Surveillance of Deer Tick Abundance and Pathogen Prevalence in the Lehigh Valley

Julia Leep-Lazar
Muhlenberg College

Samantha Stuppi
Muhlenberg College

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Surveillance of Deer Tick Abundance and Pathogen Prevalence in the Lehigh Valley

Julia Leep-Lazar and Samantha Stuppi

Lehigh Valley Health Network, Allentown, Pennsylvania

BACKGROUND / INTRODUCTION

- *Ixodes scapularis* (black-legged) ticks serve as a vector for several human pathogens, most notably *Borrelia burgdorferi* which causes Lyme disease. They can also transmit *Babesia microti* (babesiosis), *Anaplasma phagocytophilum* (anaplasmosis) and *Borrelia miyamotoi* (tick-borne relapsing fever).
- The nymphal stage of black-legged ticks is particularly relevant for human disease transmission due to its small size and tendency for attachments to remain unnoticed for more than 24 hours.
- The risk for infection with a tick-borne microbe can be evaluated on the basis of two factors: **1.** the local abundance of black-legged ticks and **2.** the proportion of those ticks that are infected with human pathogens.
- In this study, both the relative abundance and the percentage of infection with pathogenic microbes were assessed. Eleven publicly accessible, forested sites were chosen the Lehigh Valley region for this three-year study.

MATERIALS AND METHODS

TICK COLLECTION

- Nymphal-stage black-legged ticks were collected at 11 sites distributed throughout the Lehigh Valley region.
- Ticks were collected by dragging a 1 m^2 corduroy flag along the forest floor and periodically checking for ticks and transferring them to 70% ethanol for identification and DNA testing.
- The iPhone Trails GPS application was used to record the time, distance and location for each 30 min. collecting session, or "drag".

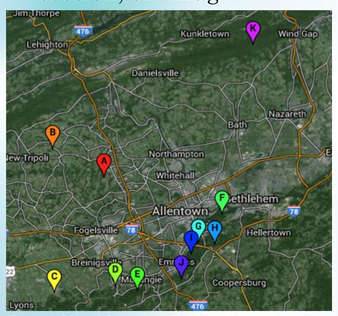


Figure 2. Map of the 11 sites distributed throughout the Lehigh Valley region

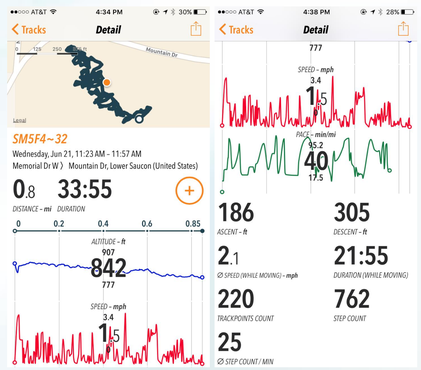


Figure 3. Screenshots from the Trails, the iPhone Trails GPS application

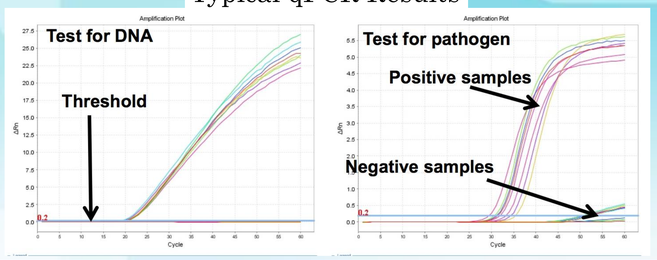
Figure 1. Lab students using corduroy flags for collecting tick samples

MATERIALS AND METHODS

DNA TESTING

- 50 ticks from each site were selected for further analysis and DNA was extracted from these ticks using the Qiagen DNeasy kit.
- qPCR was used to assay for tick DNA, indicating a successful DNA extraction. DNA samples that were of sufficient concentration were further analyzed using a set of qPCR assays that were specific for each of the respective pathogens. Two different tests were used to verify the identity of each pathogen.

Typical qPCR Results



RESULTS

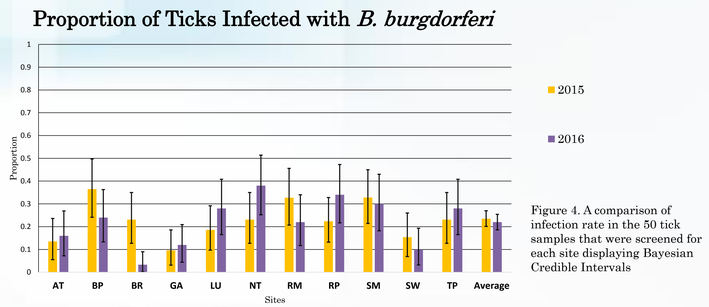


Figure 4. A comparison of infection rate in the 50 tick samples that were screened for each site displaying Bayesian Credible Intervals

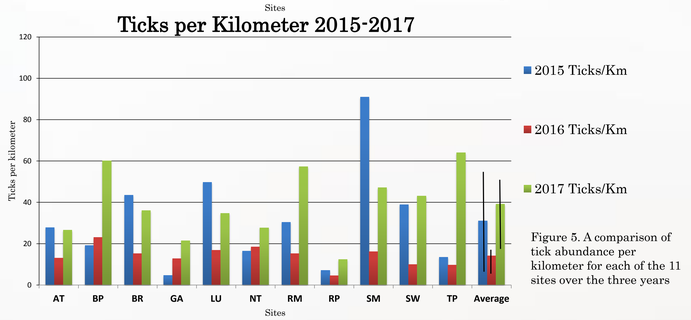


Figure 5. A comparison of tick abundance per kilometer for each of the 11 sites over the three years

CONCLUSIONS

- Using a consistent sampling strategy each year, a total of **2921** black-legged tick nymphs were collected in early summer 2017. This compares to **841** in 2016 and **1491** in 2015.
- There was a significant difference in tick abundance (ticks/km) between 2016 and 2017 ($P<0.0001$, unpaired t-test).
- There was no significant difference in tick abundance (ticks/km) between 2015 and 2017. ($P<0.38$, unpaired t-test).
- Among-site variability in tick abundance was evaluated. In 2015 and 2016, two sites differed by more than one standard deviation from the annual average abundance at all sites. In 2017, five sites differed from the annual average. Importantly, no single site consistently differed from the annual average for more than two years. Thus, we conclude that black-legged ticks are widely and somewhat evenly distributed throughout our study sites.
- 2015 and 2016 infection rates for *B. burgdorferi* at each of the 11 sites were assessed. Each value was assigned a 95% Bayseian Credible Interval.
- Our percentage of ticks infected with *B. burgdorferi* was .235 and .220 in 2015 and 2016 respectively.

  Our infection percentages of the other pathogens has shown a consistent low rate of infection among collected ticks which is in accordance with past research.

ONGOING RESEARCH

- We are currently working on qPCR pathogen assays for ticks that were collected in 2017 to compare results with previous years.
- With the caveat that correlation does not indicate causation, we will be analyzing local weather patterns to assess whether any correlation can be detected between tick abundance and environmental conditions. We will also test the predictions of other researchers that 2017 would be a high-density nymphal tick season.

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