11-1-2018

Multistate Infestation with the Exotic Disease-Vector Tick Haemaphysalis longicornis - United States, August 2017-September 2018

C. B. Beard
James Occi
Denise L. Bonilla
Andrea M. Egizi
Dina M. Fonseca

See next page for additional authors

Follow this and additional works at: https://touroscholar.touro.edu/nymc_fac_pubs

Part of the Medicine and Health Sciences Commons

Recommended Citation

This Article is brought to you for free and open access by the Faculty at Touro Scholar. It has been accepted for inclusion in NYMC Faculty Publications by an authorized administrator of Touro Scholar. For more information, please contact touro.scholar@touro.edu.
Multistate Infestation with the Exotic Disease–Vector Tick

Haemaphysalis longicornis — United States, August 2017–September 2018

C. Ben Beard, PhD1; James Occi, MA, MS2; Denise L. Bonilla, MS3; Andrea M. Egizi, PhD4; Dina M. Fonseca, PhD2; James W. Mertins, PhD3; Byron P. Backenson, MS5; Waheed I. Bajwa, PhD6; Alexis M. Barbarin, PhD7; Matthew A. Bertone, PhD8; Justin Brown, DVM, PhD9; Neeta P. Connally, PhD10; Nancy D. Connell, PhD11; Rebecca J. Eisen, PhD1; Richard C. Falco, PhD3; Angela M. James, PhD3; Rayda K. Krell, PhD12; Kevin Lahmers, DVM, PhD12; Nicole Lewis, DVM13; Susan E. Little, DVM, PhD14; Michael Neault, DVM15; Adalberto A. Pérez de León, DVM, PhD16; Adam R. Randall, PhD17; Mark G. Ruder, DVM, PhD18; Meriam N. Saleh, PhD19; Brittaney L. Schappach20; Betsy A. Schroeder, DVM13; Leslie L. Seraphin, DVM3; Morgan Wehtje, PhD3; Gary P. Wormser, MD20; Michael J. Yabsley, PhD21; William Halperin, MD, DrPH22

Haemaphysalis longicornis is a tick indigenous to eastern Asia and an important vector of human and animal disease agents, resulting in such outcomes as human hemorrhagic fever and reduction of production in dairy cattle by 25%. H. longicornis was discovered on a sheep in New Jersey in August 2017 (1). This was the first detection in the United States outside of quarantine. In the spring of 2018, the tick was again detected at the index site, and later, in other counties in New Jersey, in seven other states in the eastern United States, and in Arkansas. The hosts included six species of domestic animals, six species of wildlife, and humans. To forestall adverse consequences in humans, pets, livestock, and wildlife, several critical actions are indicated, including expanded surveillance to determine the evolving distribution of H. longicornis, detection of pathogens that H. longicornis currently harbors, determination of the capacity of H. longicornis to serve as a vector for a range of potential pathogens, and evaluation of effective agents and methods for the control of H. longicornis.

H. longicornis is native to eastern China, Japan, the Russian Far East, and Korea. It is an introduced, and now established, exotic species in Australia, New Zealand, and several island nations in the western Pacific Region. Where this tick exists, it is an important vector of human and animal disease agents. In China and Japan, it transmits the severe fever with thrombocytopenia syndrome virus (SFTSV), which causes a human hemorrhagic fever (2), and Rickettsia japonica, which causes Japanese spotted fever (3). Studies in Asia identified ticks infected with various species of Anaplasma, Babesia, Borrelia, Ehrlichia, and Rickettsia, and all of these pathogen groups circulate zoonotically in the United States (4,5). In addition, parthenogenetic reproduction, a biologic characteristic of this species, allows a single introduced female tick to generate progeny without mating, thus resulting in massive host infestations. In some regions of New Zealand and Australia, this tick can reduce production in dairy cattle by 25% (6).

Before 2017, H. longicornis ticks were intercepted at U.S. ports of entry at least 15 times on imported animals and materials (James W. Mertins, U.S. Department of Agriculture [USDA], personal communication).

The USDA Animal and Plant Inspection Service coordinated cooperative efforts through telephone conference calls with various local, state, and federal agricultural and public health agencies. Through these efforts, enhanced vector and animal surveillance were implemented to detect additional tick infestations. Suspect archival specimens that were available among previously collected ticks were also examined. Ticks were identified definitively by morphology at the USDA National Veterinary Services Laboratories or by DNA sequence analysis (molecular barcoding) at Rutgers University Center for Vector Biology, Monmouth County (New Jersey) Mosquito Control Division; College of Veterinary Medicine, University of Georgia; and Center for Veterinary Health Sciences, Oklahoma State University. By definition, a “report” is any new morphologic or molecular identification of H. longicornis ticks with a new county or host species from that county, identified from August 2017 through September 2018. Subsequent repeat collections are not reported here.

From August 2017 through September 2018, vector and animal surveillance efforts resulted in 53 reports of H. longicornis in the United States, including 38 (72%) from animal species (23 [61%] from domestic animals, 13 [34%] from wildlife, and two [5%] from humans), and 15 (28%) from environmental sampling of grass or other vegetation using cloth drags or flags or carbon dioxide–baited tick traps. With the exception of one report from Arkansas, the remaining reports of positively identified ticks are from eight eastern states: New Jersey (16; 30%), Virginia (15; 28%), West Virginia (11; 21%), New York (three; 6%), North Carolina (three; 6%), Pennsylvania (two; 4%), Connecticut (one; 2%), and Maryland (one; 2%) (Figure). Among the 546 counties or county equivalents in the nine states, ticks were reported from 45 (8%) counties (1.4% of all 3,109 U.S. counties and county equivalents) (Table 1).

1 Drags consist of white cloth (usually 1 m2) that have a wooden leading frame and are dragged by a cord through grass or a leafy forest floor. Flags are similar but are used to brush uneven surfaces such as small bushes in wooded areas. Drags and flags are used to sample the environment for ticks trying to locate a host.

2 Carbon dioxide traps consist of dry ice–filled small boxes with holes that allow the CO2 to escape which are placed on a white cloth or mat in a grassy area or forest floor. Ticks, attracted by the CO2, crawl on to the cloth or mat surface, which is inspected for ticks after a period of time.
Excluding 15 reports of positive environmental sampling using flagging, dragging, or carbon dioxide traps, the remaining 38 reports reflect collection of ticks from infested host species (Table 2). Surveillance efforts did not include testing the ticks or hosts for pathogens. No cases of illness in humans or other species were reported. Concurrent reexamination of archived historical samples showed that invasion occurred years earlier. Most importantly, ticks collected from a deer in West Virginia in 2010 and a dog in New Jersey in 2013 were retrospectively identified as *H. longicornis*.

**Discussion**

Cooperative efforts among federal, state, and local experts from agricultural, public health, and academic institutions during the last year have documented that a tick indigenous to Asia is currently resident in several U.S. states. The public health and agricultural impacts of the multistate introduction and subsequent domestic establishment of *H. longicornis* are not known. At present, there is no evidence that *H. longicornis* has transmitted pathogens to humans, domestic animals, or wildlife in the United States. This species, however, is a potential vector of a number of important agents of human and animal diseases in the United States, including *Rickettsia*, *Borrelia*, *Ehrlichia*, *Anaplasma*, *Theileria*, and several important viral agents such as Heartland and Powassan viruses. Consequently, increased tick surveillance is warranted, using standardized animal and environmental sampling methods.

The findings in this report are subject to at least two limitations. First, the findings are limited by the variable surveillance methods used to identify the geographic and host distribution of *H. longicornis*. These methods included both passive and active surveillance. Conclusions about the geographic and host distribution might reflect the biases in the collection and submission of samples to states and USDA and the paucity of available information. Second, the data in this report reflect the collection of specimens that were positively identified by morphology or molecular barcoding. These represent sentinels that *H. longicornis* is present in different U.S. states and regions, and not a comprehensive assessment of the distribution of *H. longicornis*.
The recently documented occurrence of *Haemaphysalis longicornis* in the United States presents an opportunity for collaboration among governmental, agricultural, public health agencies and partners in academic public health, veterinary sciences, and agricultural sciences to prevent diseases of potential national importance before onset in humans and other animal species.

**Acknowledgments**

Wes Watson, Andrew D. Haddow, Naomi Drexler, Gleeson Murphy, Harry Savage, Howard Ginsberg, Kimervante, field and laboratory personnel.

Corresponding author: C. Ben Beard, cbeard@cdc.gov, 970-221-6418.

1Division of Vector-Borne Diseases, National Center for Emerging and Zoonotic Infectious Diseases, CDC; 2Center for Vector Biology, School of Environmental and Biological Sciences, Rutgers, The State University of New Jersey, New Brunswick, New Jersey; 3Animal and Plant Health Inspection Service, Veterinary Services, U.S. Department of Agriculture, Riverdale, Maryland; 4Tick-borne Disease Laboratory, Monmouth County Mosquito Control Division, and Center for Vector Biology, Department of Entomology, Rutgers, The State University of New Jersey, New Brunswick, New Jersey; 5Tick-borne Disease Laboratory, New York City Department of Health and Mental Hygiene, Communicable Disease Branch, New York State Department of Health; 6City Mosquito Control Board of New York City, New York, New York; 7Bureau of Communicable Diseases Control, New York State Department of Health; 8New York City Department of Health and Mental Hygiene, Communicable Disease Branch, New York, New York; 9Department of Entomology and Plant Pathology, North Carolina State University, Raleigh, North Carolina; 10Pennsylvania Game Commission, Animal Diagnostic Laboratory, Harrisburg, Pennsylvania; 11Department of Biological and Environmental Sciences, Western Connecticut State University, Danbury, Connecticut; 12Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland; 13Virginia-Maryland College of Veterinary Medicine, Virginia Polytechnic Institute and State University, Blacksburg, Virginia; 14Division of Animal Health, New Jersey Department of Agriculture; 15Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, Oklahoma; 16Veterinary Division, North Carolina Department of Agriculture and Consumer Services; 17Agricultural Research Service, Knipling-Bushland U.S. Livestock Insects Research Laboratory, U.S. Department of Agriculture, Kerrville, Texas; 18Animal and Plant Health Inspection Service, Wildlife Services, U.S. Department of Agriculture, Riverdale, Maryland; 19Southeastern Cooperative Wildlife Disease Study, Department of Population Health, University of Georgia, Athens, Georgia; 20Bureau of Epidemiology, Pennsylvania Department of Health; 21Department of Health, College of Public Health, College of Veterinary Medicine, and the Warnell School of Forestry and Natural Resources, University of Georgia, Athens, Georgia; 22Department of Epidemiology, School of Public Health, Rutgers, The State University of New Jersey, New Brunswick, New Jersey.

All authors have completed and submitted the ICMJE form for disclosure of potential conflicts of interest. Susan E. Little reports grants, personal fees, and nonfinancial support from several veterinary pharmaceutical and diagnostic companies, outside the submitted work. Mark G. Ruder reports grants from U.S. Department of Agriculture during the conduct of the study and grants from U.S. Department of Agriculture, outside the submitted work. Gary P. Wormser reports unpaid board membership in the American Lyme Disease Foundation; fees for expert medical/legal testimony regarding Lyme disease and babesiosis; grants to New York Medical College from Immuneics, Inc., Quidel Corporation, and Rarecyte, Inc. for diagnostic tests for Lyme disease and babesiosis, Tufts University for xenodiagnoses to assess persistence of *Borrelia*, and Institute for Systems Biology for exploration of biomarkers for Lyme disease outcomes; U.S. Patent Application, “High Sensitivity Method for Early Lyme Disease Detection” (Application No. 15/046,204); and U.S. Provisional Patent Application, “Use of Metabolic Biosignatures for Differentiation of Early Lyme Disease from Southern Tick-Associated Rash Illness (STARI)” (Application No. 62/277,252); and stock/stock options in Abbott/AbbVie. No other potential conflicts of interest were disclosed.
References