About the Author

Dr. Canuti is assistant professor at the University of Copenhagen. Her primary research interests are virus discovery and emergence, and her studies focus on virus epidemiology, ecology, and evolution.

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Address for correspondence: Marta Canuti, Department of Veterinary and Animal Sciences, University of Copenhagen, Stigbøjlen 4, 1870 Frederiksberg, Denmark; email: marta.canuti@gmail.com

Heartland Virus in Lone Star Ticks, South Carolina, USA, 2021–2024

Emily Owens Pickle, Madeleine M. Meyer Torelli, Harrison Knapp, Diana L. Zychowski, Sean Sweeney, Kayla Bramlett, Kyndall Dye-Braumuller, Stella Self, Ross M. Boyce, Scott P. Commins, Melissa S. Nolan

Author affiliations: University of South Carolina, Columbia, South Carolina, USA (E.O. Pickle, M.M. Meyer Torelli, H. Knapp, S. Sweeney, K. Bramlett, K.C. Dye-Braumuller, S. Self, M.S. Nolan); University of North Carolina at Chapel Hill School of Medicine, Chapel Hill, North Carolina, USA (D.L. Zychowski, R.M. Boyce, S.P. Commins)

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Tickborne arboviruses are a serious health threat, but surveillance gaps remain. We tested lone star nymphs collected in South Carolina, USA, for Heartland and Bourbon viruses. Six pools were positive for Heartland virus; none were positive for Bourbon virus. Longitudinal surveillance provides insights into the emergence and distribution of tickborne pathogens.

Heartland virus (HRTV; family *Phenuiviridae*, genus *Bandavirus*) and Bourbon virus (BRBV; family *Orthomyxoviridae*, genus *Thogotovirus*) are emerging tickborne pathogens. Both viruses were detected in the contiguous United States within the past 15 years (*1*,*2*). Symptoms of identified infections included acute febrile illness characterized by thrombocytopenia and leukopenia, with progression to multiorgan failure and death in severe cases (*3*). Wildlife serosurveillance suggests both pathogens are more widely spread than reported cases indicate (Appendix, https://wwwnc.cdc.gov/EID/article/32/12/26-0320-App1.pdf).

The lone star tick (*Amblyomma americanum*) is the primary vector for both Heartland and Bourbon viruses (*4*,*5*). Lone star tick range is well established across the eastern United States and continues to expand northward and westward, driven by host movement, land use changes, and climate change (*6*). White-tailed deer (*Odocoileus virginianus*) are a keystone host for lone star ticks; a retrospective wildlife serosurvey conducted in South Carolina reported HRTV antibodies in 20% (1/5) of white-tailed deer samples collected in 2001 and in 40% (2/5) of samples collected in 2008 (*7*). Similar studies have reported evidence of BRBV in neighboring states (*3*). Although

South Carolina lies within the established range of lone star ticks, has a history of tickborne bacterial disease transmission (*8*), and has documented HRTV circulation in wildlife (*3*), testing of ticks collected in the state has not included HRTV or BRBV.

For our study, we used data from a multiyear surveillance program in South Carolina to test field-collected lone star ticks for HRTV and BRBV and assess potential risk. Statewide tick collection occurred April 2021–August 2024 with the use of standard drag/flag and CO_2-baited trapping methods (*8*). To maximize the likelihood of detecting viral infection, we limited testing to nymphal lone star ticks because of the epidemiologic importance and abundance of this life stage in human exposure. We identified specimens morphologically by using established dichotomous keys and maintained specimens under cold-chain conditions. We bisected ticks longitudinally, processing one half for RNA nucleic acid extraction and the other for DNA extraction. For viral detection, we extracted RNA by using the QIAamp Viral RNA Kit (QIAGEN, https://www.qiagen.com) according to the manufacturer's protocol. We pooled ≥5 nymphs by collection site, date, and method before multiplex testing. Over a 4-year period, we collected a total of 1,665 nymphs, which we separated into 368 pools. Pools were distributed by year as follows: 2021, n = 223; 2022, n = 106; 2023, n = 21; and 2024, n = 18.

After assay optimization, we performed real-time reverse transcription PCR by using previously published primers targeting the HRTV small (S) segment and the BRBV nucleoprotein gene (*9*). We optimized the assay by performing gradient real-time reverse transcription PCR (54°C–64°C) and testing 10-fold serial of the positive control to generate standard curves and determine the optimal annealing temperature (62°C). We confirmed amplicon size and quality by electrophoresis. We classified pools as positive if they demonstrated exponential amplification with a cycle threshold (Ct) ≤35, equivocal at Ct 36–37, and negative at Ct ≥38 or no amplification. Each run included negative controls (nuclease-free water) and positive controls; we sourced HRTV and BRBV from the Centers for Disease Control and Prevention's Arbovirus Reference Collection (https://www.cdc.gov/vector-borne-diseases/php/arbovirus-reference-collection/index.html).

We tested 1,665 lone star ticks in pools of ≤5 nymphs: 6 of 368 pools were positive for HRTV and none were positive for BRBV. All HRTV-positive pools came from the same location in Colleton County, South Carolina (Figure). Positive pools comprised lone star tick nymphs collected in 2021 (5/6) and 2022 (1/6) (Table). Collection methods for HRTV-positive pools were distance dragging (2/6), carbon dioxide trapping (3/6), and removal from a collector's body (1/6). HRTV-positive pools were collected in the months of April, July, and August.

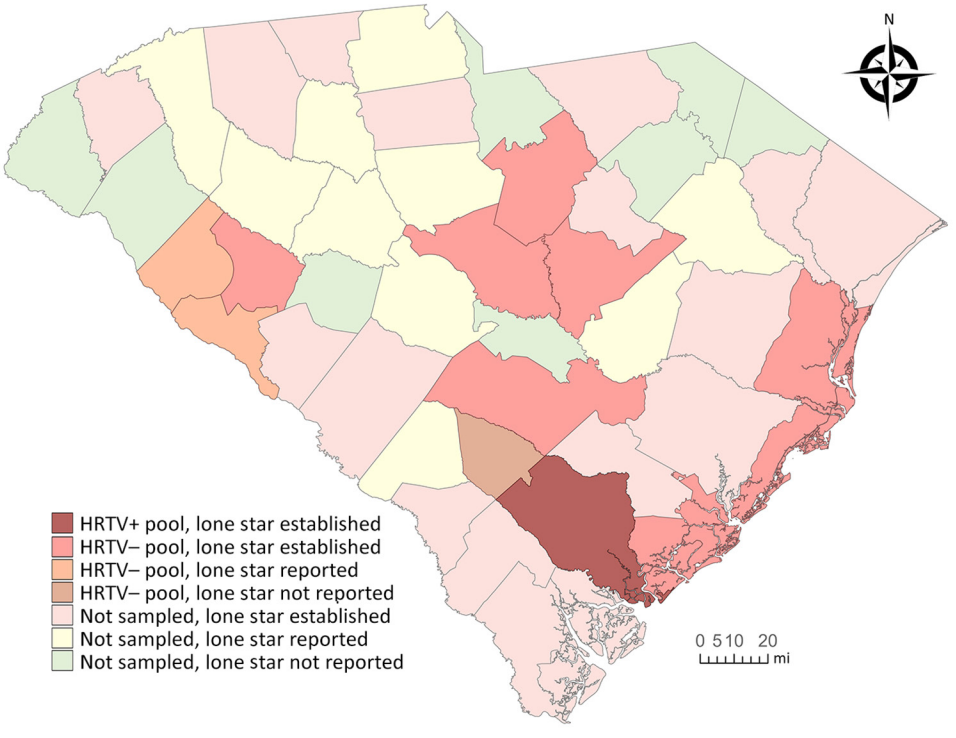


Figure. Geographic distribution of lone star ticks (*Amblyomma americanum*) and HRTV surveillance, South Carolina, USA, 2021–2024. Established counties were defined as those in which ≥6 lone star ticks of a single life stage or ticks from >1 life stage were collected within a 12-month period. HRTV, Heartland virus.

Table. Pathogen testing results in study of HRTV in lone star ticks, South Carolina, USA, 2021–2024*

Year collected	Sampling		Testing results		Collection method for positive pools		
	No. counties sampled	No. counties tested	No. pools tested	No. HRTV-positive pools	Dragging	CO_2 trap	On person
2021	16	4	223	5	1	3	1
2022	23	8	106	1	1	NA	NA
2023	25	3	21	0	NA	NA	NA
2024	45	7	18	0	NA	NA	NA
Total			368	6	2	3	1

*HRTV, Heartland virus; NA, not available.

Our study reports HRTV detection in questing South Carolina lone star tick nymphs, a widespread species associated with an increasing number of health threats in the United States (*9*). Collection of positive pools occurred during spring through late summer across 2 different years, consistent with expected nymphal host-seeking activity and demonstrating viral persistence across time. Lone star ticks use multiple strategies to find a host, as demonstrated in the HRTV-positive pools collected by dragging (ambush behavior) and by CO_2 trapping (active host-seeking). Our study results compliment previous data indicating seropositive animals and 1 human case, although the human case did not include follow-up and it remains unclear where the exposure occurred (*7*,*10*).

Healthcare providers should consider tickborne viral infections in patients who do not respond to antimicrobial therapy, because the overlapping prevalence of multiple lone star tick-associated pathogens can confound diagnosis. Supportive care is the primary management of patients with tickborne viral infections because no specific antiviral therapies are available. Continued and expanded testing can help better define the geographic range, epidemiology, and public health significance of emerging tickborne viruses in the United States. Tick bite prevention, early clinical recognition, and strengthened surveillance remain essential for treatment and control of tickborne viruses.

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About the Author

Ms. Pickle is transitioning to an assistant professor of public health at Old Dominion University from a postdoctoral fellowship at the University of South Carolina, throughout her time working on this article. Her research focuses on emerging tickborne pathogens, alpha-gal syndrome, and the ecological-epidemiologic drivers of vectorborne disease in the southeastern United States.

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Address for correspondence: Melissa Nolan, Arnold School of Public Health, University of South Carolina, 915 Greene St, Lab Rm 327, Columbia, SC 29208, USA; email: msnolan@mailbox.sc.edu

Osteomyelitis Caused by *Metamycoplasma gateae* after Cat Bite, Japan, 2026

Takehiro Hashimoto, Miyuki Uehara, Yuta Shingai, Daisuke Tamura, Kazunori Kimitsuki, Hirotaka Shibata, Kazufumi Hiramatsu

Author affiliations: Oita University Hospital, Yufu, Japan (T. Hashimoto, K. Hiramatsu); Oita University Faculty of Medicine, Yufu (M. Uehara, Y. Shingai, D. Tamura, K. Kimitsuki, H. Shibata)

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We report a case of osteomyelitis caused by *Metamycoplasma gateae* after a cat bite in an immunocompromised patient in Japan. No standardized treatment has been established; however, the patient recovered after surgery and minocycline treatment. Clinicians should consider *M. gateae* infection in immunocompromised patients with unidentified infections and cat-bite exposure.

Metamycoplasma gateae, a member of the family Mycoplasmataceae, was first isolated from cat saliva in 1967 (*1*) and reclassified from *Mycoplasma* into the genus *Metamycoplasma* in 2018 (*2*). Although *M. gateae* is known to colonize cats and cause feline infections (*3*–*6*), human infections have not been reported. We report a case of osteomyelitis caused by *M. gateae* in an immunocompromised patient with cat-bite exposure.

A 39-year-old woman was admitted to Oita University Hospital with fever and pain in her right hand, which her pet cat had bitten 42 days before admission. She had systemic lupus erythematosus treated with methylprednisolone (8 mg/d) and mycophenolate mofetil (2,000 mg/d) and type 1 diabetes mellitus managed with continuous subcutaneous insulin infusion. Swelling and pain in the right hand developed 32 days before admission and was diagnosed by a dermatologist at the hospital as cellulitis and treated with intravenous ceftriaxone, followed by oral clindamycin for 2 weeks. Magnetic resonance imaging, performed 31 days before hospital admission, had shown no osteomyelitis. The pain persisted despite treatment. Two days before admission, swelling spread to the wrist and fourth and fifth proximal interphalangeal joints, and fever (38.3°C) developed along with worsening pain.

At admission, physical examination revealed swelling and tenderness of the right hand. Laboratory tests showed elevated leukocytes (9,660 cells/μL, reference range 3,300–8,600 cells/μL), C-reactive protein (15.3 mg/dL, reference range 0.0–0.14 mg/dL), and glycated hemoglobin (7.6%, reference range 4.9%–6.0%) and markedly decreased serum immunoglobulin levels (88 mg/dL IgG [reference range 861–1,747 mg/dL]; 13 mg/dL IgA [reference range 93–393 mg/dL]; and 2 mg/dL IgM [reference range 50–269 mg/dL]). Magnetic resonance imaging revealed subcutaneous fluid collection within the dorsum of the hand and osteomyelitis of the third metacarpal bone, leading to a diagnosis of cellulitis with osteomyelitis. We performed an incision with drainage and collected pus, tissue, and blood culture specimens. We cultured the pus and tissue specimens in aerobic, anaerobic, and enrichment media under standard conditions (Appendix https://wwwnc.cdc.gov/EID/article/32/12/26-0515-App1.pdf). We initiated empirical antimicrobial drug therapy with piperacillin/tazobactam (4/0.5 g every 8 h). Pus and tissue cultures were negative; serologic testing for *Bartonella* antibodies was negative. We changed the antimicrobial drug therapy to ampicillin/sulbactam (2/1 g every 6 h) on day 5. However, pain in the right hand worsened; we changed the treatment back to piperacillin/tazobactam only on day 8.

On day 11, 16S rRNA gene sequencing of DNA from a tissue specimen identified *M. gateae* as the causative bacterium. The nucleotide sequence was deposited in GenBank (accession no. LC934417). The sequence showed 99.86% (1,450/1,452 nt) sequence