Temporal and spatial variation of Erlichia chaffeensis in the lone star tick (Amblyomma americanum)

Olivia Spencer

William & Mary

Applied Conservation and Ecology Lab

Abstract

Topic: Pathogen presence and occurrence of *E. chaffeensis* between lone star nymph and adult populations through space and time

Purpose: To understand how these patterns came to be and what that means for human risk of disease

Study design: Ticks were collected from 130 random sites in the Virginia and Middle Peninsulas and tested for pathogen presence via DNA extractions, PCR, and gel electrophoresis

Hypothesis: Adult populations should show higher pathogen presence and dispersal given the number of blood meals between life cycle stages

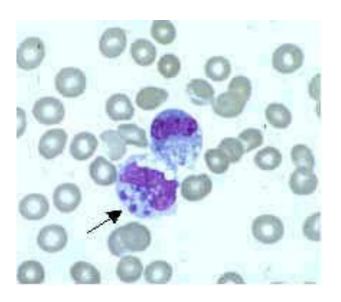
Research Questions

How does pathogen prevalence vary in both nymphs and adults through time?

How does pathogen occurrence vary geographically through time?

What does this mean for human risk of disease?

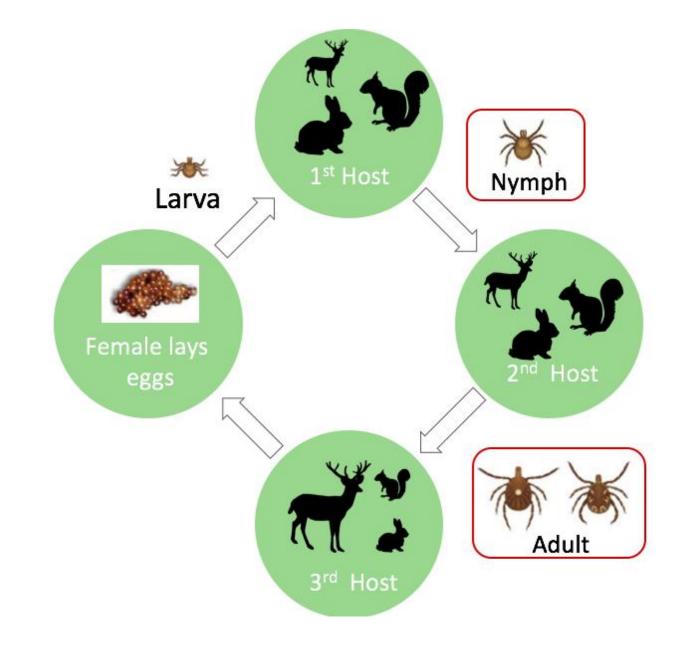




Background

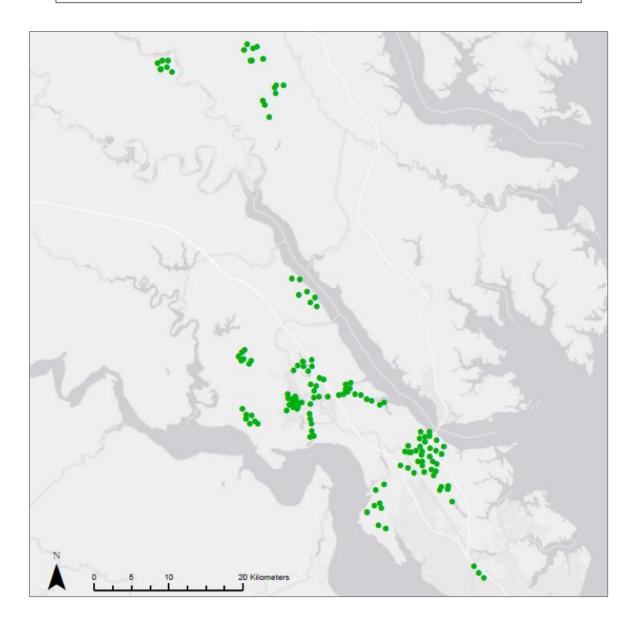
- Tick-borne illnesses pose a growing threat to human health
- Most studies investigate the blacklegged tick and Lyme disease
- The lone star tick plays a critical role in transmitting *E. chaffeensis* to animal hosts and humans
- E. chaffeesnsis is the primary bacterial pathogen that causes Human Monocytic Erlichiosis (HME)
- Common symtoms of HME include: Fever, headache, muscle pain, nausea, vomiting, diarrhea, confusion, conjunctival infection

Life cycle of the lone star tick



Methods: Study Area

Virginia and Middle Peninsulas







Methods: Sampling

- 30m x 30m perpendicular transects
- Ticks collecting via flagging methods
 - 1 m² white canvas tarp was dragged across the ground transects and ticks were checked for every 3 meters
- Ticks were placed in 70% ethanol and stored in a -80°C freezer to prevent DNA degradation

Methods: DNA and Molecular Analysis

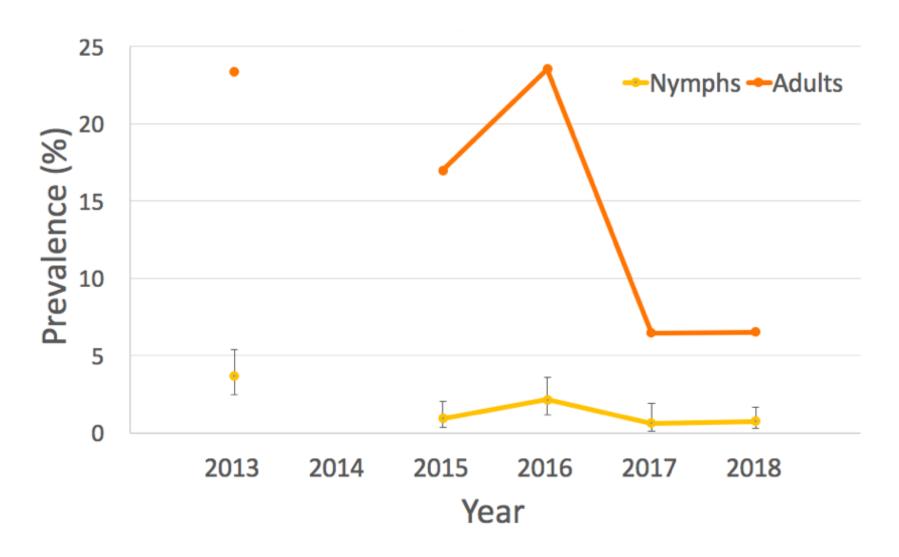
After identification, adults were cut in half and nymphs were pooled into groups of 20 or fewer

Lone star tick and *E. chaffeensis* bacterial DNA were extracted

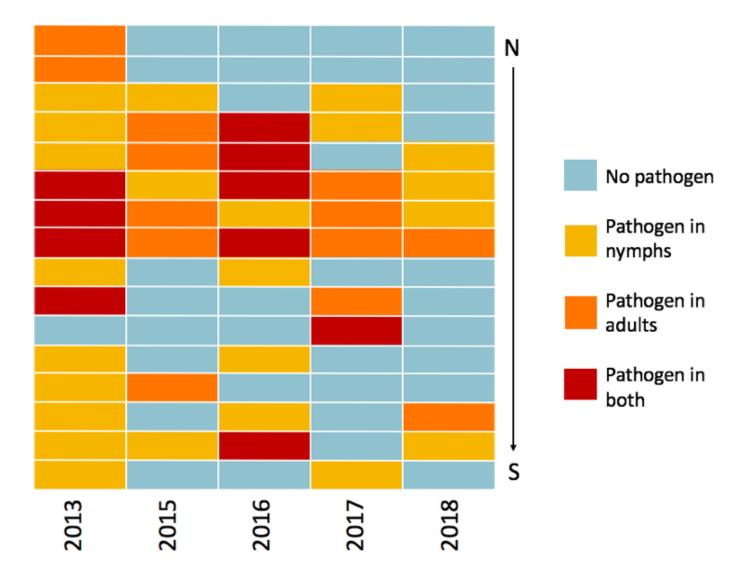
DNA was amplified via PCR with species and pathogen specific primers

PCR products were then tested via gel electrophoresis to confirm presence of tick DNA and pathogens

Results: Temporal variation in prevalence



Spatial variation in pathogen presence



Discussion

Prevalence across time

- Adult rates are consistently higher, though pattern is similar to nymphs
- Adults have higher likelihood of carrying pathogen after having fed on more hosts than nymphs

Spatial and temporal variation of pathogen occurrence

- Pathogen occurrence contracts and expands on a spatial and temporal scale
- Only 19% (n=16) of sites show annual turnover
- Adult and nymph pathogen presence do not follow the same geographic pattern, potentially due to sampling error or differing host preference

Implications for human risk of disease

Both nymph and adult lone star ticks can cause HME in humans

Adults are more likely to carry *E. chaffeensis* while nymphs are harder to find on the body

Precautions must be taken when spending time in areas where lone star ticks reside

Occurrence and prevalence are not constant across time so one must always be cautious

Future Directions

Further analysis to understand the spatial trends

Regression analysis to investigate factors impacting dispersal and prevalence of the pathogen in nymph and adult populations

Test for other pathogens using the already extracted DNA to gain deeper understanding of human risk of disease

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