Epizootic Hemorrhagic Disease in White-Tailed Deer, Canada

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Epizootic hemorrhagic disease affects wild and domestic ruminants and has recently spread northward within the United States. In September 2017, we detected epizootic hemorrhagic disease virus in wild white-tailed deer, Odocoileus virginianus, in east-central Canada. Culicoides spp. midges of the subgenus Avaritia were the most common potential vectors identified on site.

Epizootic hemorrhagic disease viruses (EHDVs) and bluetongue viruses (BTVs) are Culicoides spp. midge–transmitted orbiviruses that represent an imminent threat to the health of ruminant livestock and wildlife. For susceptible ruminants, EHDV and BTV infections can result in high rates of illness and death, leading to severe economic hardship to the agricultural sector (1). These viruses have a historical geographic range of 40°N–50°N and 35°S, following the distribution of the Culicoides vectors. However, the epidemiology of these pathogens is changing, with decades of northward expansion into areas of Europe and North America with immunologically naive hosts (1–3).

In Canada, EHDV has rarely and sporadically been detected in the southern portions of British Columbia, Alberta, and Saskatchewan (4). We report the detection of EHDV in white-tailed deer, Odocoileus virginianus, in east-central Canada, providing further evidence of the northern range expansion of orbiviruses within North America.

On September 7, 2017, two wild white-tailed deer carcasses were found in a seminatural area adjacent to a

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EHDV may have been introduced to Ontario through the movement of infected vectors or ruminants, and its detection in Ontario may represent the northern edge of the EHDV outbreak in the eastern United States. Alternatively, low levels of previously undetected EHDV transmission may have been transient or ongoing across a wider region, including Ontario, for an unknown period. In either case, this event may preclude a much more widespread and higher-impact EHDV outbreak, such as occurred with BTV in Europe and with EHDV in the United States (2,8).

We identified numerous *Culicoides* spp. midges at the site where the EHDV-infected white-tailed deer carcasses were recovered. However, *C. sonorensis* midges, the only confirmed EHDV vector species in North America (1,9), was not among these. This species was recently identified in Ontario (10), but the density and distribution of this species in the province, as well as its role in regional EHDV transmission, is currently unknown. *Culicoides* spp. composition within areas of past EHDV outbreaks varies widely; therefore, additional *Culicoides* spp. midges may serve as competent EHDV vectors. However, this possibility has not been confirmed (1,9). In addition to vector competence, the climatic limitations for the survival and successful breeding and establishment of current *Culicoides* spp. populations in the region remain to be investigated (1,8). These factors indicate the need for ongoing *Culicoides* spp. midge and deer mortality surveillance in the region.

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About the Author
Dr. Allen is a veterinarian and PhD candidate at the University of Guelph, Canada. Her research focuses on wildlife disease, specifically vectorborne viruses and disease at the livestock–wildlife interface.

References
Mass migration from Venezuela has increased malaria resurgence risk across South America. During 2018, migrants from Venezuela constituted 96% of imported malaria cases along the Ecuador–Peru border. *Plasmodium vivax* predominated (96%). Autochthonous malaria cases emerged in areas previously malaria-free. Heightened malaria control and a response to this humanitarian crisis are imperative.

**Malaria** is a vectorborne parasitic infection caused by *Plasmodium* spp. and transmitted by *Anopheles* mosquitoes, characterized by fever and hemolysis with chronic and fatal potential (1). Despite substantial strides toward elimination in the Americas, malaria remains a major concern; ≈975,700 cases occurred and 138 million persons were at risk in 2017 (2). Most malaria cases in South America occur in the Amazon region, and *P. vivax* is more common than *P. falciparum* (3).

*P. vivax* and *P. falciparum* malaria were historically endemic to the Ecuador–Peru coastal border region. During 1990–2012, a total of 62,000 malaria cases were reported from El Oro Province, Ecuador, and 85,605 from Tumbes Region, Peru (4). Through vector control and active case surveillance and response, malaria was eliminated from El Oro Province in 2011 and Tumbes Region in 2012 (4). However, malaria cases elsewhere in Ecuador increased from 378 in 2013 (5) to 1,279 in 2017 (6). Peru and other countries in the region also reported increased malaria in 2017, indicating a major risk for reintroduction to elimination areas (2). In 2017, Venezuela alone accounted for more than half of all malaria cases in the Americas (2).

The public health sector in Venezuela is struggling with infectious disease epidemics, including malaria (7), despite a historically successful malaria control program (3). The worsening social and economic crisis has led to large-scale migration from and within Venezuela. The shortage of antimalarial drugs and lax in-country control efforts have exacerbated the situation, affecting countries throughout South America (8). Many people from Venezuela are migrating through Colombia and Ecuador to reach Peru and the southern cone of South America, stopping at various locations along the way (Figure). We report a series of imported malaria cases in migrants from Venezuela and the first autochthonous cases of malaria in the Ecuador–Peru border region since local elimination.

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**Effects of Political Instability in Venezuela on Malaria Resurgence at Ecuador–Peru Border, 2018**

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