



Prevalence of *Borrelia burgdorferi* in Central Florida Rodents

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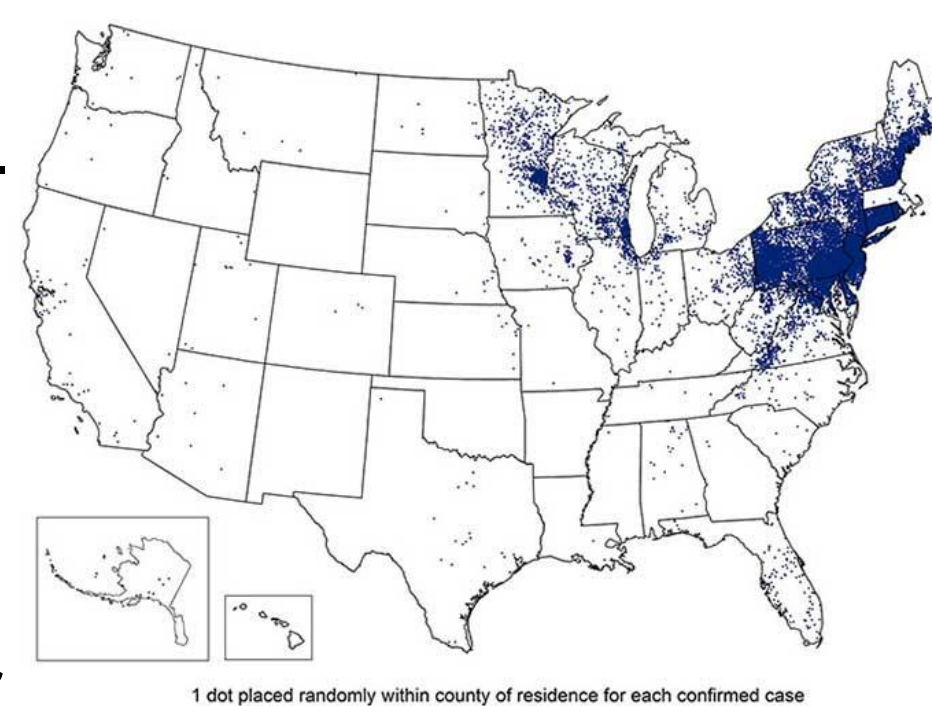
Introduction/Background

Zoonotic diseases are those that are transmitted from animals to human. Hard bodied ticks are the major vector for transmitting these diseases. Ticks transmit a large variety of pathogens, including *Borrelia burgdorferi*, the spirochete bacteria responsible for causing Lyme disease.

Lyme borreliosis is the most common zoonotic disease in the United States, affecting around 30,000 people annually. Over 80% of these infections occur in northeastern and mid-Atlantic states (Zee et al. 2015).

Ixodes scapularis, the black-legged tick, is the major vector for *B. burgdorferi* in the United States. It picks up the bacteria when it feeds on a reservoir during its larval stage and transmits it when it bites and animal or human in its nymph stage.

Reservoirs are animals that carry a pathogen and are a starting point for the spread of a disease. These animals do not always show symptoms of the disease (Oliver et al. 2003). The most common reservoir for *B. burgdorferi* is *Peromyscus leucopus*, the white-footed mouse. It is found more abundantly in the northeastern and woodland regions of the US.



Images retrieved from:
<https://www.cdc.gov/lyme/transmission/index.html>
<https://www.cdc.gov/lyme/stats/maps.html>

Methods

Species Sampled: *Peromyscus gossypinus* (cotton mouse), *Sigmodon hispidus* (cotton rat), *Neotoma floridana* (eastern woodrat), *Ochrotomys nuttalli* (golden mouse)

- Rodents were collected during summer and fall in Lake Woodruff National Wildlife Refuge
- A tissue sample was collected from each rodent, and each was identified by species
- DNA was extracted from each sample
- Nested PCR was performed to amplify the flagellin B and outer surface protein B genes
- Each PCR product was run on a gel to verify whether *B. burgdorferi* was present in each sample
- Bands that signified a positive sample were cut out and DNA purified
- The purified DNA was sent out for sequencing
- Sequences were compared to the NCBI database to confirm *B. burgdorferi*
- Logistic regression and Chi-square was used to test the significance of the data

Species Sampled



Peromyscus gossypinus (cotton mouse)



Sigmodon hispidus (cotton rat)



Neotoma floridana (eastern woodrat)



Ochrotomys nuttalli (golden mouse)

Images retrieved from:
<https://www.sciencedirect.com/science/article/pii/S09780123809209000493>
https://blancowateratlas.wordpress.com/2013/08/14/order-didelphimorphia/neotoma-floridana_eastern-woodrat/
<https://www.biolib.cz/en/taxon/id3665/>



<https://www.wildlifedepartment.com/wildlife/wildlife-diversity/wildside/insights-decade-wildlife-study>

Results

- A total of 39 rodents were captured (Figure 1)
- PCR analysis and DNA sequencing showed that *P. gossypinus* and *N. floridana* were infected with *B. burgdorferi* sensu stricto (Figure 2)
- No infections identified among *S. hispidus* or *O. nuttalli*
- Logistic regression yielded values that indicated that there was a significant effect of species on the likelihood of being infected ($p=0.0084$)
- Chi-square analysis revealed that *N. floridana* was significantly more likely to be infected than *P. gossypinus* ($\chi^2=5.99$, $p=0.014$)

Results

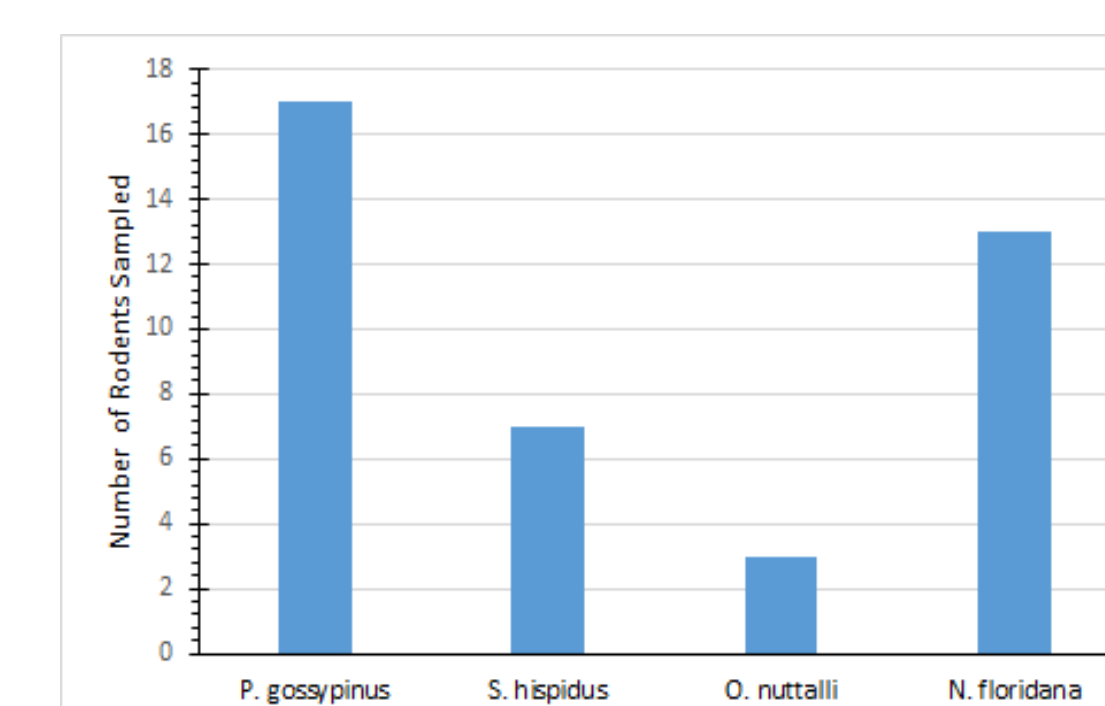
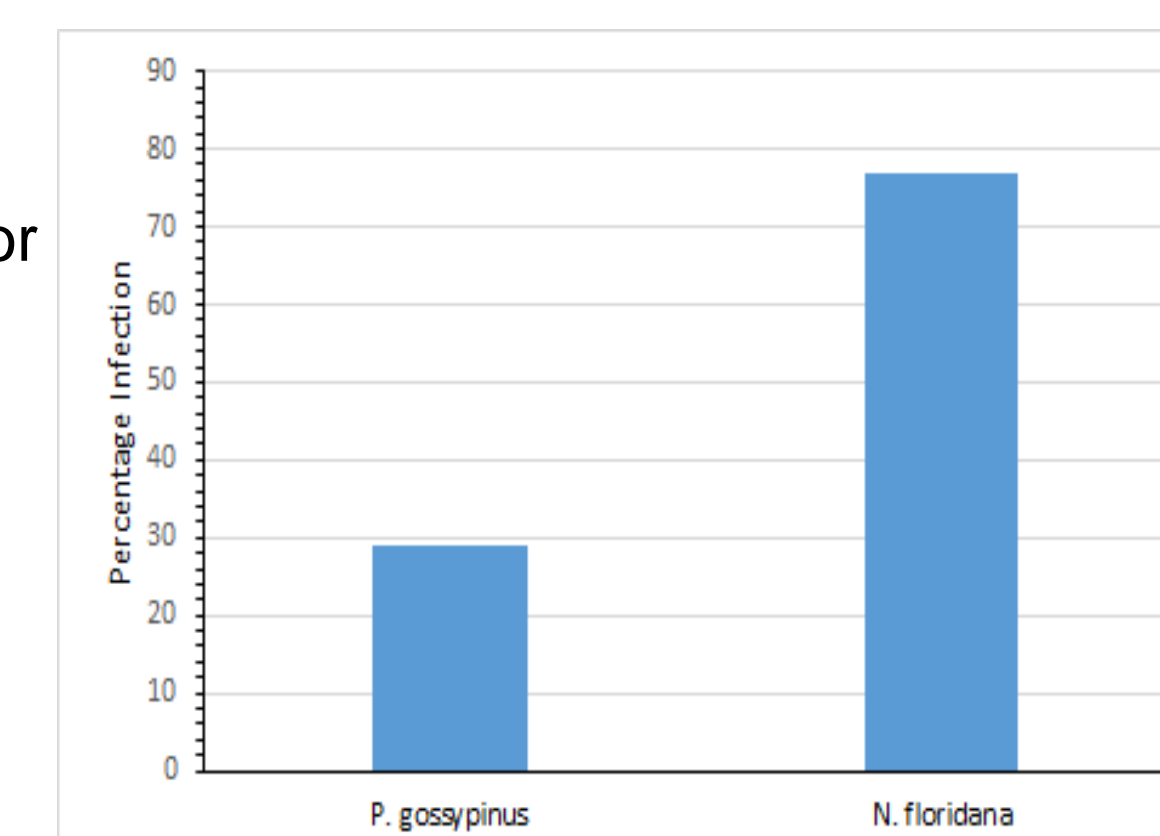


Figure 1. Total number of rodents captured and tested for *B. burgdorferi* by species. A total of 39 rodents were captured representing four species.

Figure 2. The percentage of positive samples for each species shows that significantly more *N. floridana* were infected with *B. burgdorferi* than *P. gossypinus* ($\chi^2=5.99$, $p=0.014$).



N. floridana (Eastern woodrat)

Literature Cited

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Conclusions

Previous studies identified *Borrelia burgdorferi* sensu lato strains in *N. floridana*, while sensu stricto was identified only in *P. gossypinus* (Lin et al. 2004). My research shows infection for *B. burgdorferi* sensu stricto in *N. floridana*, suggesting that it may be a novel reservoir for *B. burgdorferi* sensu stricto in Central Florida.

Acknowledgements

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