Apr 16th, 11:00 AM - 2:00 PM

Does Baylisascaris procyonis Impact Raccoon (Procyon lotor) Genetics?

Matthew E. Ingle
Cedarville University, mingle@cedarville.edu

Stephen G. Dunbar
Loma Linda University

Jaynee L. Bartsch
Cedarville University, jbartsch@cedarville.edu

Kyle J. Culbertson
Cedarville University, kylejculbertson@cedarville.edu

Taylor A. Fulton
Cedarville University, tfulton@cedarville.edu

See next page for additional authors

Ingle, Matthew E.; Dunbar, Stephen G.; Bartsch, Jaynee L.; Culbertson, Kyle J.; Fulton, Taylor A.; Guffey, Katherine R.; Juris, Aubrey J.; Nolan, Ashlie N.; Nordquist, Daniel P.; Rowlands, Carrie E.; and Sitler, Joshua A., "Does Baylisascaris procyonis Impact Raccoon (Procyon lotor) Genetics?" (2014). *The Research and Scholarship Symposium*. 17.
http://digitalcommons.cedarville.edu/research_scholarship_symposium/2014/poster_presentations/17

Presenters
Matthew E. Ingle, Stephen G. Dunbar, Jaynee L. Bartsch, Kyle J. Culbertson, Taylor A. Fulton, Katherine R. Guffey, Aubrey J. Juris, Ashlie N. Nolan, Daniel P. Nordquist, Carrie E. Rowlands, and Joshua A. Sitler

Department of
SCIENCE AND
MATHEMATICS
CEDARVILLE UNIVERSITY

Does *Baylisascaris procyonis* affect raccoon (*Procyon lotor*) genetics?

Ingle, M.E.[1,2], Dunbar, S.G.[2], Bartsch, J.L.[1], Culbertson, K. J.[1], Fulton, T. A.[1] Guffey, K.R.[1], Juris, A. J.[1], Nolan, A.N.[1], Nordquist, D. P.[1] Rowlands, C.E.[1], and Sitler, J. A.[1]
[1] Department of Science and Mathematics. College of Arts and Sciences. Cedarville University.
[2] Department of Earth and Biological Sciences. School of Medicine, Loma Linda University.

Introduction

Raccoons (*Procyon lotor*) are the final host for the raccoon roundworm nematode (*Baylisascaris procyonis*). *B. procyonis* has been found to infect more than 90 different wild and domesticated animals, including humans. Infection with *B. procyonis* is the leading cause of larva migrans encephalopathy (LMV). LMV is a type of visceral larva migrans in which the parasite migrates to the central nervous system and causes a variety of problems within the brain. In order to take preventative action against the spread of *B. procyonis* it is necessary to understand the dynamic relationship between the final host and *B. procyonis*, and how the nematode is spread into subsequent hosts. Phylogenetic trees illustrate co-evolutionary events between species living in a symbiotic relationship with each other. Throughout the coevolution of host and parasite, many aspects of a population affect the way the members interact with one another and with symbiotic species.

Hypotheses

Areas with higher rates of prevalence in the raccoon roundworm *B. procyonis* demonstrate lower genetic diversity and show signs of microevolution within the *P. lotor* population. The microevolution would result in genetic structuring, lower rates of heterozygosiity, and a departure from the Hardy Weinberg principle which would manifest itself in a change in the genetics of the population.

Methods

We collected raccoons from Greene and Clark Counties in southwest Ohio, working with 6 fur trappers, between November 10th and January 31st, 2012. The methods for collection and extraction can be found in the paper labeled "The Prevalence of Raccoon Roundworm (*Baylisascaris procyonis*) in the North American raccoon (*Procyon lotor*), and the Relation to Diet"(Ingle).

We necropsied the small intestines and removed anything attached to the mesentery. The full length of the intestines were necropsied and any *Baylisascaris procyonis* were collected and stored in 70% ethanol solution contained in cups labeled with the same number as those assigned to the raccoon from where they were extracted. We recorded the worms and set them aside for future analysis.

In order to evaluate the relationship between host and parasite in regards to diet, we isolated DNA from intestinal wall tissue, amplifying a portion of exon 2 from MHC II. We isolated the DNA from the raccoons using the methods and equipment highlighted in the packet from the QIAmp DNA Mini Kit labeled, *Protocol: DNA Purification from Tissues (QIAmp DNA Mini Kit).*

We sent our samples to The Ohio State University for sequencing. We calculated heterozygosities for the nine townships we surveyed. We used a χ^2 test for equality of distributions to determine whether raccoons from townships with above 60% prevalence have different rates of heterozygosity for this locus than other raccoons. These data will help us to understand the relationship between raccoons and raccoon roundworm.

Results:

Expected	Below 60% Prevalence	Above 60% Prevalence
Number Heterozygous	43.87704918	57.12295082
Number Homozygous	9.12295082	11.87704918

Table 1 offers the results of a c^2 test to determine the expected number of individuals above and below 60% prevalence heterozygous and homozygous at gene DRB.

Observed	Below 60% Prevalence	Above 60% Prevalence	Total
Number Heterozygous	47	54	101
Number Homozygous	6	15	21
Total	53	69	122

Table 2 offers the observed results on the number of heterozygous and homozygous individuals at gene DRB, as well Lower variation because there is very little mixing.
as the total number of both types of gene combinations observed overall.

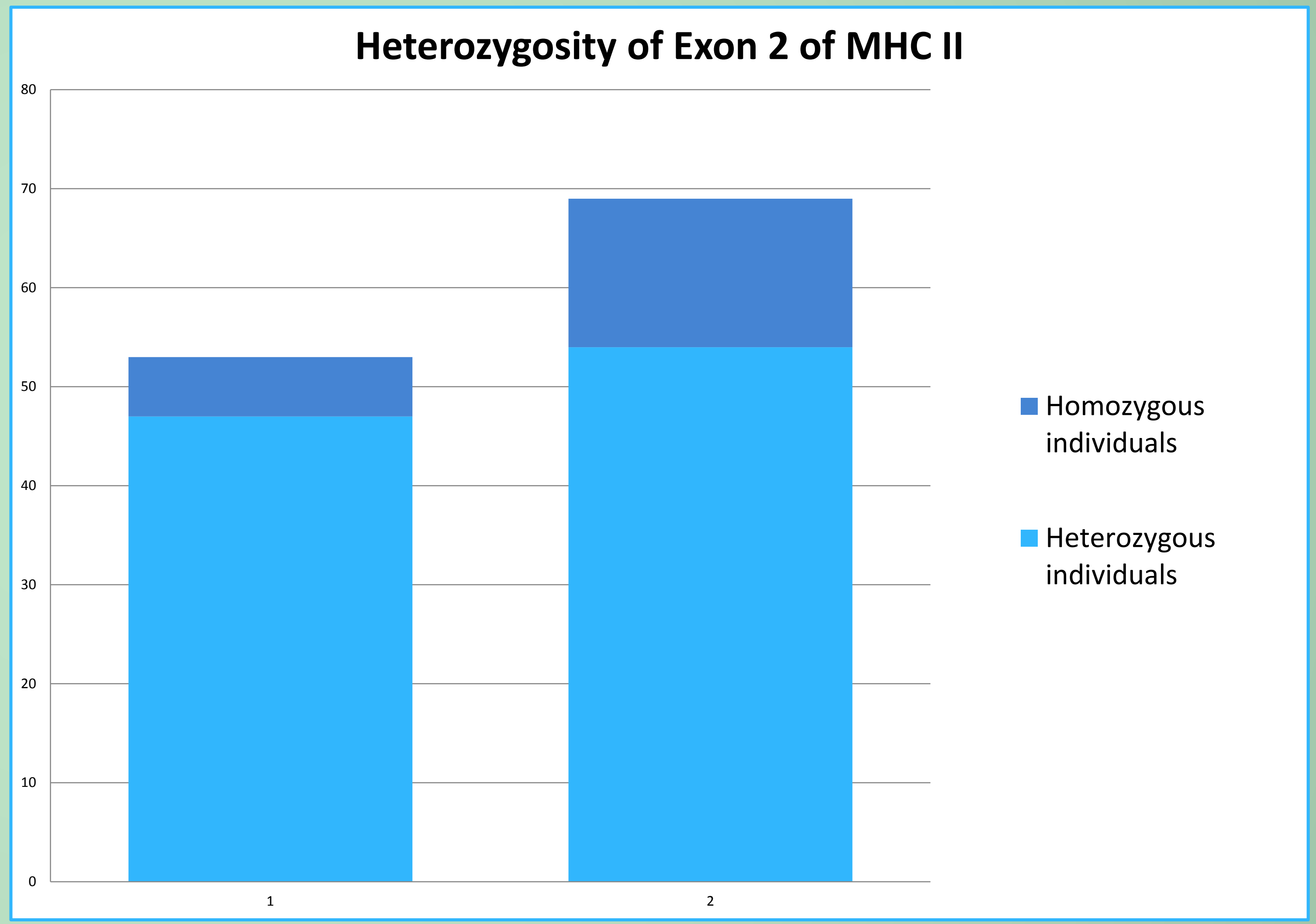

Figure 1 offers a visual representation of the heterozygous portion within populations categorized by prevalence rates. Bar 1 represents individuals below 60% prevalence, and bar 2 represents individuals above 60% prevalence.

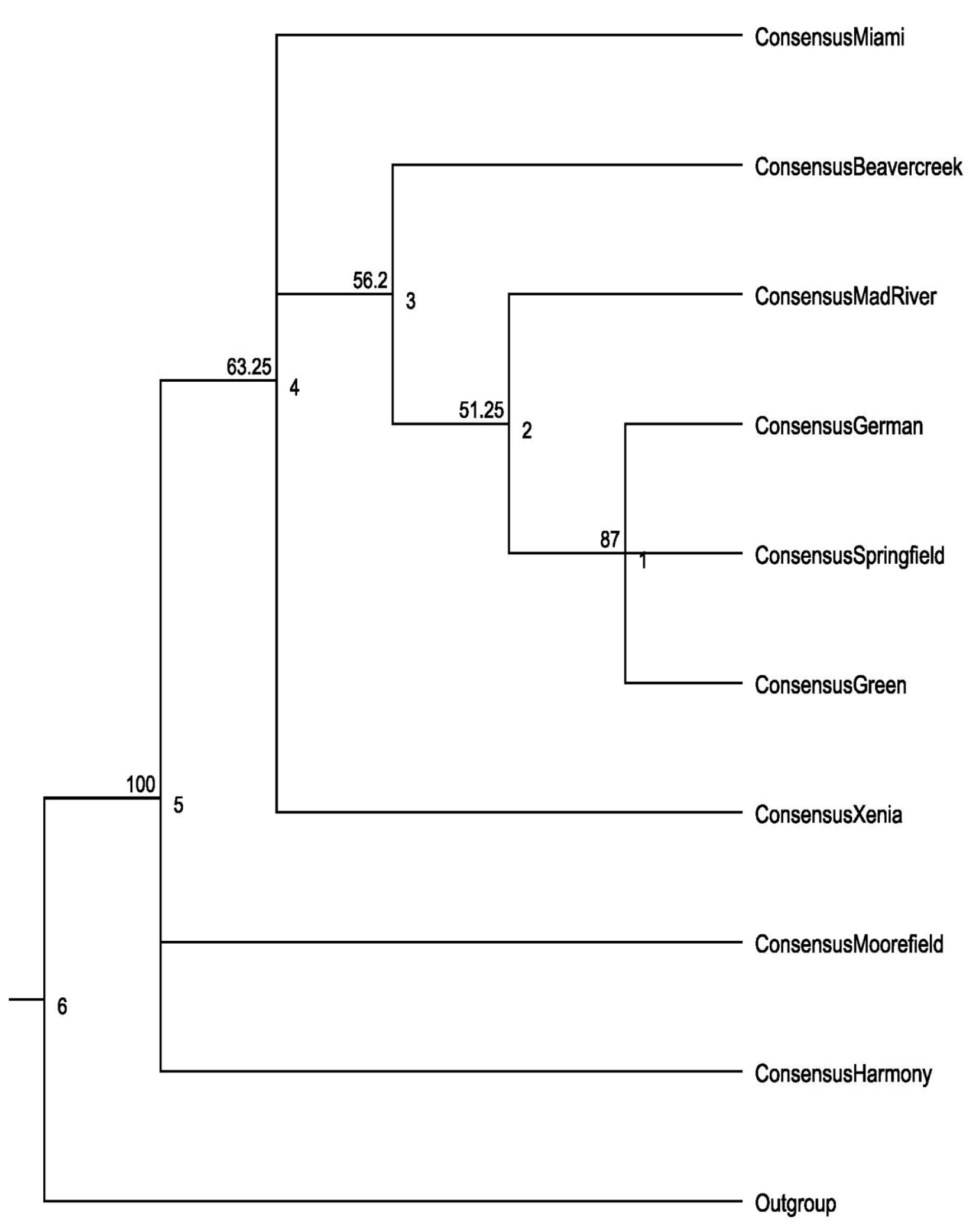

Figure 2 offers a phylogenetic tree of *Pyrocon loctor*, as can be determined from the data gathered in this study.

Conclusions

The number of homozygous individuals was significantly lower than expected in communities experiencing less than 60% prevalence, with a χ^2 value of 39.011, and a p value of < 0.0001. Based on the data collected, genetic diversity is observed at lower levels in regions with higher prevalence rates. These findings would suggest that prevalence of raccoon roundworm (*B. procyonis*) acts as a genetically selective agent among *Procyon lotor* populations in southwest Ohio, inducing microevolutionary changes.

Acknowledgements

We would like to thank Dave Pitstick, Dave Linkhart and Steve Hiller for providing the raccoons for us. We would also like to thank Mindy Vasser, Kara Yutzy and Kelsey Cowen for their work in the field. Finally, we would like to thank Dr. Mark Gathany and Dr. Kristen Page for guidance and encouragement.

References

Beasley, J. C., Devault, T. L., & Rhodes Jr., O. E. (2007). Home-range attributes of raccoons in a fragmented agricultural region of northern Indiana. *Journal of Wildlife Management, 71*(3), 844-850.

Blizzard, E. L., Yabsley, M. J., Beck, M. F., & Harsch, S. (2010). Geographic Expansion of *Baylisascaris procyonis* Roundworms, Florida, USA. *Emerging Infectious Diseases, 16*(11), 1803-1804.

Page, K. L., Beasley, J. C., Olson, Z. H., Smyser, T. J., Downey, M., Kellner, K. F., . . . Rhodes Jr., O. E. (2011). Reducing *Baylisascaris procyonis* Roundworm Larvae in Raccoon Latrines. *Emerging Infectious Diseases, 17*(1), 90-93.

Page, K. L., Gehrt, S. D., Titcombe, K. K., & Robinson, N. P. (2005). Measuring prevalence of raccoon roundworm (*Baylisascaris procyonis*): a comparison of common techniques. *Wildlife Society Bulletin, 33*(4), 1406-1412.

Page, K. L., Swihart, R. K., & Kazacos, K. R. (2001a). Changes in transmission of *Baylisascaris procyonis* to intermediate hosts as a function of spatial scale. *Oikos, 93*, 213-220.

Page, K. L., Swihart, R. K., & Kazacos, K. R. (2001b). Seed preferences and foraging by granivores at raccoon latrines in the transmission dynamics of the raccoon roundworm (*Baylisascaris procyonis*). *Canadian Journal of Zoology, 79*, 616-622.