texas, US indicating the origin and number of animals sampled by species. Counties of Texas from which samples originated are in blue. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

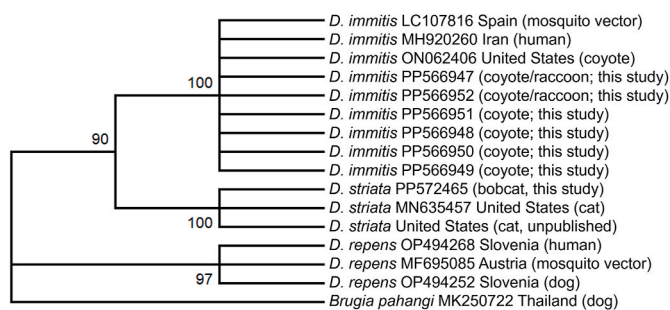


Fig. 2. Phylogenetic tree created using a maximum likelihood method (2000 bootstrap replicates) showing the relationship of identified *Dirofilaria immitis* and one isolate of *Dirofilaria striata*. *Brugia pahangi* sequence was used as outgroup.

The apparent absence of *D. immitis* in gray foxes could be attributed to the limited opportunistic sample size available in the current study. There have been several reports of *D. immitis* in gray foxes across areas of the U.S. and Mexico, often in low prevalence (Simmons et al., 1980; Carlson and Nielsen, 1983; Hernández-Camacho et al., 2016).

In this study, we detected *D. immitis* DNA in 2.99% (2/67) of raccoons. In North America, *Dirofilaria* infections in raccoons are primarily attributed to *Dirofilaria tenuis* (Sauerman and Nayar, 1985; Izasa and Courtney, 1988; Telford and Forrester, 1991; Richardson et al., 1992; Pung et al., 1996). The absence of *D. tenuis* DNA sequences in GenBank is a limitation for studies in which blood samples of raccoons are molecularly assessed. Hence, molecular characterization of *D. tenuis* genes is urgently needed, especially because it is the third most common *Dirofilaria* species reported in humans (Perles et al., 2024). A single juvenile male raccoon was previously reported to be naturally infected by two immature female *D. immitis* in Parramore Island, Virginia (Snyder et al., 1989).; In addition, a previous experimental study had demonstrated that raccoons could not support the development of *D. immitis* (Christensen and Shelton, 1978); however only two adult female raccoons were used in this study. While generally considered an aberrant host with no significant role in the epidemiology of *D. immitis*, the detection of parasite DNA in blood suggests the presence of circulating microfilariae, and hence, a patent infection (Negron et al., 2022; Soboty

et al., 2022). Nevertheless, the role of raccoons as a susceptible, relevant reservoir host for *D. immitis* remains questionable and may deserve further investigation.

Dirofilaria striata, a scarcely studied filarioid nematode of felids, was found in a single bobcat (1/5). This positive bobcat was captured within a neighborhood illustrating their epidemiological importance as reservoir to other hosts, including domestic cats. This parasite has been reported in bobcats in Louisiana (Orihel and Ash, 1964), South Carolina (Miller and Harkema, 1968), Florida panthers (*Puma concolor*) (Forrester et al., 1985; Lamm et al., 1997), and dogs in Florida (Courtney et al., 1985). More recently, the detection of this parasite in a cat from Florida provided the first molecular data based on the partial sequence of the *COI* gene (Wyatt et al., 2020). The molecular characterization of novel *D. striata* isolates across its range is paramount for establishing a robust database for future comparisons among filarial populations.

Despite being underdiagnosed in humans, the zoonotic role of *D. immitis* is known worldwide (Theis, 2005; Fontes-Sousa et al., 2019; Oshima, 2023; Perles et al., 2024). Classical infections in humans are characterized by nodules on the lungs with minimal pathogenic relevance (Hirano et al., 2002; Malik et al., 2016; Palicelli et al., 2022). However, erratic ocular parasitism by *D. immitis* may pose additional risk to human health (Somsap et al., 2021; Aykur et al., 2021). Additionally, human infection by *D. striata* was reported in the intraorbital tissue of a 6-year-old boy living in Buncombe County, North Carolina (Orihel and Isbey, 1990).

The presence of both *D. immitis* and *D. striata* in wild carnivores, especially those adapted to live in areas inhabited by domestic animals and humans, is essential for understanding dirofilariosis epidemiology. While in endemic areas, chemoprophylactic treatments impact the overall prevalence of the infection in dogs and cats (Labarthe et al., 2015; Brianti et al., 2023; Mosley et al., 2023). However, the lack of measures to prevent infection in coyotes, raccoons and bobcats may negatively impact any prevention or eradication program, like has been suggested in the Linosa Island, in Italy, where, most likely, the presence of feral cats could impact the eradication program (Brianti et al., 2023). Finally, data from this study indicate that *D. immitis* infection in raccoons is likely more common than expected and reinforces the importance of monitoring both coyotes and raccoons in heartworm endemic areas. Additionally, it provides additional molecular data on *D. striata*, a little known filarioid of felids.

CRediT authorship contribution statement

Rafael A.N. Ramos: Writing – original draft, Methodology, Data curation, Conceptualization. **Hassan Hakimi:** Writing – review & editing, Methodology, Data curation. **Jordan Salomon:** Writing – review & editing, Methodology, Data curation. **Rachel E. Busselman:** Writing – review & editing, Methodology, Data curation. **Rachel Curtis-Robles:** Writing – review & editing, Methodology, Data curation. **Carolyn L. Hodo:** Writing – review & editing, Methodology, Data curation. **Sarah A. Hamer:** Writing – review & editing, Supervision, Funding acquisition, Data curation, Conceptualization. **Guilherme G. Verocai:** Writing – review & editing, Supervision, Funding acquisition, Data curation, Conceptualization.

Declaration of competing interest

None.

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