

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

# Does Baylisascaris procyonis Phylogeny Correlate with That of the Raccoon (*Procyon lotor*)

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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 Phylogeny Correlate with That of the Raccoon (*Procyon lotor*)" (2014). *The Research and Scholarship Symposium*. 18.  
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**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

## Introduction

Raccoons (*Procyon lotor*) are the final host for the raccoon roundworm nematode (*Baylisascaris procyonis*). As a final host is able to support the parasite for an extended period of time, there is sufficient opportunity for both the host and parasite to have a significant mutual impact. The two species can act as selective agents on one another, driving the selection of alleles that would propagate the survival of both species in the next generation of a parasitic relationship.

## Hypothesis

Our hypothesis is that the phylogenetic trees of the *Procyon lotor* and *Baylisascaris procyonis* will express high correlations. We would expect the phylogenetic trees of the two species to line up very similarly, having similar patterns of genetic structuring.

## Methods

We extracted the DNA from the *Baylisascaris procyonis* we had previously harvested from necropsied *Procyon lotor* according to protocol for the DNA Mini kit (Qiagen). The DNA was then sent to The Ohio State University for amplification and sequencing. We amplified a portion of cytochrome C. We constructed two cladograms according to maximum parsimony to better understand how the raccoons and raccoon roundworms from different townships are related to each other.

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## Results:

Figure 1 offers a phylogenetic tree of *Baylisascaris procyonis*, as can be determined from the data we gathered in this study.

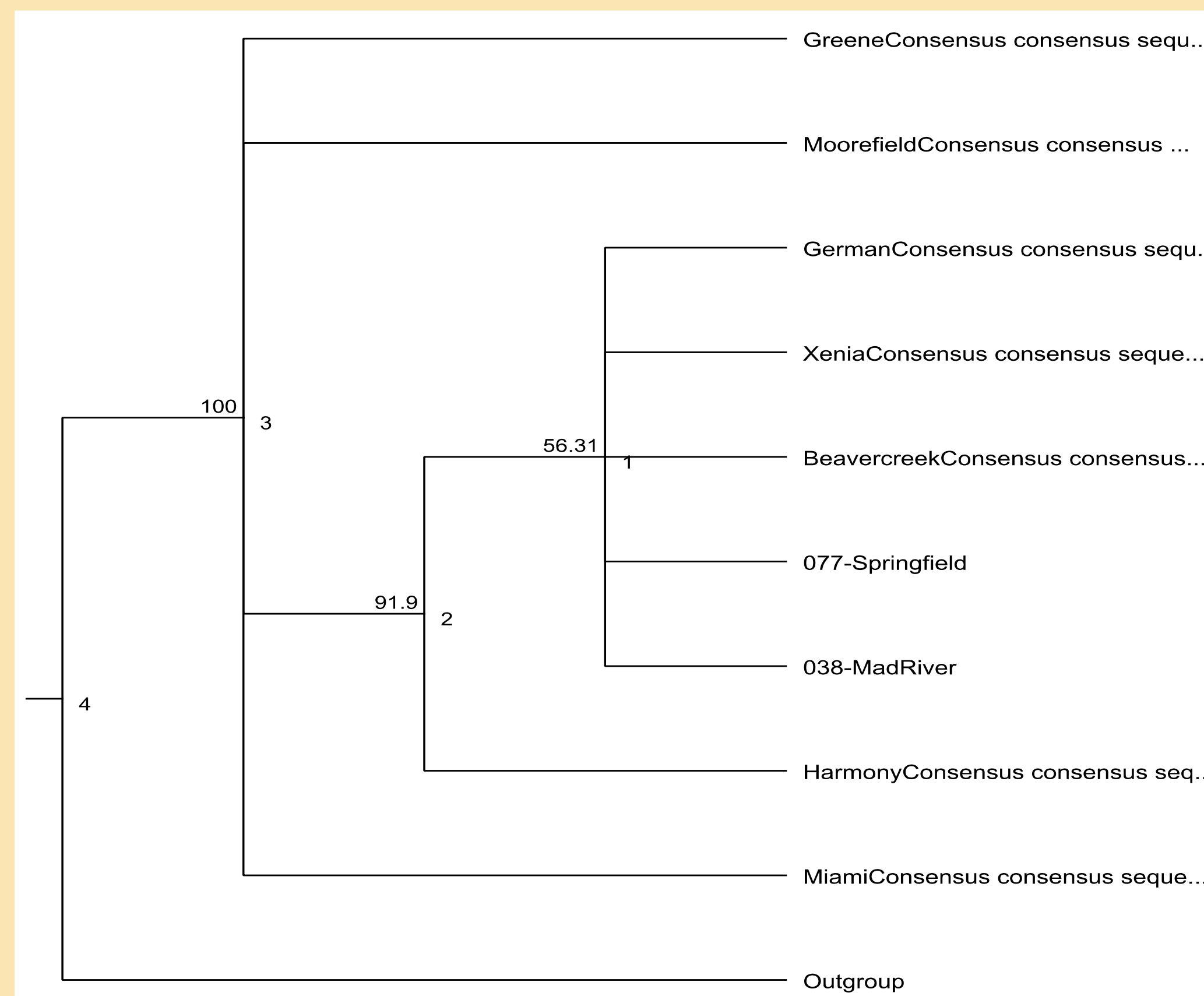
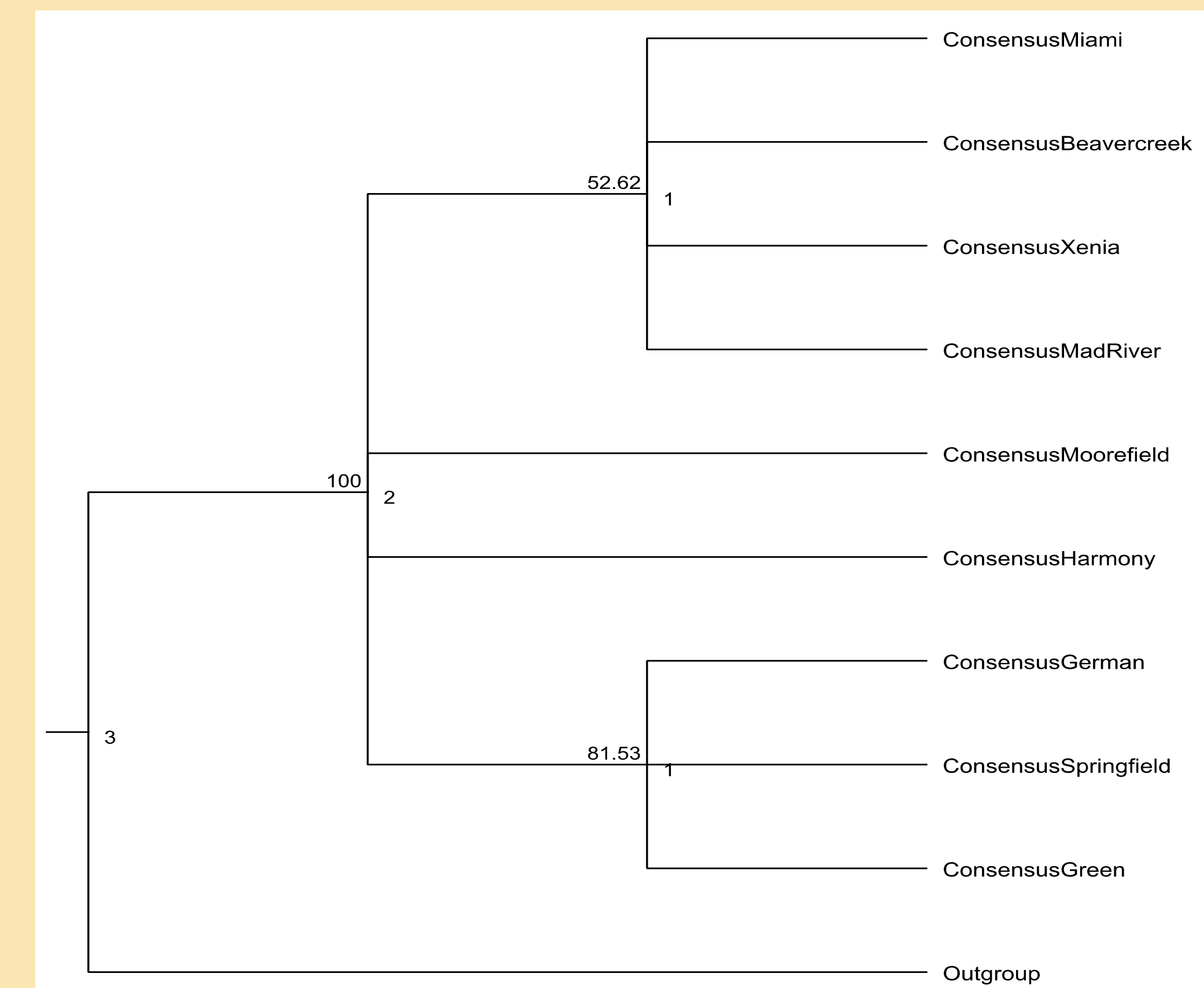


Figure 2 offers a phylogenetic tree of *Procyon lotor*, as can be determined from the data we gathered in this study.



## Conclusions

The maximum parsimony cladograms indicate genetic structuring in the raccoons and raccoon roundworms and the cladograms show similar groupings. The outgroup is shown to have the least commonality in both charts, which is expected, confirming that the local populations for both *Procyon lotor* and *Baylisascaris procyonis* are more closely related to each other than to distant populations. Moorefield showed up as a sister group to more closely related groups in both cladograms. German and Springfield are paired together for both species, as well as Beaver creek, Xenia and Mad River. Harmony showed a stronger relation to other townships among raccoon roundworms than it did raccoons. Green and Miami demonstrated an opposite relationship, appearing as sister groups to groups of townships more closely related to each other in *Baylisascaris procyonis*, but appearing quite similar to other populations among raccoons. There are enough correlations to confirm that genetic structuring interplay between the two species is a very real factor, but explaining the lack of total cladogram conformity would require additional research.

## 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.