Assessing the Prevalence of Human Pathogens in Lehigh Valley’s Deer Ticks

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Deer Ticks and their Pathogens

Deer ticks (Ixodes scapularis) are known vectors of several human pathogens including Borrelia burgdorferi, Anaplasma phagocytophilum (ha strain), Babesia microti, and the emerging infectious agent, Babesia miyamotoi. One or more of these pathogens can be transmitted to humans through a single tick bite.

Lyme disease is caused by the spirochete, B. burgdorferi (sensu lato). In the northeastern United States, deer ticks are abundant and tick-borne infections such as Lyme disease are endemic in this region. Pennsylvania alone reported 19% of the nation’s total cases of Lyme disease in 2011 (Adams et al., 2013). Many of these cases were reported from eastern Pennsylvania, where the density of infected ticks is high (Dulk-Wasser 2012). A regional investigation of the prevalence of infectious agents in deer ticks in the Lehigh Valley has not been conducted prior to this study.

Anaplasma phagocytophilum (Ha strain) causes a strain of the intracellular bacterium, Anaplasmaphagocytophilum that infects neutrophils. Babesia microti, a protozoan parasite of red blood cells, causes babesiosis. Babesiosis is emerging in the Lehigh Valley where three cases were reported in 2013.

B. miyamotoi is a causative agent of tick-borne relapsing fever. One human case of infection was reported in New Jersey in 2012 (Gugliotta et al., 2013).

Testing Tick DNA Using Real-Time PCR

The objective of this study is to determine the infection rates of B. burgdorferi, A. phagocytophilum, B. microti, and B. miyamotoi in deer ticks in the Lehigh Valley. Assessing the prevalence of these human pathogens in ticks can guide health care providers in time-sensitive clinical decision-making regarding prophylaxis and treatments.

Screening was achieved using a primer/probe set corresponding to genes from each pathogen. A TaqMan® probe adapted from Courtney et al. (2004) targets the 23S rRNA sequence of B. burgdorferi (sensu lato). This probe also detects B. miyamotoi. In order to distinguish between B. burgdorferi and B. miyamotoi, a second TaqMan® reaction specific for the B. burgdorferi Csp-A gene was performed (Dibernardo et al., 2014). Csp-A negative samples were analyzed by sequencing the flagellin gene.

A probe based on the msp2 gene was designed to detect A. phagocytophilum (Courtney et al. 2004). A B. microti 18S rRNA gene-specific probe was used to detect these protozoa (Teal et al. 2012). In the literature, this probe was reported to be specific only for B. microti and no other Babesia species.

Rates of Infection in the Lehigh Valley

as of 07/18/14

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>N positive/ N tested</th>
<th>% Positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>B. burgdorferi (sensu lato)</td>
<td>101/427</td>
<td>23.7%</td>
</tr>
<tr>
<td>B. miyamotoi</td>
<td>1/427</td>
<td>0.23%</td>
</tr>
<tr>
<td>A. phagocytophilum</td>
<td>8/427</td>
<td>1.9%</td>
</tr>
<tr>
<td>B. microti</td>
<td>2/427</td>
<td>0.47%</td>
</tr>
<tr>
<td>B. odocoilei</td>
<td>1/427</td>
<td>0.23%</td>
</tr>
</tbody>
</table>

References


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