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Model-informed risk assessment for Zika virus outbreaks in the Asia-Pacific regions



Yue Teng ^{a,b,*,g}, Dehua Bi ^{b,c,g}, Guigang Xie ^b, Yuan Jin ^{b,d}, Yong Huang ^{a,b}, Baihan Lin ^e, Xiaoping An ^{a,b}, Yigang Tong ^{a,b,**}, Dan Feng ^{f,***}

^a Beijing Institute of Microbiology and Epidemiology, Beijing 100071, China

^b State Key Laboratory of Pathogen and Biosecurity, Beijing 100071, China

^c Department of Mechanical and Mechatronics Engineering, University of Waterloo, 200 University

Avenue West, Waterloo, Ontario N2L 3G1, Canada

^d Beijing Institute of Biotechnology, Beijing 100071, China

^e Computational Neuroscience Program, Department of Psychology, Physics, and Computer Science and Engineering, Institute for Protein Design, University of Washington, Seattle, WA 98195, USA

^f Division of Standard Operational Management, Institute of Hospital Management, Chinese PLA General Hospital, Beijing 100853, China

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KEYWORDS Zika virus; Endemic; Risk factors; Modeling; Forecasting; Surveillance	Summary Recently, Zika virus (ZIKV) has been recognized as a significant threat to global public health. The disease was present in large parts of the Americas, the Caribbean, and also the western Pacific area with southern Asia during 2015 and 2016. However, little is known about the factors affecting the transmission of ZIKV. We used Gradient Boosted Regression Tree models to investigate the effects of various potential explanatory variables on the spread of ZIKV, and used current with historical information from a range of sources to assess the risks of future ZIKV outbreaks. Our results indicated that the probability of ZIKV outbreaks increases with vapor pressure, the occurrence of Dengue virus, and population density but decreases as health expenditure, GDP, and numbers of travelers. The predictive results revealed the potential risk countries of ZIKV infection in the Asia-Pacific regions between October 2016 and January 2017. We believe that the high-risk conditions would continue in South Asia and
	January 2017. We believe that the high-risk conditions would continue in South Asia and Australia over this period. By integrating information on eco-environmental, social-econom- ical, and ZIKV-related niche factors, this study estimated the probability for locally acquired

^{*} Corresponding author. State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, 20 Dong-Da Street, Fengtai District, Beijing 100071, China. Fax: +86 10 68164807.

*** Corresponding author.

E-mail addresses: yueteng@sklpb.org (Y. Teng), tong.yigang@gmail.com (Y. Tong), danfeng@sklpb.org (D. Feng).

^g Y.T. and D.H.B. contributed equally to this work.

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^{**} Corresponding author. State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, 20 Dong-Da Street, Fengtai District, Beijing 100071, China. Fax: +86 10 68164807.

mosquito-borne ZIKV infections in the Asia-Pacific region and improves the ability to forecast, and possibly even prevent, future outbreaks of ZIKV.

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Introduction

Zika virus (ZIKV) was first identified in a monkey in Africa in 1947, and was first reported in Asia in 1969.^{1,2} The first documented outbreak of ZIKV in humans occurred on Yap State (Federated States of Micronesia) in 2007.³ The most recent outbreak of ZIKV began in early 2015 in South America, and then spread to other parts of South and North America and the Caribbean.⁴ It also reached several Pacific islands and Singapore by mid-2016.⁵ The World Health Organization declared it a Public Health Emergency of International Concern in February 2016.⁶ Confirmed cases were reported in 40 countries and territories in America and the Caribbean, as well as 16 in the western Pacific and one in Africa, in 2015 and 2016.⁷

ZIKV belongs to the virus family Flaviviridae and the genus Flavivirus, which also contains West Nile virus, Dengue virus, Yellow fever virus, and Japanese encephalitis virus.⁸ Zika virus disease (ZVD) also causes an illness that resembles a mild form of dengue fever.⁹ Currently, there is no medication or vaccine that can prevent the ZIKV infection. ZIKV is mainly spread by the Aedes aegypti and Aedes albopictus mosquitoes, which are common throughout tropical and sub-tropical regions of the world.¹⁰ Previous publications have highlighted a complex set of human and environmental factors that determine the spatial distribution of this disease.¹¹ Additionally, researchers found that travel from ZIKV affected areas and socio-economic conditions in countries facing potential abundant mosquito populations may play important roles in the ZIKV transmission.¹² Finally, researchers believe that high-risk factors for transmission exist along the borders of affected countries.¹³

However, the various risk factors that affected the progress of the ZIKV outbreaks remain unidentified.^{14,15} We, therefore, collected data from 50 countries with evidence of local mosquito-borne ZIKV infections, and 80 countries without ZIKV infection reports, to investigate potential explanatory variables. We considered ecological, environmental, meteorological and social-economical niche factors. These included precipitation, vapor pressure, population density, the number of travelers, temperature, health expenditure per capita, Gross Domestic Product per capita, water coverage and ZIKV transmission in nearby countries. Because the ZIKV-related mosquitoes often carried other viruses, we also extracted occurrence data for these mosquito species and Dengue virus (DENV), West Nile virus (WNV), Yellow Fever virus (YFV) and Chikungunya virus (CHIKV). We used a Gradient Boosted Regression Tree (GBRT) model to evaluate the effect of these factors on the probability of ZIKV transmission and to estimate risk levels for ZVD outbreaks, at the country level, in Asia and two countries in Oceania between October 2016 and January 2017. Our approach estimates the relative influence of these potential risk factors and their importance for surveillance systems that attempt to provide early warning of outbreaks and inform decision-making in countries within the Asia-Pacific region.

Materials and methods

Data collection

The countries with locally acquired mosquito-borne ZIKV infections, and the number of confirmed cases during the 2015-2016 outbreaks, were obtained from the World Health Organization (WHO)'s latest Zika situation report (http://www.who.int/emergencies/zika-virus/situationreport/8-september-2016/en/) and the Pan America Health (http://www.paho.org/hq/index.php? Organization option = com_content&view = article&id = 11599&Itemid = 41691&lang=en). The distribution of confirmed cases was linked to a global geographic map to plot the thematic figure using GIS technologies. The map was created in Arc-GIS 9.3 software (ESRI Inc., Redlands, CA, USA) (http:// www.esri.com/). We collected data from 50 countries with evidence of local mosquito-borne ZIKV infections and 80 countries without ZIKV infection reports. The data concerning ecological, environmental, meteorological and social-economical niche factors, in addition to various factors concerning phylogenetic relatedness to ZIKV, were included in the mathematical model used in this study.

Among these data, the ecological niche data of monthly temperature, vapor pressure and precipitation were from the dataset of CRU-3.23 (http://iridl.ldeo.columbia.edu/ SOURCES/.UEA/.CRU/.TS3p23/) and the water coverage and population density were extracted from the World Factbook (https://www.cja.gov/library/publications/theworld-factbook/). We further examined the borders of the countries in this database to identify neighboring countries to those affected by ZIKV (a value of 1 indicated a country that neighbored a ZIKV affected country, and 0 meant it had no such neighbor). GDP, health expenditure per capita and the annual number of travelers for each country were downloaded from the World Bank dataset (http://data.worldbank.org/). The occurrence data for mosquitoes, Dengue virus, Chikungunya virus, Yellow Fever virus and West Nile virus was obtained from a previous publication,^{16,17} WHO's report (http://www.who.int/csr/don/ archive/disease/yellow_fever/en/) and the CDC (http:// www.cdc.gov/westnile/statsmaps/). The detailed list of the factors with their descriptions was given in Table 1 and Table S2. The data was split into a learning set (40 ZIKV affected countries and 70 none ZIKV countries) and a prediction set (10 ZIKV affected countries and 10 none ZIKV countries) for the prediction model.

Model summary

A Gradient Boosting Regression Tree (GBRT) model was built on the learning dataset at the country level in this study to Download English Version:

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