Applied Geography 64 (2015) 66–73

Contents lists available at ScienceDirect

Applied Geography

journal homepage: www.elsevier.com/locate/apgeog

Mapping eastern equine encephalitis virus risk for white-tailed deer in Michigan

Joni A. Downs [a,*], Garrett Hyzer [a], Eric Marion [a], Zachary J. Smith [a], Patrick Vander Kelen [b], Thomas R. Unnasch [c]

[a] School of Geosciences, University of South Florida, 4202 E. Fowler Ave., Tampa, FL 33620, USA
[b] Washington State Department of Health, Olympia, WA 98504, USA
[c] College of Public Health, University of South Florida, 4202 E. Fowler Ave., Tampa, FL 33620, USA

ARTICLE INFO

Article history:
Received 27 March 2015
Received in revised form
16 September 2015
Accepted 16 September 2015
Available online 28 September 2015

Keywords:
Arbovirus
Disease mapping
GIS
Odocoileus virginianus
Wildlife

ABSTRACT

Eastern equine encephalitis (EEE) is a mosquito-borne viral disease that is often fatal to humans and horses. Some species including white-tailed deer and passerine birds can survive infection with the EEE virus (EEEV) and develop antibodies that can be detected using laboratory techniques. In this way, collected serum samples from free ranging white-tailed deer can be used to monitor the presence of the virus in ecosystems. This study developed and tested a risk index model designed to predict EEEV activity in white-tailed deer in a three-county area of Michigan. The model evaluates EEEV risk on a continuous scale from 0.0 (no measurable risk) to 1.0 (highest possible risk). High risk habitats are identified as those preferred by white-tailed deer that are also located in close proximity to an abundance of wetlands and lowland forests, which support disease vectors and hosts. The model was developed based on relevant literature and was tested with known locations of infected deer that showed neurological symptoms. The risk index model accurately predicted the known locations, with the mean value for those sites equal to the 94th percentile of values in the study area. The risk map produced by the model could be used refine future EEEV monitoring efforts that use serum samples from free-ranging white-tailed deer to monitor viral activity. Alternatively, it could be used focus educational efforts targeted toward deer hunters that may have elevated risks of infection.

1. Introduction

Eastern equine encephalitis (EEE) is a mosquito-borne disease caused by the EEE virus (EEEV). EEEV is endemic to the eastern United States and infects a variety of vertebrate species. EEEV is primarily found along the Atlantic and Gulf coasts, although it also occurs in some inland areas near the Great Lakes. An estimated 30–70% of human cases and 90% of horse cases of EEE are fatal, and survivors often suffer severe neurological complications (CDC, 2014). Mortality rates are also high for some species of exotic birds, such as ring-necked pheasants (*Phasianus colchicus*) (Williams, Fulton, Jon, & Reed, 2000) and emu (*Dromaius novaehollandiae*) (Tengelsen et al., 2001). Mortality from EEE has been reported in some native wildlife, including the endangered whooping crane (Dein et al., 1986). EEEV infections have been reported in domestic pigs (Elvinger, Baldwin, Liggett, Tang, & Stallknecht, 1996), cattle (McGee, Littleton, Mapp, & Brown, 1992), sheep (Bauer, Gill, Poston, & Kim, 2005), dogs (Farrar, Miller, Baldwin, Stiver, & Hall, 2005), and chickens (Griffiths & McClain, 1985), although these species typically do not show signs of disease and instead develop detectable antibodies against the virus. Similar resistance to EEEV has been observed in a variety of wildlife, including some passerine birds (Sun et al., 2013), wading birds (Gottdenker, Howerth, & Mead, 2003), ungulates (Berl et al., 2013; Lubelczyk et al., 2014; Schmitt et al., 2007), and snakes (Bingham et al., 2012).

EEEV is maintained in ecosystems through an enzootic cycle that involves mosquitoes (vectors) and competent avian reservoirs (hosts) that amplify the virus. Throughout much of the eastern US, this cycle primarily involves mosquitoes of the genus *Culiseta* (*Cs. melanura* and *Cs. morsitans*) and the bird species that they feed upon, such as northern cardinals (*Cardinalis cardinalis*) and other

* Corresponding author.
E-mail addresses: jdowns@cas.usf.edu, downs@usf.edu (J.A. Downs).

http://dx.doi.org/10.1016/j.apgeog.2015.09.006

song birds (Cohen et al., 2009; Estep et al., 2011; Estep et al., 2013; McLean et al., 1985; Molaei, Andreadis, & Armstrong, 2007; Molaei et al., 2010). EEEV is then transmitted to humans, horses, and other susceptible species via bridge vectors—mosquitoes that feed on both birds and mammals. Common bridge vectors include *Aedes vexans*, *Coquillettidia perturbans*, *Ochlerotatus sollicitans*, and *Ochlerotatus canadensis* (Armstrong & Andreadis, 2010a, 2010b). In the Northeast and Great Lakes regions, EEEV transmission peaks during summer and early fall, and not every year, while transmission is typically observed year-round in Florida (CDC, 2014).

Though EEE is relatively rare, high fatality rates in humans, horses, and other susceptible species prompt many government agencies to implement prevention, monitoring, and control programs. A vaccine is commercially available to prevent EEE in horses (Pandya, Gorchakov, Wang, Leal, & Weaver, 2012). As the equivalent is unavailable for humans, reducing exposure to mosquitoes is the most reliable way to prevent human EEEV infections. Recommended approaches include using insect repellents, wearing protective clothing, installing screens on windows and doors, and removing mosquito breeding sites from yards and gardens. Monitoring efforts typically involve testing blood samples from collected mosquitoes or avian sentinel flocks of chickens (Loftin et al., 2006; Morris, Baker, Stark, Burgess, & Lewis, 1994; Oprandy, Olson, & Scott, 1988; Ottendorfer & Stark, 2006) or wild birds (Williams, Young, Watts, & Reed, 1971). A recent innovation in EEEV surveillance involves screening free-ranging wildlife that are resistant to the disease for antibodies. Serum samples can be collected from hunter harvests, road kill surveys, or other methods (Berl et al., 2013; Eisen et al., 2011). If EEEV is detected by any of these means, attempts to curb its transmission generally involve aerial spraying of insecticides over impacted areas in order to kill any potentially infected mosquitoes (Carpenter, Lee, & Chancy, 1981; Howard & Oliver, 1997). Programs like these are vital for protecting public health, although the costs incurred can be large, reaching more than $100 million annually in some states.

A potential way to reduce costs is to target efforts in locations with higher risks of transmission. Predictive modelling using GIS offers one approach for identifying priority areas. A popular approach involves the development of index models. Typically, these models measure physical, biotic, or human variables for spatial units—either raster cells or polygons—and combine them mathematically to derive final index values that measure the outcome of interest. Index models have found utility in a variety of geographic applications, such as assessing the suitability of lands for wildlife habitat (Downs, Gates, & Murray, 2008), agricultural production (Wilson, Gerhart, Nielsen, & Ryan, 1992), and urban activities (Rybarczyk & Wu, 2010). Index models are also widely applied for measuring socio-economic (Weber, Sadoff, Zell, & de Sherbinin, 2015) and environmental vulnerability (Malcomb, Weaver, & Krakowka, 2014; Kovarik & van Beynen, 2015), as well as quantifying risk associated with natural hazards (Platt, 2014), environmental dangers (Santini, Caccamo, Laurenti, Noce, & Valentini, 2010), and a host of other threats. Index models are particularly useful for mapping risk of disease and predicting future outbreaks. Index models and closely related approaches have been widely used to map high risk locations for a variety of mosquito-borne diseases, such as West Nile Virus (LaBeaud et al., 2008; Rochlin, Turbow, Gomez, Ninivaggi, & Campbell, 2011; Young, Tullis, & Cothren, 2013) and Dengue (Machado–Machado, 2012; Wen, Lin, Teng, & Chang, 2015). Once high risk areas are identified using these approaches, efficient monitoring and control strategies can be developed and implemented (Chu, Chan, & Jao, 2013).

This paper develops and tests a risk index model for mapping EEEV risk for white-tailed deer (*Odocoileus virginianus*) in Michigan. EEEV can cause encephalitis and abnormal behaviour in white-tailed deer (Schmitt et al., 2007), though mortality is thought to be relatively uncommon. The first fatal infection was reported in a single deer in Georgia during 2001 (Tate et al., 2005) and subsequently a small number of other cases have been documented in Michigan (Schmitt et al., 2007). It is generally thought that EEEV poses only a minimal threat to deer populations, since they are generally resistant to the virus and produce antibodies upon infection. EEEV antibodies are widespread in deer populations in the Northeast, with 7.1% of sampled deer testing positive in Maine (Eisen et al., 2011) and 10.2% in Vermont (Berl et al., 2013), further suggesting mortality is insignificant. The antibodies produced by white-tailed deer can be detected using plaque-reduction neutralization assay methods in the laboratory, and testing free-ranging individuals for antibodies can be a cost-effective way to monitor viral activity over a large geographic area as is commonly done in Maine (Eisen et al., 2011) and Vermont (Berl et al., 2013). The model developed in this paper is designed to map EEEV infection risk for white-tailed in order to target surveillance, prevention, or control efforts.

2. Materials and methods

A risk index model was developed to evaluate EEEV risk to white-tailed deer in the state of Michigan. Since 1980, 16 human cases of EEE have been documented in Michigan, the highest incidence in the Great Lakes region. The state has also recently experienced high numbers of equine cases, including 8 in 2005 and 58 in 2010. Additionally, 8 white-tailed deer cases and their geographic locations were reported for 2005 in a study by (Schmitt et al., 2007). The free-ranging deer in the sample displayed signs of chronic wasting disease or other neurological symptoms. The individuals were subsequently euthanized in the field, and tissue samples were sent for analysis. Eight individuals tested positive for EEEV. The three-county area where those deer were located was selected as the study area for this research included Kent, Ionia, and Montcalm counties in the Lower Peninsula (Fig. 1). These counties support

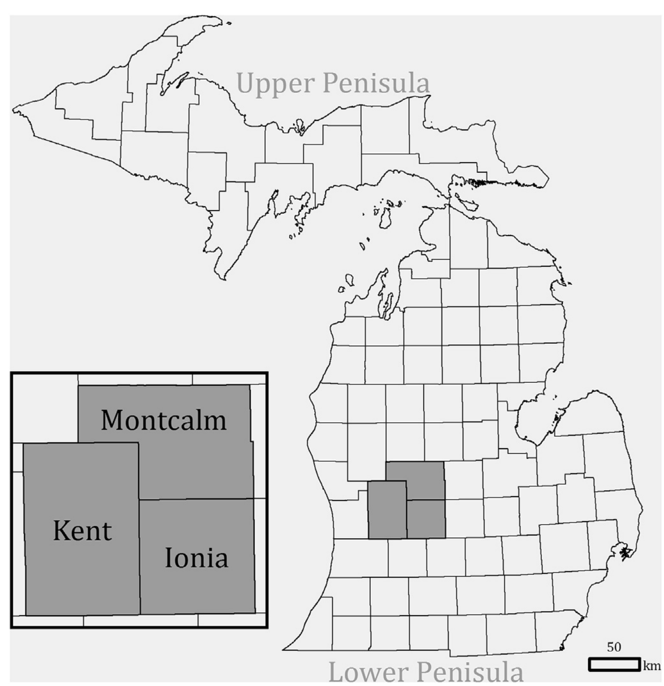

Fig. 1. Map of the three-county study area in Michigan.