

Isolation of Heartland Virus from Lone Star Ticks, Georgia, USA, 2019

Appendix

Appendix Table 1. Sequencing metrics for 3 genome segments from 3 Heartland virus–positive pools collected in Georgia, USA, 2019

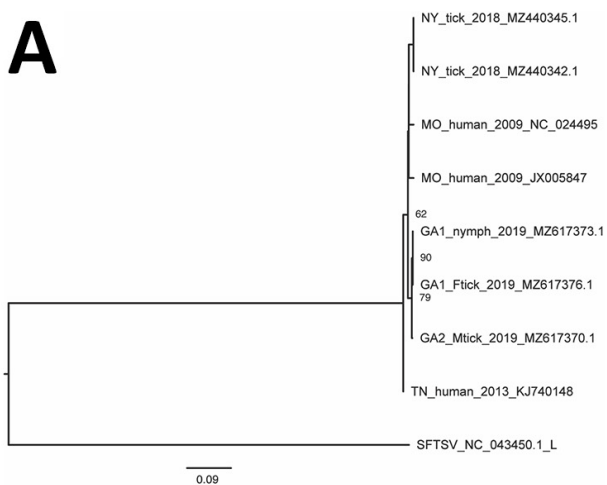
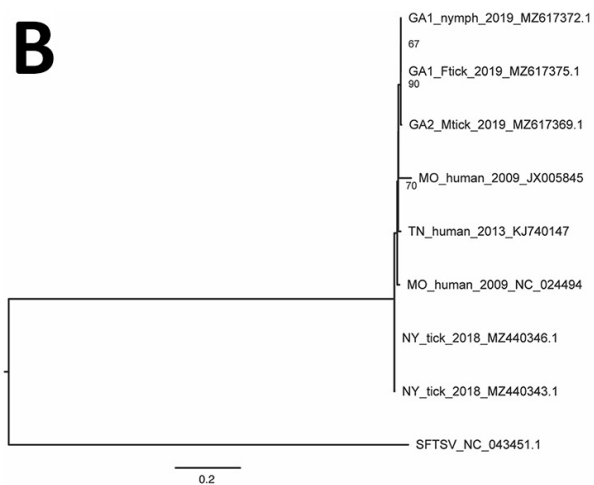
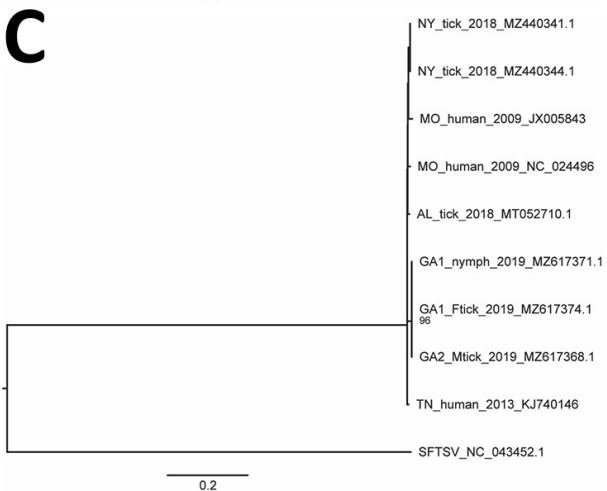
Sample no.	Total reads	Small coverage, %	Mean small depth	Medium coverage, %	Mean medium depth	Large coverage, %	Mean large depth
HRT23	3,908,804	98.0	21	99.3	52	98.7	24
HRT26	4,625,523	95.7	24	100.0	76	99.2	50
HRT504	5,575,666	85.1	8	99.5	40	88.8	7

Appendix Table 2. Pairwise nucleotide identity between 3 HRTV virus genomes sequenced in this study, Georgia, 2019, and the only 3 previously published HRTV genomes*

Sample	Location	Small segment, % nucleotide identity					Medium segment, % nucleotide identity					Large segment, % nucleotide identity				
		HRT23	HRT26	HRT 504	JX00584X	KJ74014X	HRT23	HRT26	HRT 504	JX00584X	KJ74014X	HRT23	HRT26	HRT 504	JX00584X	KJ74014X
HRT23	Site 1	/					/					/				
HRT26	Site 1	100.0					100.0					99.8				
HRT504	Site 2	97.6†	97.6†				99.7	99.8				91.6†	91.8†			
JX00584X	Missouri 2009, human	97.5	97.4	95.1†			95.6	95.6	95.5			97.8	97.9	90.1†		
KJ74014X	Tennessee 2013, human	97.6	97.4	95.2†	97.4		98.4	98.4	98.2	95.7		98.0	98.1	90.4†	98.0	
NC_02449X	Missouri 2009, human	97.9	97.8	95.6†	98.3	97.9	98.2	98.2	98.1	95.5	98.4	97.9	98.0	90.2†	98.1	98.0

*HRTV, Heartland virus; / indicates that the percentage identity shown includes sequence ambiguities.

†For sample HRT504, only partial small and large segments were sequenced.

A**B****C****D**