Introduction

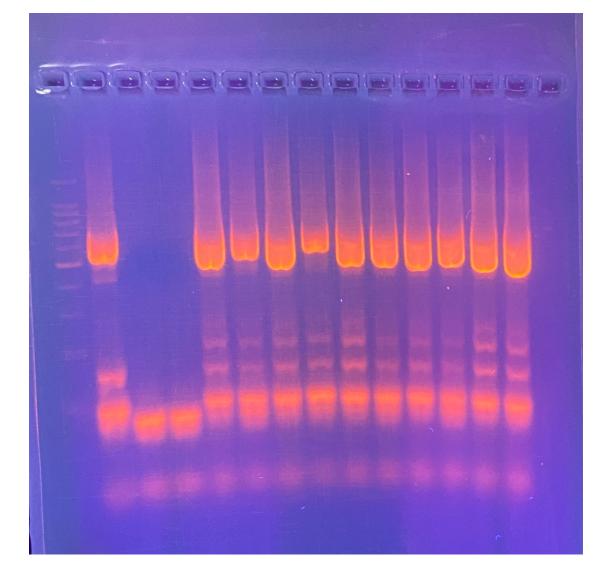
- *Dracunculus insignis* and *Dracunculus lutrae* are parasitic nematodes native to North America.
- The goal of this project was to investigate the genetic diversity of *Dracunculus* in wildlife species from the Eastern USA and investigate spatial and host patterns of infection.
- *D. lutrae* was expected from otters, and *D. insignis* was expected from remaining hosts.



Dracunculid specimens from an Arkansas otter.

Methods

- 89 *Dracunculus*-like specimens from North American river otters (*Lontra canadensis*), raccoons (*Procyon lotor*), and Virginia opossums (*Didelphis virginiana*) across the Eastern USA.
- Phylogenetic relationships were examined using the cytochrome c oxidase I (COI) gene target.
- Experimental methods included DNA extraction, gene-specific amplification (PCR), Sanger sequencing, and phylogenetic analysis using Geneious.

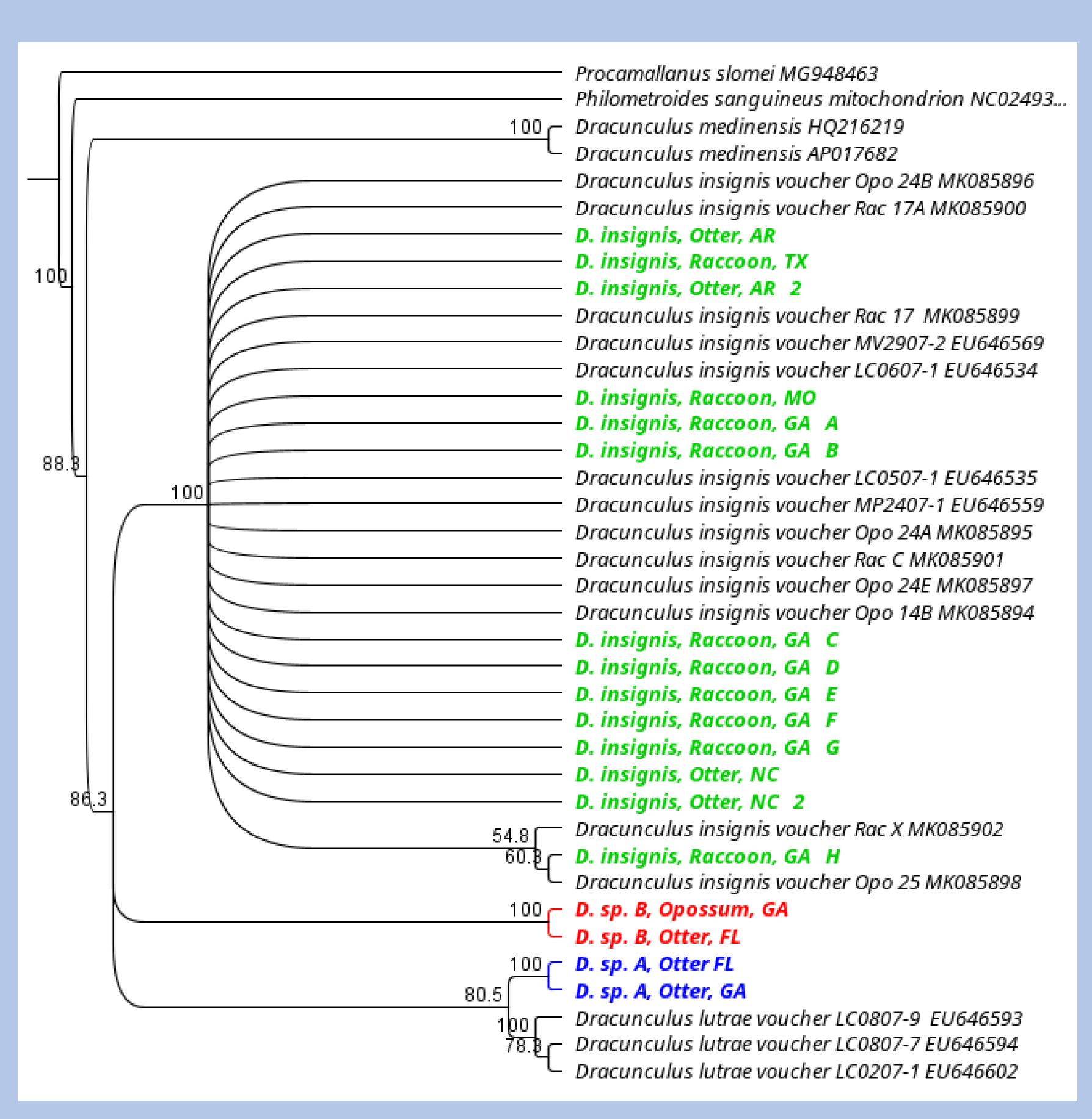


Electrophoresis gel with UV light to show PCR amplification.

Phylogenetics of *Dracunculus* Nematodes in North America

Madeline R. Giner, Erin K. Box, Sarah M. Coker, Ellen Haynes, Michael J. Yabsley, and Christopher A. Cleveland

Wildlife in North America are infected with a wide, previously undetected, diversity of *Dracunculus* species.



<u>Key</u> D. insignis

D. sp B

D. sp A

Neighbor-joining phylogenetic tree showing the relationships of selected *Dracunculus* spp. Bi-directionally sequenced specimens resulting from this project are shown in color.









Results

 48 of the 89 specimens were successfully sequenced and identified.

	D. insignis	D. sp. A	D. sp. B
Raccoon	20 GA, 1 TX, 1 MO		
Otter	13 AR, 6 NC	1 GA, 1 FL, 1 SC	1 FL
Opossum	2 GA		1 GA

Conclusions

- *D. insignis* was present in most locations and hosts, *D. lutrae* was absent in tested otters.
- Two novel species were identified:
 - D. sp. A was closely related to D. lutrae (92.8% shared genetic identity)
- D. sp. B had its own unique clade and was present in the Southeastern U.S.
- More research is needed to examine the prevalence of the two novel species.

<u>Acknowledgements</u>

- I thank all Cleveland Lab members for their mentoring and support.
- I thank the Carter Center for funding and the Southeastern Cooperative Wildlife Disease Study for support.









The University of Texas at San Antonio™