Does Baylisascaris procyonis Impact Raccoon (Procyon lotor) Genetics?

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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 heterozygosity, 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. We isolated the DNA from the raccoons using the methods and equipment highlighted in 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 χ² 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:

Table 1 offers the results of a χ² test to determine the expected number of individuals above and below 60% prevalence heterozygous and homozygous at gene DRB.

<table>
<thead>
<tr>
<th></th>
<th>Below 60% Prevalence</th>
<th>Above 60% Prevalence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heterozygous</td>
<td>43.87704918</td>
<td>57.12295082</td>
</tr>
<tr>
<td>Number</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Homozygous</td>
<td>9.12295082</td>
<td>11.87704918</td>
</tr>
</tbody>
</table>

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

Conclusions

The number of homozygous individuals was significantly lower than expected in communities experiencing less than 60% prevalence, with a χ² 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

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References


