A risk index model for predicting eastern equine encephalitis virus transmission to horses in Florida

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ABSTRACT

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A GIS-based risk index model was developed to quantify EEEV transmission risk to horses in the State of Florida. EEEV is a highly pathogenic arbovirus that is endemic along the east coast of the United States, and it is generally fatal to both horses and humans. The model evaluates EEEV transmission risk at individual raster cells in map on a continuous scale of 0–1. The risk index is derived based on local habitat features and the composition and configuration of surrounding land cover types associated with EEEV transmission. The model was verified and validated using the locations of documented horse cases of EEEV. These results of the verification and validation indicate that the model is able to predict locations of EEEV transmission to horses broadly across the state. The model is relatively robust to regional variation in EEEV transmission and habitat conditions in Florida, and it accurately predicted nearly all verification and validation cases in the Panhandle, North, and Central regions of the state. The model performed less accurately in the South, where relatively few cases are documented. Despite these differences, the model provides a useful way to assess EEEV risk both from a regional perspective and at more localized scales. The resulting predictive maps are designed to guide EEEV surveillance and prevention efforts by county mosquito control districts.

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Introduction

The most pathogenic arbovirus—or arthropod-borne virus—to affect the United States is eastern equine encephalitis virus (EEEV). Viral transmission of EEEV is found predominately along the east coast of the United States from Maine to Florida with cases of neuro-invasive EEE reported in 20 states (Bigler et al., 1976). EEEV circulates in a transmission cycle involving freshwater swamp mosquitoes, competent avian reservoirs, and mammals (Crans, 1962; Moncayo, Edman, & Finn, 2000; Morris, 1988). The mosquito *Culiseta melanura* is thought to be the primary enzootic vector for EEEV in North America, although numerous other species can carry the virus. The primary reservoir hosts are thought to be passerine songbirds for which the virus is generally non-fatal. Recent studies have also implicated reptiles as potential hosts of the virus (Bingham et al., 2012). The transmission cycle also involves bridge vectors—mosquitoes that feed on both birds and mammals—which transmit EEEV to humans, horses, and other mammals during epizootic outbreaks (Weaver, 2005).

Currently, there is no approved human vaccine or effective treatment available for those infected with EEEV. Symptoms of EEEV in humans include swelling of the brain, chills, fever, and malaise, among others. The case fatality rate of symptomatic humans can be 35% or more with surviving cases often suffering from neurological complications, including brain impairment, and resulting in million dollar health care costs (Villari, Spielman, Komar, McDowell, & Timperi, 1995). Therefore, prevention and surveillance still remain the best options for controlling the risk of infection to humans. A vaccine is available to protect horses, although horse fatalities are still common in North America. Florida has the greatest burden of EEE cases in the United States, accounting for 25% of all human fatalities since 1964 (CDC, 2010). In Florida, EEEV claims an average of 70 horse fatalities a year (Vander Kelen, Downs, Burkett-Cadena, et al., 2012; Vander Kelen, Downs, Stark, et al., 2012). EEEV continues to be widespread across Florida, with transmission reported in 64 of Florida's 67 counties (Lobo, Jimenez-Valverde, & Real, 2008; Zweig & Campbell, 1993). Unlike the Northeast and Central United States, which observe epizootic outbreaks of human and horse cases in August and September

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(Letson, Bailey, Pearson, & Tsai, 1993), EEEV transmission in Florida occurs throughout the year, with most human and horse cases occurring in June and July (Bigler, Lassing, Buff, Lewis, & Hoff, 1975).

In addition to EEEV, Florida has several other endemic mosquito borne diseases, including West Nile Virus (WNV) and St. Louis encephalitis virus (SLE). As a result, most counties in Florida maintain active surveillance and control programs aimed at reducing the threat of arboviruses. The surveillance activities undertaken by these programs involve mosquito collections to monitor increases in putative vector populations and screening of sentinel chicken flocks to monitor virus activity. These data are used to guide mosquito control activities. Florida spends approximately $150 million per year on these activities (Jaing, 2010), which represents one of the largest state expenditures in the country. Traditionally, the locations of many of the sentinel chicken flocks in Florida were determined based upon the proximity to human cases of SLE during the last major human outbreak of this virus in the 1970s (Monath & Tsai, 1987; Nelson et al., 1983). Since EEEV, SLE, and WNV do not necessarily share the same environmental risk variables (LaBeaud et al., 2008; Moncayo et al., 2000), it is important to modify existing surveillance efforts to improve public protection from multiple arboviruses.

Geographic information systems (GIS) are commonly used to map disease occurrence and predict potential high risk areas for arboviral disease transmission. For instance, a number of studies have used climate, vegetation, elevation, and other environmental variables to predict West Nile Virus (Crowder et al., 2013; Day & Shaman, 2008; LaBeaud et al., 2008; Rochlin, Turbow, Gomez, Ninivaggi, & Campbell, 2011; Ruiz et al., 2010; Yoo, 2013; Young, Tullis, & Cothren, 2013). Similar approaches have also been used to map Dengue (Dickin, Schuster-Wallace, & Elliott, 2014; Machado-Machado, 2012) and Malaria (Fuller, Troyo, Alimi, & Beier, 2014) risk, as well. While risk maps developed to predict arboviral transmission can be used to guide prevention efforts such as chemical spraying (Chu, Chan, & Jao, 2013), such a model has not previously been developed to predict EEEV in Florida. Developing a model capable of identifying EEEV foci would be very useful in assisting the county mosquito control districts in targeting their surveillance and vector control efforts to those areas most likely to support viral transmission. Such a targeted surveillance and control program would result in more efficient detection of viral activity, thereby providing increased protection to Florida's residents.

This study reports development and application of a risk index model for predicting EEEV transmission to horses in the state of Florida. This is the first reported attempt, to our knowledge, to predictively map EEEV transmission risk. The model incorporates previously published habitat risk variables derived from Florida's 2005–2010 horse cases (Vander Kelen, Downs, Burkett-Cadena, et al., 2012; Vander Kelen, Downs, Stark, et al., 2012). The GIS-based model is applied using publicly available land use-land cover data. The index model estimates transmission risk to horses on a continuous scale from 0 to 1. The risk index model was verified using the previously published dataset and validated with independent cases documented during 2004 and 2011. The overall goal is to develop an accurate model that can be applied to assist county mosquito control districts in their EEEV surveillance and prevention efforts.

Methods

A spatially-explicit GIS-based risk index model was developed to quantify EEEV transmission risk to horses in Florida. The model inputs and parameters were derived from a recent study published by Vander Kelen, Downs, Burkett-Cadena, et al. (2012) and Vander Kelen, Downs, Stark, et al. (2012) that quantified habitats associated EEEV horse cases in Florida (hereinafter referred to as the previous

study). The previous study examined habitat composition and configuration associated with 438 horse cases of EEEV reported during 2005–2010 within four regions of the state: Panhandle, North, Central, and South (Fig. 1). Development of the risk index model was consistent with that for spatially-explicit habitat suitability index (HSI) models used to evaluate habitat for wildlife, where suitability is measured on a continuous scale that ranges from 0 (unsuitable) to 1 (optimal) (Brooks, 1997; Dijak, Rittenhouse, Larson, Thompson, & Millspaugh, 2007; Downs, Gates, & Murray, 2008; Rickers, Queen, & Arthaud, 1995; Roloff & Kernohan, 1999). The risk index model assesses EEEV transmission risk for horses on a similar scale extending from 0 (minimal risk) to 1 (maximal risk), where intermediate values measure relative levels of risk. The model relies on land cover data in raster format and assesses EEEV transmission risk at each grid cell. Land cover data at a 30 m spatial resolution generated by the Florida Department of Environmental Protection's Bureau of Watershed Restoration and distributed by the state's five Water Management Districts was used in both this and the previous study. This dataset includes land use and cover classified at four levels, with Level 1 being the most generalized and Level 4 the most specific. This study utilized Level 2 descriptions, as they differentiated between various wetland types and residential classes which were necessary for the model. The forty-two Level 2 classes were aggregated into 14 classes (Table 1) relevant to the model. Coastal habitats were excluded, as the vectors for EEEV are freshwater species of mosquito. EEEV risk is quantified based on the local land cover at each cell, as well as habitat composition and configuration in the surrounding area. The developed model includes five individual risk variables—all scaled 0–1—which are integrated into a final index that assesses overall risk on the same scale. These risk variables include: local habitat, wetland proximity, wetland composition, tree plantation–coniferous forest proximity, and tree plantation–coniferous forest composition.

Risk model formulation

Risk variable 1 (RV1): local habitat

RV1 measures EEEV transmission risk associated with the land cover type at each cell. Values for RV1 were derived from the
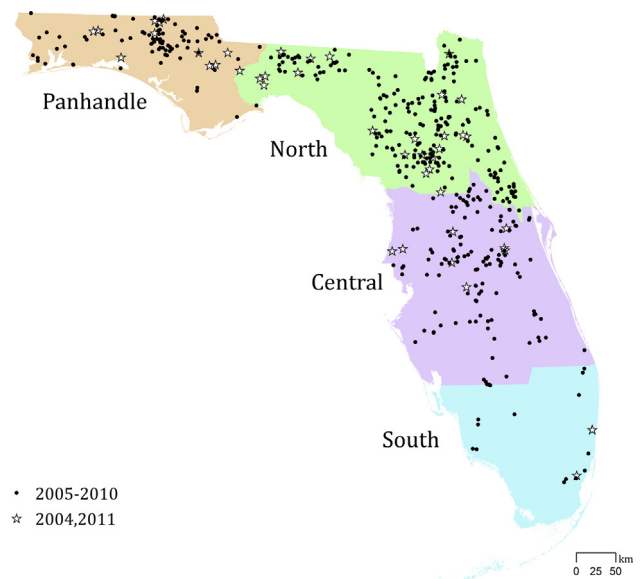

Fig. 1. Locations of documented horse cases of EEEV during 2005–2010 (Vander Kelen, Downs, Burkett-Cadena, et al., 2012; Vander Kelen, Downs, Stark, et al., 2012) and 2004 and 2011 (validation sites) within four regions of Florida.