

Emerging Tickborne Disease: A Study of Heartland Virus in Georgia Ticks

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Georgia Mosquito Control Association Annual Meeting

Oct 21st, 2021

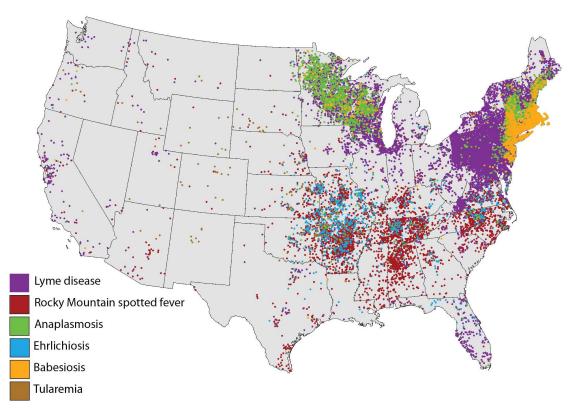






Tickborne Disease in the US

Distribution of tickborne disease in the US, 2016



NOTE: Each dot represents one case. Cases are reported from the infected person's county of residence, not necessarily the place where they were infected.

NOTE: Babesiosis was reportable in AL, AR, CA, CT, DE, IA, IL, IN, LA, KY, ME, MD, MA, MI, MN, MO, MT, NE, NH, NJ, NY, ND, OH, OR, RI, SC, SD, TN, TX, UT, VT, WA, WV, WI, and WY.

NOTE: No cases of tickborne illness were reported from HI. AK reported 6 travel-related cases of Lyme disease and 1 case of tularemia.

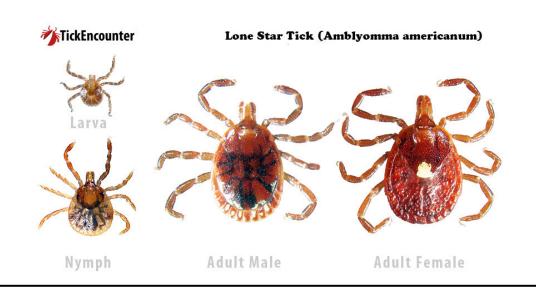
NOTE: Anaplasmosis and ehrlichiosis were not reportable in CO, ID, NM, AK, or Hl.

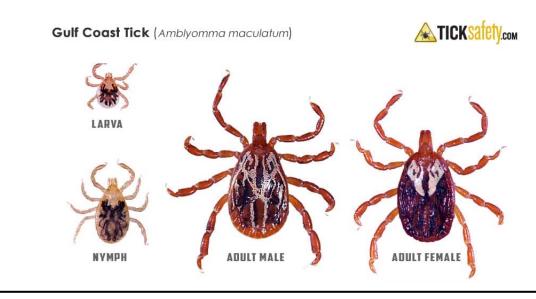
NOTE: Spotted fever rickettsiosis was not reportable in AK and HI.

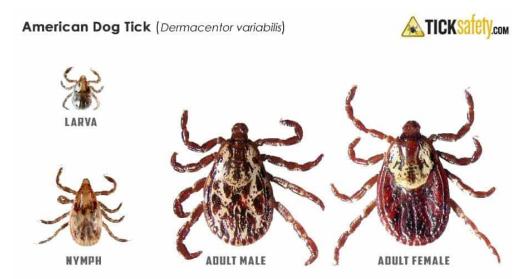
https://news.mayocliniclabs.com/2018/06/02/tick-borne-diseases-testing-at-mayo-clinic/

BACKGROUND: GENERAL BACKGROUND: HRTV SAMPLING STRATEGY RESULTS CONCLUSIONS & FUTURE DIRECTIONS

Main Tick Species Found in GA









Asian Longhorned Tick Confirmed in Georgia

★ SEPTEMBER 24, 2021 /

The Georgia Department of Agriculture (GDA) Animal Health Division has confirmed the presence of the Haemaphysalis longicornis tick, otherwise known as the Asian Longhorned tick. It was found affecting a cow in Pickens County, located in the northern part of the state.

This is the first case of the invasive tick identified in Georgia, and while it is native to

eastern Asia, an investigation is ongoing to determine the extent of the tick's presence in this area.



Asian Longhorned Tick (Haemaphysalis longicornis)

Pinterest



The Discovery of Heartland Virus: Missouri 2009

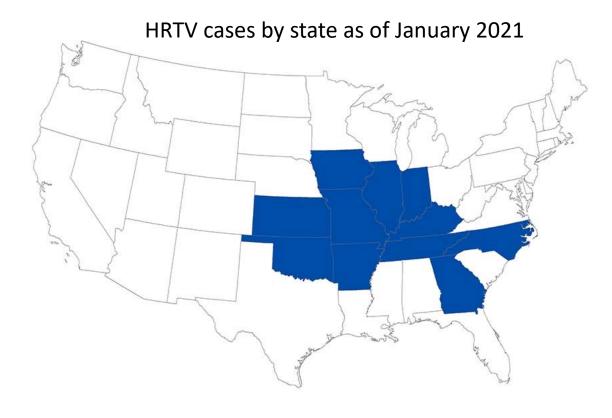


Savage HM, Godsey MS, Lambert A, et al. First detection of heartland virus (Bunyaviridae: Phlebovirus) from field collected arthropods. Am J Trop Med Hyg. 2013;89(3):445-452. doi:10.4269/ajtmh.13-0209

SAMPLING STRATEGY

Heartland Virus (HRTV) Epidemiology

- RNA virus (Genus: Bandavirus) most closely related to severe fever with thrombocytopenia syndrome (SFTS) virus vectored by the Asian longhorned tick in Asia
- Since then, more than 50 cases have been reported in Midwestern and Southern states (CDC)
- Cases mostly in older adults with onset from May to September, most common tick association (and only one with HRTV isolation) is the lone star tick
- Infection rates (MIR/MLE) reported in ticks range from 0.32 / 1000 to 9.46 / 1000

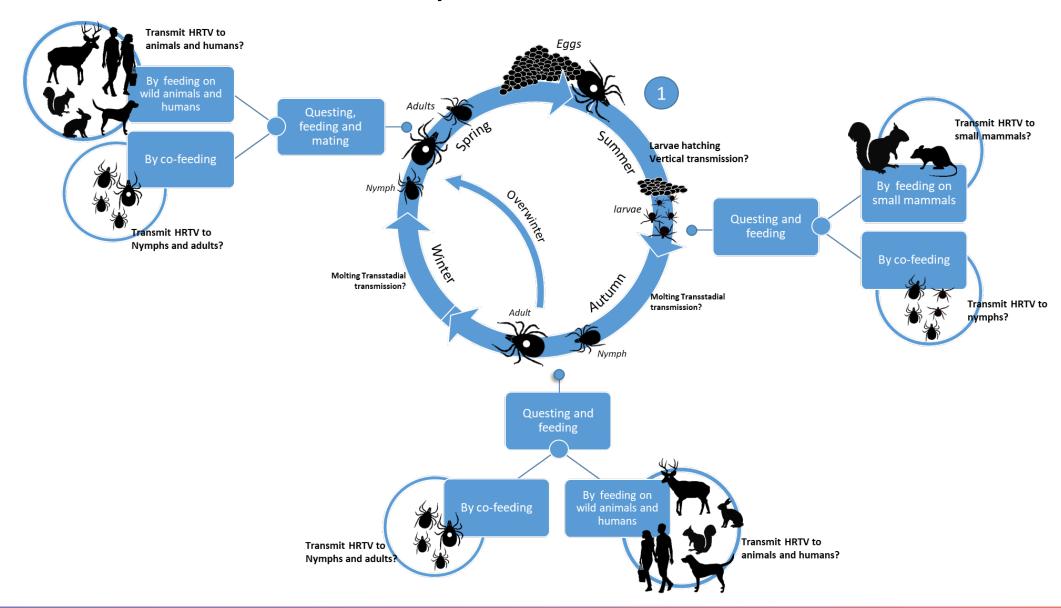


https://www.cdc.gov/heartland-virus/statistics/index.html

HRTV Clinical Features

- Symptoms:
 - Fever
 - Fatigue
 - Anorexia
 - Nausea
 - Diarrhea
 - Depressed cell counts (leukopenia, thrombocytopenia)
 - Elevation of liver enzymes
- Severe illness requiring hospitalization, can be **fatal** (especially in people with comorbidities)

HRTV Transmission Cycle



BACKGROUND: GENERAL BACKGROUND: HRTV SAMPLING STRATEGY RESULTS CONCLUSIONS & FUTURE DIRECTIONS

Heartland Virus in GA

- In GA, there was a human case identified retroactively occurring in 2005 and serological evidence of infection in white-tailed deer dating back to 2001
- Amblyomma americanum is one of the most common tick species found in GA so represents a potential threat to GA residents in vectoring HRTV, among other pathogens
- Before our study, HRTV had not been isolated directly from any ticks in GA

Study Objectives



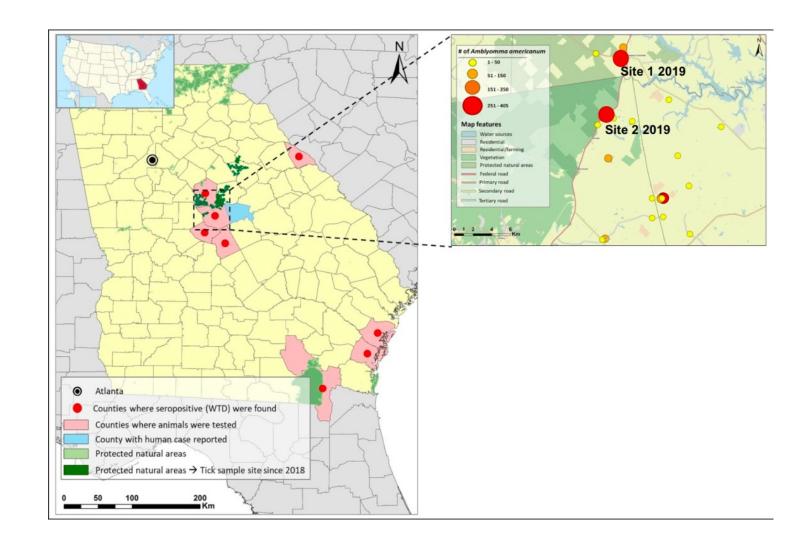
Isolate HRTV from primary tick samples in GA using a sampling strategy with adequate sample size to allow for viral detection



Compare genetic diversity in collected HRTV samples and those already existing on NCBI

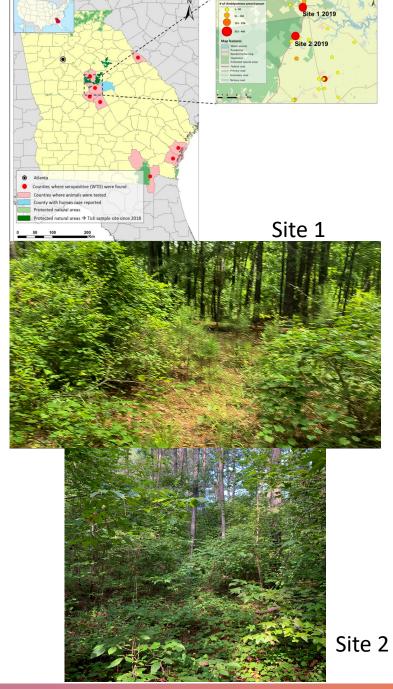
Sampling information

- In 2018 flag sampling for questing ticks was conducted at 26 sites close to seropositive deer and the reported human case
- After initial sampling, sites were narrowed down to two with the highest collections in 2018 where additional flag sampling took place in 2019
- Sampling took place between April and October ~weekly both years



Results: Ticks Collected

Tick Species	Life Stage	2018 (N)	2019 (N)	2019: Site 1	2019: Site 2	
Amblyomma americanum	Adult	646	1530	790	740	
	Nymph	2265	4853	2844	2009	
	Total	2911	6383	3634	2749	
	Pools	272	677	339	338	
Amblyomma maculatum	Adult	30	10	6	4	
	Pools	6	9	5	4	
Dermacentor variabillis	Adult	14	74	57	17	
	Pools	3	37	27	10	
Ixodes scapularis	Adult	5	3	3	0	
	Pools	2	2	2	0	



RESULTS **BACKGROUND: GENERAL BACKGROUND: HRTV** SAMPLING STRATEGY **CONCLUSIONS & FUTURE DIRECTIONS**

Results: HRTV+

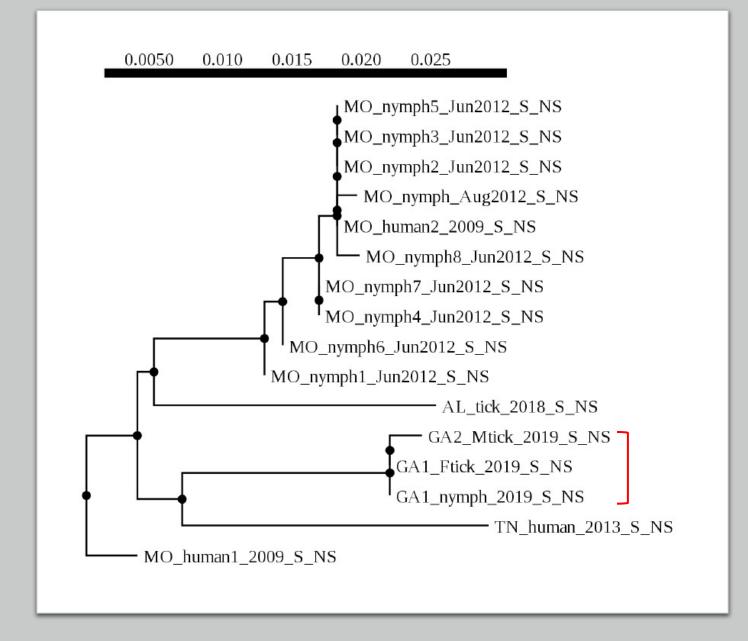
- Ticks were sorted into 283 and 677 pools respectively in 2018 and 2019 by species, stage, sex and collection site
- Samples were then homogenized, RNA was extracted, and RT-PCR was run for detection of HRTV and Bourbon virus. Those identified to be positive were cultured for evaluation of cytopathic effect
- Detected 3 HRTV positive pools 1 with 5 females, 1 with 5 males and 1 with 25 nymphs
- MIR = 0.46 per 1000 in 2019

			Number of	HRTV RT-PCR	Culturing: Vero E6					
Pool	Collection		specimens	from	Passage 1		Passage 2		Passage 3	
Number	Date	Site	per pool	homogenate	СРЕ	PCR	СРЕ	PCR	СРЕ	PCR
23	4/28/19	1	5	+	-	-	ı	-	-	ı
26	4/28/19	1	25	+	+	+	1	+	-	1
504	6/14/19	2	5	+	-	+	-	+	-	+

SAMPLING STRATEGY

Results: Genomics and Phylogenetics

- HRTV genomes were sequenced from the 3 positive pools yielding complete genome sequences for pool 23 and 26 (100% coverage for S/M/L segments) and partial for pool 504 (97%/100%/89% for S/M/L segments)
- Sequences from pools 23 and 26 were nearly identical in all 4 open reading frames
- 23 and 26 were more closely related to pool 504 then previously published full HRTV genomes (x3, 2 from MO 2009, 1 from TN 2013, human cases)
 - Synonymous changes > nonsynonymous changes
 - 6 AA positions where all 3 tick samples differed from the 3 reported human samples



Conclusions

- High density sampling allowed for adequate sample size for HRTV detection in both adult and nymph lone star ticks, the first identified in GA
- Two positive pools in April suggest potential overwintering of HRTV
- Our MIR calculated is similar to low compared to other IR estimations
- HRTV genome sequences were relatively highly conserved between the three samples in the study obtained 2 months and 5 km apart; 2-5% difference in genomes compared to the human cases in the previous decade; next most recent ancestor branch with TN

Future Directions

- Continued surveillance for HRTV infection in Amblyomma americanum ticks in GA
- Spatial distribution of HRTV in GA
 - Are certain areas at higher risk of Heartland virus persistence/spillover?
 - How related are the genomes isolated of Heartland virus across the state?





Thank you Prokopec, Piantadosi, and Mead labs

- Yamila Romer
- Gonzalo Vazquez-Prokopec
- Anne Piantadosi
- Daniel Mead
- Kayla Adcock
- Zhuoran Wei
- Oscar Kirstein
- Sebastian Duran
- Tim Walsh
- Ellie Fausett
- +so many more!!!

