Distribution and Prevalence of a Keystone Parasite in the Eastern United States

Steven L. Kohler¹, Elaine R. Cooper¹, and Michael J. Wiley²
¹Western Michigan University, Kalamazoo, MI, USA 49008
²The University of Michigan, Ann Arbor, MI 48109

We attempted to collect G. nigrior larvae and pupae from five streams in Georgia, 14 in Virginia, 17 in Pennsylvania, and 10 in Vermont. At each site we tried to collect 100 individuals. All individuals collected were preserved immediately in 70% ethanol.

To screen for Cougourdella infection, individuals were homogenized in ~ 0.5 mL distilled water in 1.5 mL centrifuge tubes. Homogenates for each individual were examined for infection using phase contrast microscopy at 400X. We first screened 10 individual larvae. If no infections were detected, the remaining larvae were screened in groups of two (i.e., 2 larvae per centrifuge tube). Larvae and pupae were tested separately because disease prevalence is often lower in pupae. Cougourdella prevalence in each G. nigrior population was estimated using procedures described in Hoenig et al. (1987).

We used DNA sequencing of the SSU rDNA gene to determine if the same species of Cougourdella was present in G. nigrior populations in the eastern United States as in Michigan. DNA was extracted from Cougourdella spores from isolates obtained in Georgia, North Carolina, and Pennsylvania, amplified by PCR using microsporidian-specific, primers, and gel-extracted PCR products were sequenced at the University of Michigan DNA Sequencing Core.

Cougourdella prevalence in G. nigrior populations ranged from 0 to 100% (Fig. 3). Disease prevalence was ≥ 20% in 15 of 31 streams (48.4%) in which Cougourdella was present. G. nigrior populations supporting high disease prevalence were present in all regions surveyed (Fig. 3). For comparative purposes, mean disease prevalence in Michigan and Maine streams that have been surveyed for > 10 years is shown in Figure 3. The incidence of disease in Michigan and Maine G. nigrior populations (62 of 70 streams; 88.6%) and prevalence levels are quite similar to those observed in the streams surveyed in 2009 (Fig. 3).

Table 1. The number of streams sampled in each state in which Glossosoma was found, the number of streams in which at least 10 Glossosoma individuals were collected, and the number of those streams in which Cougourdella was detected.

<table>
<thead>
<tr>
<th>State</th>
<th>G. nigrior</th>
<th>G. nigrior</th>
<th>G. nigrior</th>
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<tbody>
<tr>
<td>Georgia</td>
<td>5</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>Virginia</td>
<td>13</td>
<td>9</td>
<td>8</td>
</tr>
<tr>
<td>Pennsylvania</td>
<td>15</td>
<td>11</td>
<td>13</td>
</tr>
<tr>
<td>Vermont</td>
<td>8</td>
<td>6</td>
<td>5</td>
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</tbody>
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Cougourdella epizootics regulate Glossosoma dynamics. We used DNA sequencing of the SSU rDNA gene to determine if the same species of Cougourdella was present in G. nigrior populations in the eastern United States as in Michigan. DNA was extracted from Cougourdella spores from isolates obtained in Georgia, North Carolina, and Pennsylvania, amplified by PCR using microsporidian-specific, primers, and gel-extracted PCR products were sequenced at the University of Michigan DNA Sequencing Core.

Results

SSU rDNA gene sequences from Georgia, North Carolina, Pennsylvania and Michigan Cougourdella isolates were nearly identical (> 98% similarity), which suggests that a single Cougourdella species infects G. nigrior populations in the eastern United States.

Cougourdella was present in streams supporting Glossosoma nigrior populations in all regions surveyed (Table 1). Overall, 75.6% of G. nigrior populations were infected by Cougourdella. The proportion of populations infected was very similar for the subset of streams where ≥ 10 G. nigrior were collected (74.2%; Table 1).

Conclusions

The microsporidian parasite Cougourdella sp. is associated with Glossosoma nigrior populations throughout G. nigrior’s range in the eastern United States.

Available evidence suggests that a single species of Cougourdella is responsible for disease epizootics in G. nigrior populations.

Nearly 50% of infected G. nigrior populations exhibited relatively high disease prevalence. This suggests that disease epizootics are common, and that Cougourdella likely has keystone effects on stream food web structure throughout the eastern United States.

Future Research

We will apply pyrosequencing techniques to the Cougourdella genome to search for microsatellite markers.

Candidate markers will be screened and a set of markers will be used to determine the genetic structure of Cougourdella populations throughout G. nigrior’s range in the eastern United States.

Analysis of Cougourdella population genetic structure over this broad spatial scale should help to answer questions about the history of the host-parasite relationship and Cougourdella’s life cycle.

References


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